Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession accession number.
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein. If you encounter an accession number from an older search run against UniProt (results file Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or numbers.

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Sequence 101, App
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1 GLDTVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251
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/ cgn2_6/ptodata/1./iaa/6A_COMB.pep:*
/ cgn2_6/ptodata/1./iaa/BECOMB.pep:*
/ cgn2_6/ptodata/1./iaa/PCTUS_COMB.pep:*
/ cgn2_6/ptodata/1./iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-425-334-99
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US-08-445-99
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US-08-4477-4848-99
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US-08-646-360-99
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Maximum Match 1008
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Maximum DB seq length: 251
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Sequence 110, App Sequence 2, Appli Sequence 10 App Sequence 110, App Sequence 247, App Sequence 2, Appli		Ribsome-Inactivating rray & Borun Drive
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		T 1 -425-336-101 enece 101, Appligation US ener No. 5621083. NERAL INFORMATION: APPLICANT: Better, Marc APPLICANT: Better, Marc APPLICANT: Better, Marc APPLICANT: Studnika, Gar TITLE OF INVENTION: Drow NUMBER OF SEQUENCES: 140 CORRESPONDENCE ADDRESS: ADDRESSEE: Marshall, O STREET: 6300 Sears Tow STREET: 6300 Sears Tow STREET: 60606-6402 COMPUTER: Illinois COMPUTER: EADABLE FORM: MEDIUM TYPE: Floppy di COMPUTER: EADABLE FORM: MEDIUM TYPE: PC-PRY MEDIUM TYPE: PLOPPY SOFTWARE: PAPPLICATION DATA: APPLICATION NUMBER: US FILING DATE: 19-10N-19 APPLICATION NUMBER: TELEFORMUMICATION INFORMA THE
66699999999999999999999999999999999999		RESULT 1 US-08-425-336-101 Sequence 101, Applipé Patent No. 5621083; Batent No. 5621083; Batent No. 5621083; BAPLICANT: Better APPLICANT: Better APPLICANT: Studni TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: MATE STREET: 6300 Se COUNTRY: Chicago STATE: 1111nois COUNTRY: USA ZIP: 60606-6402 COMPUTER READABLE MEDIUM TYPE: F1 COMPUTER: F2 COMPUTER: PATE SOFTWARE: PATE COMPUTER: BATE COMPU
00000000000000000000000000000000000000		APP

TELEPAX: 312/474-0446
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 101: SEQUENCE CHARACTERISTICS: LENGTH: 251 amino acids: TYPE: amino acid: TOPOLOGY: linear: MOLECULE TYPE: protein US-08-425-336-101

100, App 99, Appl

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Sequence Sequence Sequence

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US-08-425-336-110 US-08-488-113B-2

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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carcoll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating VUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       Length 251;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-20N-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: US 08/064,691
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STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
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                                          TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
312/707-8889
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Best Local Similarity 100.
Matches 251; Conservative
                           312/707-9155
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MOLECULE TYPE: protein
US-08-488-113B-101
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                         TELEFAX:
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US-08-488-113B-101

| Sequence 101, Application US/08488113B
| Patent No. 5744580.
| Patent No. 5744580.
| Patent No. 5744580.
| APPLICANT: Better, Marc D.
| APPLICANT: Studnika, Gary M.
| TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
| TITLE OF INVENTION: Proteins
| TITLE OF INVENTION: About Note of Street, 34th floor
| STATE: Illinois
                                                                                                                                                    1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                      100.0%; Score 1277; DB 1; Length 251; 100.0%; Pred. No. 6.8e-119; tive 0; Mismatches 0; Indels 0
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COMPUTER KEALABLE FURDER

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,1138

FILING DATE: 07-MN-1995

CLASSIPICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430

FILING DATE: 19-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567

FILING DATE: 39-JUN-1991

ATTORNEY/ASCAT INFORMATION:
NAME: MCNICADIAS, Janet M.
REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A

TELECOMMUNICATION INFORMATION:
                                                                        Matches 251; Conservative
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MEDIUM TYPE: Floppy
                                                  Best Local Similarity
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFPKDAPDAAYEGLFKOYIKTRLHFGGSYPSLEGEK 120
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proceins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDREWS, Held & Malloy, Ltd.
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APPLICATION NUMBER: US 07/901,707
PILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: MCANICATION:
NAME: MCANICATION NUMBER: 32,918
REFERENCE POCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-8889
TELEPHONE: 12/707-8889
TELEPHONE: 12/707-8889
TELEPHONE: 12/707-8889
TELEPHONE: 312/707-8155
TELEPHONE: 312/707-8155
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-8155
TELEPHONE: 312/707-8
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COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; DB 1;
6.8e-119;
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500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1277;
Pred. No. 6.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101, Application US/08646360 Patent No. 5837491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Sc
Best Local Similarity 100.0%; P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ALLKFVDKDPK 251
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CITY: Chicago
STATE: Illinois
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US-08-646-360-101
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181 POORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Batent No. 6146631

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carcoll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proceins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANGTEWS, Held & Malloy, Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1277; DB 2; Best Local Similarity 100.0%; Pred. No. 6.8e-119; Matches 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor CITY: Chicago
                             APPLICATION NUMBER: PCITUS94/U5348
FILING DATE: 12-WAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-WAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-WOY-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAB: Janet M.
REGISTRATION NUMBER: 32,919
                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                    PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ALLKFVDKDPK 251
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PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GLDTVSFSTKGATYITTVVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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      TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS: ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor STREET: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1277; DB 3; Length 251; Best Local Similarity 100.0%; Pred. No. 6.8e-119; Matches 251; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 09-DEC-1992
FRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/87,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 200-70.P4
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-136-389-101
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11022US09/200-70.P3.C3
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                 CLASSIFICATION DATA:

APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MONICATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
TELEPHONE: 312/707-9889
TELEPHONE: 312/707-8899
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MOLECULE TYPE: protein
US-08-839-765-101
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US-09-136-389-101
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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI

181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI

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Sequence 101, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.

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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSBAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                              61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                        121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101, Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Garcil, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: .
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
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INFORMATION FOR SEQ ID NO: 101:
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STATE: Illinois
COUNTRY: USA
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APPLICANT: Carroll, Stephen F.

APPLICANT: Studmika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173.

ADDRESSEE: MCANDERSE: Hold & Malloy, Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRION APPLICATION DATA:

APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-AMY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-AMY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 10-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INPORMATION:
NAME: MCNISCHOLAS, JANCTO, PA
                                                                                                                                                  Sequence 101, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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TOPOLOGY: ):-
  241 ALLKFVDKDPK 251
                                        241 ALLKFVDKDPK 251
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: USA
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SEQUENCE CHARACTERISTICS LENGTH: 251 amino aci
                                GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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SEQUENCE CHARACTERISTICS
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STATE: Illinois
COUNTRY: USA
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                      LENGTH:
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                                                                                                                                                                     1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                             Gaps
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
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                                                                                 Query Match 100.0%; Score 1277; DB 4; Length 251; Best Local Similarity 100.0%; Pred. No. 6.8e-119; Matches 251; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chloago STATE: Illinois COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-AMY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATPONDEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 99, Application US/08425336 Patent No. 5621083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Thomas C. REGISTRATION NUMBER: P-36,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALLKFVDKDPK 251
                 MOLECULE TYPE: protein
TOPOLOGY: linear
  ; TOPOLOGY:
; MOLECULE TYPE
US-09-711-485-101
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US-08-425-336-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Patent No. 5621083
GENERAL INFORMATION
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDERSE:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                     Length 251;
                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                  Score 1273; DB 1;
Pred. No. 1.7e-118;
0; Mismatches 1;
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APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIPICATION 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US/07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US/07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-36,989
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                                                                                                                                                  Query Match
Best Local Similarity 99.6%;
Matches 250; Conservative
: 251 amino acids
amino acid
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                                         TOPOLOGY: linear
MOLECULE TYPE: protein
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRRKKADDPGKCFVLVALSNDN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS: 169
CORRESPONDENCE ADDRESS: ADDRESSE: MCANdrews, Held & Malloy, Ltd.
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                                                                                                                                                                                                                                                                                                                                                               Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: US-JUN-1995
RIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: US/08/48,1136
FILING DATE: 18-APR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION
                                                                                                                                                                                                                                                                                                                                                           Score 1273; DB 1;
Pred. No. 1.7e-118;
0; Mismatches 1;
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500 West Madison Street, 34th floor
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APPLICATION NUMBER: US 07/901,707
TELEFAX: 312/474-0448
TELEX: 25-3856
INPORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                        Query Match 99.7%;
Best Local Similarity 99.6%;
Matches 250; Conservative
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                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-425-336-100
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-08-488-113B-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
TUTLE OF INVENTION: Proteins
TUTLE OF SEQUENCES: 169
CORRESPONDENCE ADDRESS: 169
ADDRESSEE: MCANDRESS: Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.7%; Score 1273; DB 1; Length 251; 99.6%; Pred. No. 1.7e-118; tive 0; Mismatches 1; Indels (
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY PARTY INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 100, Application US/08488113B
Patent No. 5744580
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.6
Matches 250; Conservative
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us-10-717-243-101.closed.rai

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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPK1 240
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Releat No. 5786699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
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500 West Madison Street, 34th floor
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCMICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 312/707-9155
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Matches 250; Conservative
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: Illinois
FY: USA
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STREET: 50
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US-08-477-484B-99
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STATE: I
COUNTRY:
ZIP: 606
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61 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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COMPUTER: PLODS/MS.DOS

COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CONFIGNARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-UJN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,4691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,430
FILING DATE: 19-UJN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UJN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCANISCHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
RESERRICATION NUMBER: 32,918
REGISTRATION NUMBER: 312/707-9155
TELLEPAN: 312/707-9155
TELLEPAN: 312/707-9155
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Patent No. 5756599
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen P.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 650 388-1248
INPORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
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mino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GQLAEIAIDVISVYVVGYQVRNRSYPFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKKADDPGKAFVLVALSNDN
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       Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DATE Floppy disk
COMPUTER: DATE FORM:
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-UN-1995
CLASSIFICATION NUMBER: US 08/425,336
FILING DATE: 12-MAY-1995
FILING DATE: 12-MAY-1993
RAPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
RAPLICATION NUMBER: US 07/989,430
FILING DATE: 12-MAY-1993
RAPLICATION NUMBER: US 07/989,430
FILING DATE: 19-UN-1992
RAPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
RAPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: MCANICADIAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA
TELECOMMUNICATION NUMBER: 1102ZUS07/200-70.P3.CZA
TELECOMMUNICATION NUMBER: 1102ZUS07/200-70.P3.CZA
TELECOMMUNICATION NUMBER: 100.P3.CZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1273; DB 1;
Pred. No. 1.7e-118;
0; Mismatches 1;
                                                                                                    E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Imm
TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDERSWS,
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Best Local Similarity
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STREET: DAL
TTY: Chicago
                                                                                                                                                      CITY: Chi
STATE: Il
COUNTRY:
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Sequence 99, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Carroll, Stephen F.
APPLICANT: Studika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating VITLE OF INVENTION: Proceins NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDELES:
ADDRESSEE: MCANDELES:
ADDRESSEE: MCANDELES:
ADDRESSEE: MCANDELES:
ADDRESSEE: MCANDELES:
ADDRESSEE: MCANDELES:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOCTAME: Patentin Release #1.0, Version #1.25
SOCTAMEN: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: US 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: US 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: US 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: US 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NUMBE: MONICAN WINDER:
NUMBER: WONLOCHORN NUMBER:
NUMBER:
NUMBER: WONLOCHORN NUMBER:
NUMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,91
REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-646-360-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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²⁴¹ ALLKFVDKDPK 251 ||||||||||| 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 09:49:13 Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein
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protein
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Run on:

June 20, 2005, 09:34:33 ; Search time 25 Seconds (without alignments) 966.016 Million cell updates/sec

1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251 US-10-717-243-101 1277 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

130334 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 251

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rRNA N-glycosidase	abrin (clone 7.2)	karasurin - Mongol		· luffin-b - smooth	rRNA N-glycosidase	rRNA N-glycosidase	abrin (clone 3.7)	unknown protein, 6	tRNA pseudouridine	pseudouridylate sy	carbonyl reductase	conserved hypothet	hypothetical prote	hypothetical prote			hypothetical prote	2	hypothetical prote		hypothetical prote		hypothetical prote	ino	polyhedrin - Antic	hypothetical prote	precorrin-6Y methy	hypothetical prote
SUMMARIES	ID	JC4840	C39761	JU0393	JC5032	JN0108	S17574	S17932	B39761	D96702	B95186	B98053	A28053	B70247	F72769	S26074	T47996	B82472	F82403	AB3024	AE1826	E96957	D86753	G86681	AE1143	C90415	JQ1607	G70452	A64490	A90523
	DB	7	~	~	N	~	N	~	~	N	N	~	Н	~	~	~	7	~	~	7	~	~	~	~	7	~		N	N	N
	Length	245	251	247	247	250	40	236	106	220	249	249	244	245	246	202	249	220	169	204	222	234	139	139	221	242	245	246	211	223
de	Query	27.7	25.8	24.8	•	21.5	15.3	11.7	9.5	6.4	6.2	6.1	5.9	٠	5.8	5.7	5.7	5.7	5.6	•	5.6	5.6	•	5.6	٠	•	•	5.5	5.4	5.4
	Score	353.5	330	317	312	274	195	149	121	82	79.5	78.5	75.5	74	73.5	73	\sim	72.5	71.5	71.5	71.5	71.5	71	. 71	71	7.1	71	70.5	69.5	69.5
	Result No.	-	7	m	4	ហ	9	7	80	6	10	11	12	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29

179 NNFQORIRPANNTISLENKWGKLSFQIRTSG--ANGMFSEAVELERANGKKYYV--TAVD 234

8 6 8 6

hypothetical prote flavodoxin homolog	rie pyrophosphokin rfaY protein - Esc thiamin-phosphate hypotherical prote	beta-crystallin Bl hypothetical prote	noustinctural pro- dTDP-4-dehydrorham hypothetical prote partial transposas	conserved hypothet hypothetical prote glucose-inhibited gtp-binding protei
AG2275 AE1714	A84006 S47846 A82814 T33345	CYCHB1 C84994	MILY 23 D97187 T16560 C90330	AI1682 C75011 S77879 AH3543
000	1000	- 22	1000	0000
112	232 234 194	238	122 185 205 211	181 191 231 241
7. U. I.		44.		
000	11 0 0 0 0 0 0 0 0 0 0 0 0 0	68.5	8 8 8 8	67.5 67.5 67.5
310	 	37	8 4 4 0 0 0 1	4 4 4 4 0 6 4 0

ALIGNMENTS

 1 1.11.71.71	
 JC4840	
 rRNA N-glycosidase (EC 3.2.2.22) trichoanguina	na - snake gourd
C;Species: Trichosanthes anguina (snake gourd)	- F
 C;Date: 15-Aug-1996 #sequence revision 24-Oct-1997 #text_change 05-Dec-1997	:-1997 #text_change 05-Dec-1997
D. Chockession: UC4040; UIO/UI; UIOO//	2 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
 Ajomed, Sci. 3, 178-186, 1996	i dello, I.; Isagica, A.
 A; Title: Amino acid of sequence of trichoangu	A. Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from 7
A; Reference number: JC4840	
A;Accession octobro	
 A;Residues: 1-132,'S',134-245 <cho1></cho1>	
 A; Experimental source: seed	
 A; Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table	it with the sequence data presented in Table
 R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.;	Tsugita, A.
1. Description to Oistly, August 1979 1	namina a ribosomal inactuating protein from
A; Description: Amilio acid sequence of critical	miguina, a tiposomai-tinacevacing process trom
A:Accession: JT0701	
A:Molecule type: protein	
A;Residues: 1-50,'L',52-245 <cho2></cho2>	
C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology	cosidase homology
C; Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed	lase; phosphoprotein; seed
 F;4-242/Domain: rRNA N-glycosidase homology <	<rng></rng>
 F;51,201/Binding site: carbohydrate (Asn) (co	<pre>yvalent) #status experimental</pre>
 f;/0,136,101/ACLIVE BICE: 171, GIU, AIG #Scalus predicted F;155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted	lus predicted :) (by casein kinase II) #status predicted
 Query Match 27.7%; Score 353.5	5; DB 2; Length 245;
Matches 91; Conservative 44; Mismatches 95; Indels 21; Gaps	nes 95; Indels 21; Gaps 7;
QY 5 VSFSTKGATYITYVNFLNBLRVKLKPEGNSH	HGIPLLRKKADDPGKAFVLVALSNDNGQLA 64
	וכן אממט סינסטטטטטט נפוא דוואנים דסמע
.	
Db 61 TVAVDVTNVYIVAYRADAVSYFFEDTPAEAF	61 TVAVDVINVYIVAYRADAVSYFFEDTPAEAFKLIFAGTKTVKLPYSGNYDKLQSVVGKQ- 119
Qy 122 YRETTDLGIEPLRIGIKKLDENALDNYK	KPTEJĄSSĻĻŲVIÇMVSEĄĄRFTFIĘNŲIR 178
 DD 120 -KDWIELGIPALSSAIINMVIID	JI OSTAAALLIVIL QSTABAARIKITEQQVS I / U

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F;4-243/Domain: rRNA N-glycosidase homology <RNG>
C; Keywords: abortifacient
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(Species: Trichosanthes Kirilowii (Mongolian snake-gourd)
(Species: Trichosanthes Kirilowii (Mongolian snake-gourd)
(Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
(Spacession: JU0393; PS0163
(R)TOYOKawa, S.; Takeda, T.; Katel, Y.; Wakabayashi, K.; Ogihara, Y.
(Chem. Pharm. Bull. 39, 1244-1249, 1991
A)Title: The complete amino acid sequence of an abortifacient protein, karasurin.
                                                                                                                                                   abrin (clone 7.2) precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Abrus precarcorius (Indian licorice)
C;Accession: C39761; 514471
R;Evensen, G.; Mathiesen, A.; Sundan, A.
B;Evensen, G.; Mathiesen, A.; Sundan, A.
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
A;Accession: C39761
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A; Molecule type: DNA
A; Molecule type: DNA
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A; Molecule type: DNA
A; Cross-references: Mole; Molecule type: DNA: A; Cross-references: Molecule type: DNA: Cross-references: D
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A;Residues: 1-247 <TOX>
A;Cross-references: UNIPROT:P24478
A;Note: a sequence which lacks Ala-247 is also shown in this publication
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-251 <EVE>
A;Cross-references: UNIPROT:Q38760
A;Cross-references: UNIPROT:Q38760
B;Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Reference number: S14471
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Agreedes: Trichosanthes kirilowii var. Japonica
C;Species: Trichosanthes kirilowii var. Japonica
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Rocession: JCSO32
A;Ritle: Amino acid sequences and ribosome-inactivating activities of karasurin-B and kan
A;Reference number: JCSO32; MUID:97108848; PMID:8951169
A;Recession: JCSO32
A;Retus: preliminary
A;Molecule type: protein
A;Residues: 1-247 <KON>
A;Cross-references: UNIPROT:041216; UNIPROT:094KE4; UNIPROT:08LPV7
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic
C;Superfamily: FRNA N-glycosidase; RRNA N-glycosidase homology <RNG>
F;4-243/Domain: FRNA N-glycosidase homology <RNG>
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37.8%; Pred. No. 2.9e-18;
tive 34; Mismatches 105; Indels 14; Gaps
                                                                                                                                                                                               14;
                                       24.8%; Score J., 38.2%; Pred. No. 1.1e-18; State 33; Mismatches 105; Indels ive 33; Mismatches 105; Indels state 33; Mismatches 33; 
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Local Similarity 37.8%
tes 93; Conservative
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Query Match
Best Local Similarity 25.2%;
Warches 58; Conservative
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Best Local Similarity
Matches 36; Conserv
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Inffin-b - smooth loofah
Cispecies: Luffa cylindrica (smooth loofah)
Cjoate: O4-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
CjAccession: JN0108
Rislam, M.R.; Hirayama, H.; Funatsu, G.
Ryislam, M.R.; Chem. 55, 229-238, 1991
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from A;Reference number: JN0108; MUID:91248488; PMID:1368666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRNA N.glycosidase (EC 3.2.2.22) GAP31 - Gelonium multiflorum (fragment)
C;Species: Gelonium multiflorum
C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: 517574
R;Lee-Huang, S.; Kung, H.; Huang, P.L.; Huang, P.L.; Li, B.Q.; Huang, P.; Huang, H.I.;
FEBS Lett. 291, 139-144, 1991
A;Title: A new class of anti-HIV agents: GAP31, DAP8 30 and 32.
A;Reference number: S17574; MUID:92037998; PMID:1936243
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                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGOLA
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                           20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7 $17932 rRNA N-glycosidase (EC 3.2.2.22) Sap3 - common soapwort (fragment) N/Alternate names: saporin 3
                                                                                                                                                                                                                                                                                                                                   Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 195; DB 2; Length 40;
Pred. No. 1e-09;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-40 <LEE>
A;Cross-reences: UNIPROT:P24475
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P22851
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;5-246/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                               ; Score 274; DB 2; Length 25; Pred. No. 3.9e-15; 47; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.0%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 31.74
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 IXDVNSKLLLNK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 VDQVKPKIALLK 244
                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-250 <ISL>
                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                   A; Accession: JN0108
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C;Species: Saponaria officinalis (common soapwort)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S17932; S15458
R;Fordham-Skelton, A.P.; Taylor, P.N.; Hartley, M.R.; Croy, R.R.D.
Mol. Gen. Genet. 229, 460-466, 1991
A;Fitle: Characterisation of Saporin genes: in vitro expression and ribosome inactivation A;Reference number: S17932; MulD:92049247; FMID:1719367
A;Reference number: S17932
A;Rolecule type: DAA
A;Residues: 1-236 <FOR>
A;Residues: 1-236 <FOR>
A;Coss-references: UNIPROT:P27560; EMBL:X59256; NID:g21322; PIDN:CAA41949.1; PID:g21323
A;Note: the authors translated the codon CTC for residue 75 as Phe and GCA for residue 1;C;Superfamily: TRNA N-glycosidase; nRNA N-glycosidase homology
C;Superfamily: TRNA N-glycosidase homology (fragment) <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 ANQKALEYTEDYQSIEKONAKIT------EGDKT-RKELGLGINLLSTLMDAVNKK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 EIASSLLVVIQMVSEAARFTFIENQIRNNFQ--QRIRPANNTISLENKWGKLSFQIRTSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CjDate: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 05-Jun-1998 C;Accession: B39761
R;Bronsen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chi A;Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----YEGLFKNTIKTRLHFGGSYPSLEGEKAYRETTDLGIEPLRIGIKKLDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 A--IDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQRIRPANNTISLENKWGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 EKARTLIVIIOMVSEAARFRYISNRVGVSIRTGTAFQPDPAMISLENNWDNLSGGVQOS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
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A.Molecule: type: DNA
A.Molecules: 1-106 < EVE>
A.Cross-references: GB.X54873
C.Superfamily: ricin; rRNA N-glycosidase homology
C.Superfamily: ricin; rRNA N-glycosidase, hydrolase; lectin; toxin
F.1-106/Product: abrin chain A (fragment) #status predicted <ACH>F:1-101/Domain: rRNA N-glycosidase homology (fragment) < RNG>
F:19,22/Active site: Glu, Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKP-KIALLKFVDKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 149; DB 2; Length 23
25.2%; Pred. No. 6.6e-05;
tive 39; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 FVLVALSNDNGQLAEIAIDVTSVYVVGYQVR----NRSYFFKD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 ANGMFSEAVELERANGKKYYVTAVDQ-VKPKIALLKFVDKDP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 VQGTFPHPVTLRNICNEPVIVDSLSHPTVAVLALMLFVCNPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    abrin (clone 3.7) precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 121; DB 2; 35.3%; Pred. No. 0.0044; ative 16; Mismatches 4.
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σ RESULT D96702 9

Gaps

171

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A;Cross-references: UNIPROT:Q8CWQ1; GB:AE007317; PIDN:AAL00255.1; PID:g15459107; GSPDB:GR-C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Streptococcus pneumoniae
Cibate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
Cibate: Balta, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M.
Y. Pr.; Sun, Winkler, M.E.
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A.Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A.Reference number: A97872; MuID:21429245; PMID:11544234
A.Reference number: A97872; MuID:21429245; PMID:11544234
A.Resiques: 1-249 <KUR>
A.Residues: 1-249 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pseudouridylate synthase (EC 4.2.1.70) [imported] - Streptococcus pneumoniae (Btrain R6)
                                                                                                                                                                                                                                                                                         189 FSGNGFLYKQIRNMVGTLLKIGNNRMPVEQIDLILEKKORQLAGP--TAAPNGLYLKEIR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAA------RFT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIEN----QIRNNFQQRIRPANN-----TISLENKWGKLSFQIRTSGANGMFSEAVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 PSGNGFLYKQIRNMVGTLLKIGNNRMPVEQIDLILEKKDRQLAGP--TAAPNGLYLKEIR 246
                                                                                                                  69 IDVTSVYVVG-----YQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKA 121
                                                                                                                                                                                                                                                                                                                                                                                    172 FIEN-----QIRNNFQQRIRPANN-----TISLENKWGKLSFQIRTSGANGMFSEAVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 IDVTSVYVVG-----YQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carbonyl reductase (NADPH2) (EC 1.1.1.184) - mouse
NiAlternate names: adipocyte p27 protein
C.Species: Mus musculus (house mouse)
C.Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: 503382; 869141; 869142; A28053
S.R.Nave, M.; Ringold, G.M.
J. Cell Biol. 107, 279-286, 1988
                                                                                                                                                                                                                                                      122 YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAA-----RFT
                                                    49;
                                                                                                                                                                                 88 ibvisielvaddfhcryakhsktyer----tvdrgrpknpm--rrhyathfp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 IDVISIELVADDFHCRYAKHSKTYEF----IVDRGRPKNPM--RRHYATHFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 249;
                                                    60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.7%; Pred. w. tive 28; Mismatches
                 Similarity 24.7%; Pred. No. 36; 45; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 78.5;
4.7%; Pred. No. 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: tRNA-pseudouridine synthase I
C;Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45; Conservative
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Best Local Similarity
Matches 45; Conserv
             Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 YE 248
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unknown protein, 64612-65506 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D96702
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J., Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzaberg, S.L.; Schwartz, J.R.; Suthmis, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wishin, P.; Southwick, A.W.; Sun, H.; Tallon, A;Reference number: AB6141; MUID:21016719; PMID:11130712
A;Etus: preliminary
A;Accession: D96702
A;Etus: preliminary
A;Accession: D96702
A;Ender type: DNA
A;Reference L-200, SETO.
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A,Experimental source: strain TIGR4
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9C9W1; GB:AE005173; NID:g6553900; PIDN:AAF16566.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | | : | | | 62 -NGFSVKKAEDVVNIMVGRGYALGKDAMEKAKAFDDR-----HNLISNASAT-----1 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSLEGEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 ASLDDKMGLSEKLSIGTTVVNEKLRDIDE----RYQVREITKSALAAABETAISARTALM 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
Accession: B95186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 DNGQLAEIAIDVTSV----YVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 ITYVNF--------LNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
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20.8%; Pred. No. 19;
iive 34; Mismatches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 20.8 nes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 TAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :| ||:
T-LDPSSPKV 211
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A; Residues: 1-249 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-220 <STO>
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A,Map position: 1
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C;Accession: F72769
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku DNA Res. 6, 83-101, 1999
A;Tille: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Cross-references: UNIPROT:Q9YFV5; DDBJ;AP000058; NID:g5103388; PIDN:BAA79056.1; PID:d1(
;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Methanobacterium thermoformicicum plasmid pF21
C.Species: Methanobacterium thermoformicicum
C.Species: Methanobacterium thermoformicicum
C.Species: Methanobacterium thermoformicicum
C.Species: Mov-1993 #sequence revision 17-Apr-1998 #text_change 09-Jul-2004
C.Accession: S26074; S30322; S23894; S26456
R.Noelling, J.; de Vos, W.M.
Nucleic Acids Res. 20, 5047-5052, 1992
A.Title: Identification of the CTAG-recognizing restriction-modification systems MthZI ar A;Reference number: S26073; MUID:93027239; PMID:1408820
       A,Genome: plasmid
C,Superfamily: Lyme disease spirochete plasmid probable stage 0 sporulation protein
                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                        175 -----NISI-----VVNQFIKWR-ILKEVEDALYK-RYSNYIKGKIHYYNSIKVPI 219
                                                                                                                                                                                                                                                                                                                 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 IAIDVTSVY-VVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAYRE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ENAIDNY-KPTEIASS 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105 IVENMKRQLTEEIKKLKIKAEEAKTRIKERIAEIDDEMLHIAGATANLQMLYFSGEISDR 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C.Accession: F72769
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                                                                                                                                                                                                                                                                                        58 NDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSY----
                                                                                                                                                                             42; Gaps
                                                                                                      / Match 5.8%; Score 74; DB 2; Length 245; Local Similarity 26.4%; Pred. No. 99; neg 37; Conservative 23; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Aeropyrum pernix hypothetical protein APE0145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein APE0145 - Aeropyrum pernix (strain Kl)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.8%; Score 73.5; DB 2;
21.0%; Pred. No. 1.1e+02;
tive 39; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 SYTSGMNHLRKLNDSLEREKSDAKR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 ----PSLEGEKAYRETTDL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 INRLEPDIK-SKYYKEAKDV 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 21.0
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A;Status: preliminary
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                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Pescription: catalyzes the reduction of various carbonyl compounds to corresponding all A; Pathway: involved in pulmonary metabolism of endogenous carbonyl compounds and xenobic A; Note: member of short-chain alcohol dehydrogenase family
C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C; Keywords: mitochondrion, NADP; oxidoreductase
C; Keywords: mitochondrion, NADP; oxidoreductase
F; 1-244/Product: carbonyl reductase (NADPH) #status experimental <MAT>
F; 8-180/Domain: short-chain alcohol dehydrogenase homology <SADH>
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Experimental source: strain B31
Genetics:
Title: A growth factor-repressible gene associated with protein kinase C-mediated inhi-
Reference number: S03382; MUID:88273310; PMID:2455724
Accession: S03382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
                                                                                                                            A; Residues: 1-244 <NAV>
A; Residues: 1-244 <NAV>
A; Cross-references: UNIPROT: P08074; EMBL: X07411; NID: 950003; PIDN: CAA30309.1; PID: 950004
A; Cross-references: UNIPROT: P08074; EMBL: X07411; NID: 950003; PIDN: CAA30309.1; PID: 950004
A; Experimental source: strain C3H
B; Nakanishi, M.; Deyashiki, Y; Ohshima, K.; Hara, A.
Bur. J. Biochem. 228, 381-387, 1995
A; Title: Cloning, expression and tissue distribution of mouse tetrameric carbonyl reduct
A; Reference number: 869141; MUID: 95220366; PMID: 7705352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 ALGGIGPVDLLVNNAALVIMOPFLEVTKEAFDRSFSVNLRSVFOVSOMVARDMINRGVPG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLEN------KWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKIALL- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fitle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi. Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGKGIGRDŤVKA-LHASGA----KVVAVTRTNSDĽVSLAKECPGIEPVCVDLGDWDATEK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein BBJ17 - Lyme disease spirochete plasmid J/1p38
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;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-244 «NAK»
A;Cross-references: EMBL:D26123; NID:g440371; PIDN:BAA05120.1; PID:g699608
A;Experimental source: lung; strain CD-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: protein
Residues: 1-29,40-80,84-96,110-198,209-223,227-244 <NAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%; Score 75.5; Di
24.2%; Pred. No. 74;
tive 32; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Complex: homotetramer
C;Function:
A;Description: catalyzes
A;Pathway: involved in pu
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Complex: homotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues: 1-245 <KLE>
                                                                                                          A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                Accession: S69141
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8 셤 ò 셤 ò 요 ò 셤

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A; Molecule type: DNA
A; Residues: 11-202 - NODS-
A; Cross-references: UNIPROT: P29566; EMBL: X67212; NID: g44658; PIDN: CAA47652.1; PID: g80972
A; Cross-references: UNIPROT: P29566; EMBL: X67212; NID: g44658; PIDN: CAA47652.1; PID: g80972
A; Cross-references: UNIPROT: P29566; EMBL: X67212; NID: g44658; PIDN: CAA47652.1; PID: g80972
A; Noce: the nucleotide sequence was submitted to the EMBL Data Library, July 1,992
R; Noce: the nucleotide sequence was submitted to the EMBL onto the EMBL of the EMBL: A; Reference number: S30302; MUID: 93126090; PMID: 1336177
A; Reference number: S30302; MUID: 93126090; PMID: 1336177
A; Reference number: S30302; MUID: 93126090; PMID: 1336177
A; Reference number: S30302
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-202 - NOWA
A; Residues: 1-203 - NOWA
A; Residues: 1-203 - NOWA
A; Residues: 1-203 - NOWA
A; Residues: 1-204 - NOWA
A; Residues: 1-205 - N
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A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.7%; Score 73; DB 2; Length 202; Best Local Similarity 23.6%; Pred. No. 93; Matches 37; Conservative 32; Mismatches 56; Indels
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51 ---QMSDLIHECPDKSYEGWKKWYLE---HYSDRI-----EKATKKISKM-IENWKAAAME 98

8 6 8

Search completed: June 20, 2005, 09:48:08 Job time : 26 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 20, 2005, 09:22:52; Search time 111.5 Seconds (without alignments) 1152.752 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-717-243-101 1277 1 GLDTVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

827211 Total number of hits satisfying chosen parameters: 1612378 seqs, 512079187 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 251

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Q7DM12	Q6BBQ4	Q9LRE3	Q96236	Q8RXH7	096237	QBLKQS	Q8LKQ4	Q96235	Q8RY69	Q7Y1U7	Q7Y1U5	Q6J3N3	Q6J3N4	Q9ATB3	RIPB_LUFCY	Q6J3N2	Q7SIF0	RIP3 GELMU	07Y1 <u>0</u> 6	Q8SAD7	Q84LI9	Q84LJ0	Q8S2R5	Q84LI8	Q8SAG0	048859	RIP3 SAPOF	Q9S8 <u>P</u> 3	062425	O6Z4E3
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Q9K3E8	Q81FY4	633XL9	Q7P521	Q6MRY4	Q7Y1U4	RS4 FUSNN	Q63 <u>D</u> v2	Q81T42	Q6HLC7	Q9C9W1	QBRMD6	SSB MYCPE	Q7RSS9
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ALIGNMENTS

RESULT 1 OTDM12 PRELIMINARY; PRT; 251 AA. D CODM12 D CODM12 D CODM12 D CODM12 D CS-UUL-2004 (TREMBLrel. 27, Last sequence update) D CS-UUL-2004 (TREMBLrel. 27, Last annotation update) D CS-UUL-2004 (TREMBLrel. 27, Last annotation update) D CS-UUL-2004 (TREMBLrel. 27, Last annotation update) D C Edwaryort, Viridiplantes, Strepophyta, Embryophyta C Edwaryort, Windiplantes, Strepophyta, Embryophyta C Spermatophyta; Magnollophyta; endicotyledons; core of eurosids I; Fabales; Fabaceae; Papilionoideae; Abrean (TaxID-3816; RN	PRELIMINARY; PRT; 251 AA. 970M12 970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTL--PGSQRYALIHLTNYADET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPG-KAFVLVALSNDNGQL
                                                                                                                                                                  Trichosanthes sp. Bac Kan 8-98.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.

NCBI_TaxID=118182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINȚS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.8%; Score 317; DB 2; Length 24. 38.2%; Pred. No. 1.1e-17; ive 33; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AA; 27199 MW; 89811AC32892F03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Abrin A chain (E164A) (Fragment).
Name=pcONRAC-1-E164A;
Abrus precatorius (Indian licorice) (Crab's eye).
                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AA
247 AA
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PRT;
                                                (TrEMBLrel. 15, C
(TrEMBLrel. 15, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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PRELIMINARY;
                                                01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Trichobakin (Fragment).
Name-TBK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00161; RIP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 SNIALL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 PKIALL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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SEQUENCE
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                            Q9LRE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IRENIPLGLPALDSAI-----TTLFYYNANSAASALMVLIQSTSEAARYKFIEQQIGKRA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AHQSRQQIPLGLQALTHGISFFRSGGNDN---EEKARTLIVIIQMVAEAARFRYISNRVR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQRIRPANNTISLENKWGKLSFQIR-TSGANGMFSEAVELERANGKKYYVTAVDQ--VKP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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MIS.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;

"Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";

"Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";

Submitted (UNN-2004) to the EMBL/GenBank/DDBJ datubases.

-I CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-I SIMILARITY: Belongs to the ribosome-inactivating protein family.

EMBL; AY668811; AAT91090.1; -.

GO, GO:0030789; F:RRNA N-glycosylase activity; IEA.

GO, GO:0017148; P:RRNA N-glycosylase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VSFRLSGATSSSYGVFISNLRKALPNERRLYDIPLLRSTLQG-SQRYALIHLTNYADETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIAIDVISVYVVGYQVRNRSYFFKDA-PDAAYEGLFKNTI-KIRLHFGGSYPSLE-GEKA
                                                      179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichosanthes kirilowii (Mongolian snake-gourd).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
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PRINTS; PR00395; SHIGARICIN.
PROSITE; PS00275; SHTGA RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 247
247 AA; 27172 MW; BCBA762884F89CCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Trichosanchin (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   trichosanthin
                                                                                                                                                                                                                  TVAVLALMLFVCNPP 250
                                                                                                                                                               236 VKPKIALLKFVDKDP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
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01-FEB-1997 (TrEMBLrel. 02, Last sequence 01-OCT-2003 (TrEMBLrel. 25, Last annotatic PcDNAAc-1-E164A/R167L protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific adenosine on the 28S rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94139756; PubMed=8307038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=pcDNAAc-1-E164A/R167L;
                                                                                                                                                                                                                                                                                                         85; Conservative
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                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 AHQSRQQIPLGLQALTHGISFPRSGGNDN---EEKARTLIVIIQWVAAAARFRYISNRVR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 VSIQTGTAFQPDAAMİSLENNWDNLSRGVQES-VQDTFPNQVTLTNIRNEPVIVDSLSHP 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-----GKAFVLVALSND 59
                                                                                  TISSUE-Seed;
MEDLINE-94139756; PubMed=8107038;
Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
"Cloning and expression of three abrin A-chains and their mutants
derived by site-specific mutagenesis in Escherichia coli.";
Blur. J. Blochem. 219:38-87(1994).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
                                                                                                                                                                                                                                             GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:00016919; F:RNA N-glycosylase activity; IEA.
GO; GO:0006552; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
FINEPPRO1574; RIP.
FEMP PF00161; RIP? 1.
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                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Santalales; Santalaceae; Viscum.
                                                                                                                                                                                                                                                                                                                                                                                                                                      24.7%; Score 315; DB 2; Length 251; 35.3%; Pred. No. 1.7e-17; ive 39; Mismatches 108; Indels
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                            28040 MW; D57FCB182E0EECC9 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JCT-2003 (TrEMBLrel. 25, Last annotation update)
Lectin chain A isoform 2 (Fragment).
Viscum album (European mistletoe).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90; Conservative
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                                                          [1] -
SEQUENCE FROM N.A.
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                                             NCBI_TaxID=3816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 RETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRN--N 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 SGESFLPDMYMLELETSWGQQSTQVQQS-TDGVFNNPFRLAISTGNFVTLSNVRDVIASL 240
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Eur. J. Biochem. 219:83-87(1934).
-1- CATALYTIC ACTIVITY: Endohydrolygis of the N-glycosidic bond at one
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AY081148; AAL87005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITAAIDVTNLYVVAYQAGDQSYFLRDAPDGAERHLFTGTTRSSLPFTGSYTDLERYAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKA--FVLVALSNDNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 VTHOTTGDEYFRFITLLRDY---VSSGSFSNEIPLLRQSTIPVSDAORFVLVELTNEGGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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EMBL; X76722; CAA54140.1; -.
HSSP; P11140; 1ABR.
                                                                                                                                                                                                GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0031598; F:rRNA N-GJYCOSYJASE activity; IEA.
GO; GO:00031598; P:defense response; IEA.
GO; GO:0017148; P:negative response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
InterPro; IPRO01574; RIP.
Ffam; PF00161; RIP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.6%; Score 314.5; DB 2; Length 249; 34.6%; Pred. No. 1.8e-17; ive 41; Mismatches 109; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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Last annotation update)
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GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
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237 KPKIALLKFVDKD 249
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237 IASLAIMLFVCED 249
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Pfam; PF00161; RIP; 1
                                                                                                           249 AA;
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01-0CT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                     60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ- 235
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GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Santalaceae; Viscum.

NCBL TaxID=159976;
                    protein biosynthesis; IEA
                                                                                                                                                                                                                                        24.6%; Score 314; DB 2; Length 251; 35.3%; Pred. No. 2e-17; Antive 39; Mismatches 108; Indels 18;
             GO; GO:001148; p:negative regulation of protein biosynthesis GO; GO:001148; p:negative regulation of protein biosynthesis GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
PRINTS; PR00161; RIP; 1.
PRINTS; PR00196; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
NON TER.
251 251
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251 AA; 28055 MW; 6F64755C3DEAFB79 CRC64;
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01-077-2002 (TrEMBLrel. 22, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Lectin chain A isoform 2 (Fragment).
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236 TVAVLALMLFVCNPP 250
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 QRIR-----PANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQV 236
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-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AF508916; AAM46934.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKA--DDPGKAFVLVALSNDNGQ
                                                                                                                                                                                                                                                                                                                                             8 VTHQTTGDQYF---KFITLLRDHVSSGSLSNQIPLLRQSTVPVSDTQRFVLVELSNQGGD
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                                                                                                                                                                                                                                  19; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21566752; PubMed=11710524;
Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0003598; F:rRNA N-giycosylase activity; IEA.
GO; GO:0005958; P:rRNA N-giycosylase activity; IEA.
GO; GO:0017148; P:negfative regulation of protein biosynthesis; IEA.
GO; GO:0009165; P:pathogenesis; IEA.
III.erPro; IPRO01574; RIP.
Pfam; PF00161; RIP; 1.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
PRINTS; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                      ch 24.5%; Score 312.5; DB 2; Length: Similarity 35.2%; Pred. No. 2.6e-17; 89; Conservative 37; Mismatches 108; Indels
                                                                                                                    3C5870F8338BDAB5 CRC64;
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120 AHQSRQQIPLGLQALTHGISPFRSGGNDN---EEKARTLIVIIQMVAAAALFRYISNRVR 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 EGEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
                                                                                                                                           119 EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
Lin Y., Wu Z.J., Lin Q.Y., Xie L.H.;
Submitted (JUL-2002) to the EMBL/Genbank/DDBJ databases.
-!-CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AAL82822.2;
---SIMILARITY: LCPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEG--LFKNTIKTRLHFGGSYPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHG----IPLLRKKADDPGKAFVLVALSN
                                                                                                                                                                                                                          NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created) ...
01-JUN-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
03-Mostemma pentaphyllum (diaognlan).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 1; Cucurbitales; Cucurbitaceae; Gynostemma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; UNKNOWN 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22692 MW; 8CCA3228286E09EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.5%; Score 300; DB 2;
larity 38.3%; Pred. No. 2.1e-16;
Conservative 22; Mismatches 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 IRNNFQQRIRPANNTISLENKWGKLSFQI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                          236 VKPKIALLKFVDKDP 250
                                                                                                                                                                                                                                                                                                                                                 236 TVAVLALMLFVCNPP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                     09
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
OBRY69
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                                                                                                                                                                                                                                                                                                                                                                                                                182 INSGVSYLPDVYMLELEASWGQQSTQVQQS-TDGVFNNPIRLGISTGNFVWLSNVRDVIA 240
                                                                                                                                                                                                                          64 AE---IAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                 65 EDSITAAIDVTNLYVVAYQAGDQSYFLRDAPDGAERHLFTGTTRSSLPFNGSYADLERYA 124
                                                                                                                                                                                                                                                                                                        121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                181 FQQRIR--PANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-----GKAFVLVALSND 59
                                                                                                                                              63
                                                                                                                                                                   derived by site specific mutagenesis in Escherichia coli.";
Eur. J. Biochem. 219:83-87(1994).
-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 288 rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
                                                                                                                                         5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKAD-DPGKAFVLVALSNDNGQL
                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abrus precatorius (Indian licorice) (Crab's eye).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.

NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0016787; Finydrolase activity; IEA.
GO:000598; F:rRNA N-glycosylase activity; IEA.
GO:0006952; P:defense response; IEA.
GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.; "Cloning and expression of three abrin A-chains and their mutants
                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                           Score 309.5; DB 2; Length 251; Pred. No. 4.6e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 2; Length 251;
6.1e-17;
                                                                                                   40; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 308; DB 2; Length 25; Pred. No. 6.1e-17; 39; Mismatches 109; Indels
  251
28090 MW; All777489012E989 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27997 MW; 3B60351839AEFB7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 02, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                4.6e-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abrin A chain E164A/R167L (Fragment).
Name=pcDNAC-1-E164A/R167L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                             24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24.1%;
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                                    Query Match
Best Local Similarity 34...
-hog 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIALLKFVDKD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLGIMVFVCRD 251
  251. 2
251 AA;
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Pfam; PF00161; RIP;
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Best Local
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RESULT 9

116

26

28

Gaps

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SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin Y., Lin O.Y., Xie L.H.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

- CATALTYTTC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 258 rRNA.

- SIMILARITY: Belongs to the ribosome-inactivating protein family.

REMBL; AY279104; AAP40648.1; -.

REMBL; AY279104; AAP40648.1; -.

RO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0015959; F:rRNA N-glycosylase activity; IEA.

GO; GO:0015959; F:rRNA N-glycosylase activity; IEA.

GO; GO:001748; F:negative regulation of protein biosynthesis; IEA.

RO; GO:001748; P:negative regulation of protein biosynthesis; IEA.

RO; GO:0019405; P:pathogenesis; IEA.

RITEPTYO: IRRONITY; RIP.

R Pfam; PF00161; RIP; 1.

RR Pfam; PF00161; RIP; 1.

RR Pfam; PF00161; RIP; 1.

RR Pfam; PF00161; RIP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEG--LFKNTIKTRLHFGGSYPSLEGEKAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 RETTDLGIEPLRIGIKKLDENAIDNY---KPTEIASSLLVVIQMVSEAARFTFIENQIRN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 NF--QQRIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYV--TAVD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34. NIAVLKHHVYVVGFLIGINSYIFKEAPDLAYNKSLLFPGSVRENLSYTGGYDDLERRGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                    Gynostemma pentaphyllum (Jiaogulan).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Wagnoliophyta, eudicotyledons, core eudicots, rosids,
Surantophyta, Ly Cucrbitales, Oucurbitaceae, Gynostemma.
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Gynostemmin-like protein (Fragment).
Gynostemma pentaphyllum (Jiaogulan).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AA; 27515 MW; 2ACBCE270B018203 CRC64;
                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Gynostemmin-like protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 290; DB 2;
Pred. No. 1.8e-15;
                                                                                                                                                 248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Mismatches
                          IAKNLYGTFKPDRAILSLENNWGALSKOI 200
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 LVQNGIALLKYMSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 QVKPKIALLKFVDK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=182084;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                 RESULT 11
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AC Q7Y
DT Q1-
DT Q1-
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Lin Y., Lin Q.Y., Xie L.H.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

C. -- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rENA.

C. -- SIMILARITY: Belongs to the ribosome-inactivating protein family.

EMBL; AR29106; AAP40650.1; --

RESP: P24817; E:hydrolase activity; IEA.

GO; GO:0010598; F:rNNA N-glycosylase activity; IEA.

GO; GO:0010598; F:rNNA N-glycosylase activity; IEA.

GO; GO:001748; P:negative response; IEA.

GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.

GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.

RO; GO:001774; RIP.

R Pfam; PF00161; RIP; 1.

R Pfam; PF00161; RIP; 1.

Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 BIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEG--LFKNTIKTRLHFGGSYPSLEGEKAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 RETTDLGIEPLRIGIKKLDENAIDNY---KPTEIASSLLVVIOMVSEAARFTFIENDIRN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 NF--QQRIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYV--TAVD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 NITVLKHHVYVVGFLIGINSYIFKEAPDLAYNKSLLFPGSVRENLSYTGGYDDLERRGAG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen G., Lei J., Cao B., Zeng G.; Submitted (APR-2004) to the EMBL's Submitted (APR-2004) to the EMBL's Late of the N-glycosidic bond at one specific ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S IRNA.

-- SIMILARITY: Belongs to the ribosome-inactivating protein family. EMBL; AX603353; AAT12448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 INFSLAGAGGOTYKTFIAKLRQE-----LSIGTQKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Gaps
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 1; Cucurbitales; Cucurbitaceae; Gynostemma.
NCBL_TaxID=182084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Phytolaccaceae; Phytolacca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 AA; 27545 MW; CB937106550F79F7 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.4%; Score 286; DB 2; 33.5%; Pred. No. 3.7e-15; iive 31; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 AA
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Name=papal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 33.5%
85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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229
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                                                                                                                                                                                                                                                              GQLAEIAIDVTSVYVVGYQ-----VRNRSYFFKD-------APDAAYEGLFKNT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen D., Wang X., Zhou G., Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!-CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at o specific adenosine on the 28S rRNA.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL, AF338910; AAX21951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P10297; ID6A.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
GO; GO:0017148; P:negative regponse; IEA.
GO; GO:0019405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
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PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Caryophyllales, Phytolaccaceae, Phytolacca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytolacca americana (Common pokeberry) (Virginian pokeweed)
                                                      Length 237;
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                                                   Query Match 21.8%; Score 278; DB 2; Length 23 Best Local Similarity 30.2%; Pred. No. 1.6e-14; Matches 75; Conservative 45; Mismatches 96; Indels
     FE576A3C96A1F6C6 CRC64;
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Last annotation update)
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     26622 MW;
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01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 ERANGKKY 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 VDASGAKW 237
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Matches ~ 75; Conserv
     237 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQMVSEAARFTFIENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVEL 220
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Chen G., Lei J., Cao B., Zeng G.;
Chen G., Lei J., Cao B., Zeng G.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                     GO; GO:0030598; F:RRNA N-glycosylase activity; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:001148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO:0005952; P:defense response; IEA.
GO:001148; P:negative regulation of protein biosynthesis; IEA.
GO:0009405; P:pathogenesis; IEA.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Caryophyllales, Phytolaccaceae, Phytolacca.
                                                                                                                                                                                                                                                                                                                                                                                             32;
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PRINTS; PR00396; SHICARICIN.
PROSITE; PS00275; SHICAR RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
NON_TER
                                                                                                                                                                          PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=pap;
Phytolacca americana (Common pokeberry) (Virginian pokeweed)
                                                                                                                                                                                                                                                                                                                                                                                             96; Indels
                                                                                                                                                                                                                                                                                   237 AA; 26710 MW; A274F9BA402031DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                    Score 282; DB 2;
Pred. No. 7.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 AA
                                                                                                                                                                                                                                                                                                                                                                                          44; Mismatches
GO:0016787; F:hydrolase activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiviral protein PAP (Fragment).
                                                                                                                                                                                                                                                                                                                                    22.1%;
                                                                                                                                                                                                                                                                                                                                                                                     76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERANGKKY 228
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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230 VDASGAKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI TaxID=3527;
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                       Query Match
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106/31M

106/31M

107/41M

1
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Search completed: June 20, 2005, 09:47:12 Job time: 112.5 secs

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Example 3; Page 181-182; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 251 AA;
                                                                                                                                                                                                                                AAR63914;
                                                                                                                                                                                                         AAR63914
                                                                                                                                                                                                                         Aar63914 Type I RI
Aar63912 Type I RI
Aar63903 Type I ri
Aar63915 Type I RI
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Type I RI
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                                                                                               1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                        Aar63903
Aar63915
Aar63923
Aar63921
Aar63920
Aar63919
Aar63919
Aar63919
Aar63919
Aar63919
Aar63917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aar37291
Aar63913
Aay69048
Aar07518
Aar25573
Aar21605
Aaw14228
Aaw14232
                                               June 20, 2005, 09:21:47 ; Search time 113.5 Seconds
                                                                                                                                                         1545266
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                        2105692 segs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                OM protein - protein search, using sw model
                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR07518
AAR25573
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AAY69048
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                                                                                                                       Gapop 10.0 , Gapext 0.5
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geneseqp20018:*
geneseqp2003as:*
geneseqp2003as:*
geneseqp20048:*
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Match Length
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                                                                                                                BLOSUM62
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98.7
98.7
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26 316 24.7 249 2 AAW14230 27 316 24.7 250 2 AAW14229 29 315 24.7 251 7 ADC24290 31 309 24.2 244 2 AAW14234 31 309 24.2 246 2 AAW14234 32 308.5 24.2 246 2 AAW14234 34 308.5 24.2 250 2 AAW21700 35 307 24.0 247 3 AAV59043 36 307 24.0 248 4 AAB36824 37 303 23.7 24.8 2 AAW14236 38 30.2 23.4 24.8 2 AAW14236 40 293 22.9 241 2 AAW14236 41 290.5 22.7 234 2 AAW14246 42 290.5 22.7 234 2 AAW14244 45 290.5 22.7 234 2 AAW14244	Aaw14230 Mature po	. Aaw14229 Mature po	Aab19267 Amino aci	Adc24290 A. precat	Aaw14235 Mature po	Aaw14234 Mature po	Aaw14233 Mature po	Aaw21700 Abrin-A A	Aaw25137 Abrin A A	Aay69043 Amino aci		Aaw14236 Mature po	Aar52636 Bioactive	Aaw14237 Mature po	Aaw14238 Mature po	Aaw14239 Mature po	Aaw14246 Mature po	Aaw14245 Mature po	Aaw14244 Mature po	Aaw14243 Mature po
316 24.7 249 315 24.7 250 315 24.7 251 309 24.2 244 309 24.2 246 308.5 24.2 246 308.5 24.2 246 308.5 24.2 246 307 24.0 247 307 24.0 247 307 24.0 247 290 23.4 22.9 240 290.5 22.7 233 290.5 22.7 234 290.5 22.7 234	AAW14230	AAW14229	AAB19267	ADC24290	AAW14235	AAW14234	AAW14233	AAW21700	AAW25137	AAY69043	AAB36824	AAW14236	AAR52636	AAW14237	AAW14238	AAW14239	AAW14246	AAW14245	AAW14244	AAW14243
316 24.7 315 24.7 315 24.7 309 24.2 308 5 24.2 308 5 24.2 308 5 24.2 307 24.2 307 24.2 307 24.2 307 24.2 307 24.0 307 24.0 299 22.7 290 5 22.7 290 5 22.7	N	N	ო	7	N	N	~	N	N	ო	4	N	N	7	~	~	~	~	N	7
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88888	24.7	24.7	24.7	24.7	24.2	24.2	24.2	24.2	24.2	24.0	24.0	23.7	23.6	23.4	22.9	22.8	22.7	22.7	22.7	22.7
00000000000000000000000000000000000000	316	316	315	315	309	309	309	308.5	308.5	307	307	303	302	299	293	291	290.5	290.5	290.5	290.5
	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents. Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease. Type I RIP gelonin analog Gel (A44/A50) Better MD, Carroll SF, Studnicka GM; AAR63914 standard; protein; 251 AA 94WO-US005348 93US-00064691 (revised)
(first entry) Gelonium multiflorum WPI; 1995-006804/01 (XOMA) XOMA CORP. 12-MAY-1994; 12-MAY-1993; WO9426910-A1 24-NOV-1994. 25-MAR-2003 27-JUL-1995

AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

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Sequence 251 AA;

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                                                                                                                                                                                                                                                                            240
                                                                                                                                                           120
                                                                                                                                                                                        AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                              GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.
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                                                                                      GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                               GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                         AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                      GLDTVSFSTKGATY1TYVNFLNELRVKLKPEGNSHG1PLLRKKADDPGKAFVLVALSNDN
                                         Gaps
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            Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                         0; Indels
         Query Match 100.0%; Score 1277; DB 2; Best Local Similarity 100.0%; Pred. No. 4.2e-120; Matches 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 179-180; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Type I RIP gelonin analog Gel (A50/C44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                            AAR63912 standard; protein; 251 AA.
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                                                                                                                                                                                                                                                                                                         ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                   241 ALLKFVDKDPK 251
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27-JUL-1995
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                                                                                                                                                            61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.
                                                                                       1 GLDTVSFSTKGATYITYVNPLNELRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                   181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                       1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                              121 AYRETTDIGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                    Gaps
                                    ;
   Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
99.7%; Score 1273; DB 2; 99.6%; Pred. No. 1.1e-119; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type I ribosome-inactivating protein gelonin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Better MD, Carroll SF, Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR63903 standard; protein; 251 AA.
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                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                          241 ALLKFVDKDPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-006804/01.
N-PSDB; AAQ75532.
                    Local Similarity
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27-JUL-1995
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                                      250;
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 Query Match
                     Best Loca
Matches
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Gaps

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Length 251; Indels 9 9

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61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                    GLDTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKKADDPGKAFVLVALSNDN
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                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                  Score 1269; DB 2;
Pred. No. 2.7e-119;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gelonium anti-HIV protein 31kDa (GAP31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 2; 22pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG63044 standard; protein; 251
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                                                                                    Query Match
Best Local Similarity 99.6%;
Matches 250; Conservative
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correct PN field.)
                                            Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADG63044;
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                                                                                                                                                                                                                                                                    61 GQLAEIAIDVTSVYVVGYQVRNRSYFFXDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                           181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMPSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                            120
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                                                                                                                                                                             GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                           ;
0
                                                                    Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                                                                                           Indels
                                                            99.4%; Score 1269; DB 2; 99.2%; Pred. No. 2.7e-119; ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type I RIP gelonin analog Gel(C10/A44/A50).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR63915 standard; protein; 251 AA.
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                                                 Query Match
Best Local Similarity 99.2'
Marches 249; Conservative
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                     Sequence 251 'AA;
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27-JUL-1995
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The invention describes an isolated peptide or polypeptide having an anti-
tumour and antiviral activity. Also described is a composition
comprising the isolated peptide or polypeptide, and a carrier, excipient
or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or
polypeptides. The peptide or polypeptide is useful for treating HIV
infection, and tumour. This is the amino acid sequence of Gelonium anti-
HIV protein 30kDa (MAP30).
           antiviral; MAP30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and antiviral activity, useful for treating human immunodeficiency virus
anti-HIV; cytostatic; peptide therapy; anti-tumour; GAP31; HIV; tumour; gelonium anti-HIV protein 31kba.
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Sequence 251 AA;
                       Query Match
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                                                                                                                                                               180
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                                                                                                             GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                            GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                               AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                            GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                   Gaps
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          Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type I ribosome-inactivating proteins, RIPs, gelonin, cytotoxic therapeutic agents, autoimmune disease, cancer,
                                   Indels
          Score 1269; DB 8;
Pred. No. 2.7e-119;
 99.2%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 187-188; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Type I RIP gelonin analog Gel (C103)
                                                                                                                                                                                                                                                                                                                                                     AAR63923 standard; protein; 251 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 graft-versus-host disease.
                      Best Local Similarity 99.2
Matches 249; Conservative
                                                                                                                                                                                                                                                                 ALLKFVDKDPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
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    Length 251;
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                                  Indels
Score 1264; DB 2;
Pred. No. 8.7e-119;
0; Mismatches 3;
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99.0%;
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                  Similarity
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                                                                                             Length 251;
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                                                                                                                                          Indels
                                                                                             98.7%; Score 1261; DB 2; 98.8%; Pred. No. 1.7e-118;
                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type I RIP gelonin analog Gel(C244)
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                                                                                                                                            Matches 248; Conservative
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                                                                                                                   Local Similarity
correct PN field.)
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                                                   Sequence 251 AA;
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27-JUL-1995
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                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                              61 GQLAEIAIDVŢSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKWTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                         AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                    FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                     Length 251;
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                                                                       1; DB 2;
1.7e-118;
                                                                                                                   0; Mismatches,
                                                                     Score 1261;
Pred. No. 1.
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                                                                  98.7%;
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                                                                                        Best Local Similarity 98.8
Matches 248; Conservative
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                           Sequence 251 AA;
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elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
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     cancer and graft-versus-host disease. (Updated on 25-MAR-2003
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                                                                                                                                                                               Indels
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                                                                                                                            Score 1261; DB 2;
Pred. No. 1.7e-118;
                                                                                                                                                Pred. No. 1.76
0; Mismatches
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                                                                                                                            98.7%;
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Matches 248; Conservative
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ALLCFVDKDPK 251
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disease, cancer an
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                                                                             Sequence 251 AA;
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                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                    181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPCI
                                                                                                                                1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                                 121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                                                                Gaps
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0
                                Length 251;
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                                                                Indels
                                                                 3
                             Score 1261; DB 2;
Pred. No. 1.7e-118;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 188-189; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Type I RIP gelonin analog Gel(C184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR63924 standard; protein; 251 AA.
                                98.7%;
98.8%;
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                                                al Similarity 98.8
248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      (revised)
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Sequence 251 AA;
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the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 correct PN field.)
                                                                                                                                                                          GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                            AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
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                                                                                                  Length 251;
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                                                                                                                               3; Indels
                                                                                               Score 1261; DB 2;
Pred. No. 1.7e-118;
0; Mismatches 3;
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                                                                                                 98.7%;
98.8%;
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                                                                                                                             248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Carroll SF,
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                                                                                                              Local Similarity
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                                                                      Sequence 251 AA;
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targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 correct PN field.)
                                                                                                                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                                                                                                              Length 251;
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                                                                                                                                        Indels
                                                                                                            98.7%; Score 1260; DB 2; 98.8%; Pred. No. 2.2e-118; ive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type I RIP gelonin analog Gel(C247/A44/A50).
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(first entry)
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                                                                                                                            Best Local Similarity ....
Matches 248; Conservative
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                                                                                    Sequence 251 AA
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27-JUL-1995
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selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
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                                                                                                                                                                                                                                                          AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                                          FQQR1RPANNT1SLENKWGKLSFQ1RTSGANGMFSEAVELERANGKKYYVTAVDQVKPK1
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                                                                                                             Length 251;
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                                                                                                                                    Indels
                                                                                                           98.7%; Score 1260; DB 2;
ilarity 99.2%; Pred. No. 2.2e-118;
Conservative 0; Mismatches 2;
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                                                                                                                      Local Similarity
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                                                            correct PN field.)
                                                                                     Sequence 251 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                    9
       selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 correct PN field.)
used to
                                                                                                                                                                                                                        1 GLDTVSFSTKGATYITTYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                      1 GLDIVSPSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                     FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin.
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gene fusion products and immunoconjugates. CTAs may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I RIPs"
                                                                                                                                                 251;
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                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= non-Cys residue in claimed
                                                                                                                                              Score 1260; DB 2;
Pred. No. 2.2e-118;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Cys in claimed analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type I ribosome-inactivating protein gelonin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR74177 standard; protein; 251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= see above
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                                                                                                                                                98.7%;
98.8%;
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                                                                                                                                                                             Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ALLKFVDKDPK 251
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                                                                                                                                                              Local Similarity
                                                                                                                    Sequence 251 AA;
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04-JAN-1980
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                                                                                                                                                Query Match
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/label= see above label= see above label= see above /label= see above

.167

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Polynucleotide(s) encoding gelonin analogues - having a cysteine residue for intermolecular bonding for the prodn. of immuno-toxin(s).
                                                                                                                                                                                             Claim 1; Fig 1; 66pp; English
                                                                                                               09-DEC-1992; 92US-00988430
                                                                                                                          04-NOV-1991; 91US-00787567, 19-JUN-1992; 92US-00901707.
     Misc-difference 166.
                                                                                                                                                      Carroll SF,
                                                                                                                                                                  WPI; 1995-193480/25
                           Misc-difference 198
                                                                                                                                           (XOMA ) XOMA CORP
                Misc-difference
                                      Misc-difference
                                                 Misc-difference
                                                            Misc-difference
                                                                       Misc-difference
                                                                                         US5416202-A.
                                                                                                    16-MAY-1995.
                                                                                                                                                      Lei S,
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Better MD;

Bernhard SL,

Lane JA,

polypeptides that share the ribosome-inactivating activity of the natural protein but differ in AA sequence. Preferred analogues have a Cys available for disulfide bonding located at a posn. it its AA sequence from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy terminus of the analogue. (AAR74176 is the sequence of ricin A-chain RTA, which is a Type II RIP). The primary AA sequence of the Type I RIPS colonin, BRIP, mormordin II, luffin [see Islam et al. Agricultural gelonin, BRIP, mormordin II, luffin [see Islam et al. Agricultural cological Chem., 265, 8670-74 1990], momordin I [see Hobe et al., BBA, 1088, 311-14 1991], Mirabilis antiviral protein [see Hobe et al., J. Biol. Chem., 264(12) 5659-37 1989], pokeweed antiviral protein isolated from seeds [see Kung et al., Agric. Biol. Chem., 54(12), 3301-18 1990] and saporin [see Banatti et al., Eur. J. Biochem., 183, 465-70 1989] are individually aligned with the primary sequence of the ricin A-chain [see Halling et al., Nucleic Acids Res., 13, 8019-803, 1985] respectively in Figures 1-9. The AAS invariant among the ricin A-chain and the Type I RIPS are indicated in FT. Also indicated are the preferred sites of Cys substitution. It is also preferred that the gelonin cysteine residues at positions 44 and 50 be replaced with alanine residues. (Updated on 25-MAR 2003 to correct PR field.) Analogues of Type I RIP are defined as non-naturally occurring polypeptides that share the ribosome-inactivating activity of the natural

Sequence 251 AA;

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GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                              61 GOLAEIAIDVTSVXVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 120
                                                                               9
                                                                                                                  1 GLDTVSESTKGATÝITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
                                                                             GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                      Gaps
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  Length 251;
                                      Indels
Score 1257; DB 2;
Pred. No. 4.4e-118;
1; Mismatches 3;
Query Match
Best Local Similarity 98.4%;
Matches. 247; Conservative
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180

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ò	181 FQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240	240
q	181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240	240
ò	241. ALLKEYDKDPK 251.	
đ	241 ALLKFVDKDPK 251	

completed: June 20, 2005, 09:43:21 Job time : 114.5 secs Search

39. .251 label= location of Cys in claimed analogue

'label= Cys in claimed analogue

/label= see above 247. .248 /label= see above This Page Blank (Uspto)

Sequence 108, App

14 US-10-127-890-108

251

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0.66
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12
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1: /cgm2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgm2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
4: /cgm2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
4: /cgm2_6/ptodata/2/pubpaa/NSO6_NEW PUB.pep:*
5: /cgm2_6/ptodata/2/pubpaa/NSO6_PUBCOMB.pep:*
7: /cgm2_6/ptodata/2/pubpaa/NSO6_PUBCOMB.pep:*
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19: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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16: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
17: /cgm2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1714042 segs, 383979560 residues
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                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                          US-10-717-243-101
1277
1 GLDTVSFSTKGATYIT
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Maximum DB seq length: 251
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 101, App	Sequence 101, App	Sequence 99, Appl	Sequence 100, App	Sequence 99, Appl	Sequence 100, App	Sequence 247, App	Sequence 2, Appli	Sequence 110, App	Sequence 2, Appli	Sequence 110, App
ΩI	US-10-127-890-101	US-10-717-243-101	US-10-127-890-99	US-10-127-890-100	US-10-717-243-99	US-10-717-243-100	US-09-765-527-247	US-10-127-890-2	US-10-127-890-110	US-10-717-243-2	US-10-717-243-110
	14	17	14	14	11	17	0	14	14	17	17
% Query Match Length DB	251	251	251	251	251	251	251	251	251	251	251
Query Match	100.0	100.0	7.66	7.66	99.7	99.7	99.4	99.4	99.4	99.4	99.4
Score	1277	. 1277	1273	1273	1273	1273	1269	1269	1269	1269	1269
Result No.	-	8	٣	4	2	9	7	80	6	10	11

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US-10-12/-890-108 US-10-717-243-108	US-10-127-890-103	US-10-127-890-104 US-10-127-890-105	US-10-127-890-106	US-10-127-890-109	US-10-717-243-104	US-10-717-243-105 US-10-717-243-106	US-10-717-243-109	US-10-127-890-102	US-10-127-890-111	US-10-717-243-102	US-10-717-243-107 US-10-717-243-111	US-09-792-793A-39	US-10-375-209A-39	US-10-717-243-6	US-10-282-935-3	11S = 09 = 1440 = 136 = 3	US-10-375-209A-34	US-10-127-890-5	US-10-717-243-5	US-10-083-336A-10 US-10-083-336A-11	US-10-083-336A-3	US-10-083-336A-7	US-10-083-336A-5 US-10-083-336A-4	ALIGNMENTS		on US/10127890		D. Shen F.			NUMBER OF SEQUENCES: 173	C. Mallot	dison Street, 34th floor				disk	ompatible	Peleage #1 0 Vergion	Acteur #1:07 veteron	US/10/127,890	known>	PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/646.360	(-1996	: PCT/US94/05348 7-1994	US 08/064,691	(-1993
1 -	1 7		7.	17	11	11	11.	7 7	7	17	11	0	15	11	4:	9 0	, 1	14	17	1 4	14	14	4 4			US/10	14061	Marc D. . Stephen	, Gary	Immu	173	ESS:	Bt Ma		m		ORM:	25	EM: F	DATA	MBER:	- Apr	ATA: MBER:	3 - MAY	MBER: 2-may	MBER	2-MA)
251	251	251	251	251	251	251	251	251	251	251	251	247	247	247	251	247	. 247	248	248	190	198	198	199			ation		rter, rroll,	udnika	NTION:	UENCES	E ADDR	500 We	icago	USA	61	ABLE F VPR: F	: IBM	3 SYST	CATION	ION NOI	CATION	O NOIT	ATE: 1	ION NU	ION NO	ATE: 1
0.66	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	25.3	25.3	24.9	24.7	24.7	24.0	21.7	21.7	19.3	19.2	19.2	19.2		01	Applica	ORMATIO	ANT: Be	Stı	OF INVE	OF SEQ	PONDENC	TREET:	ITY: Ch	TATE: I	IP: 606	ER READ	OMPUTER	PERATIN	T APPLI	PPLICAT	LASSIFI	APPLICA'	ILING D	PPLICAT	PPLICAT	ILING D
1264	1261	1261	1261	1261	1261	1261	1261	1260	1260	1260	1260	323	323 318	318	315	307	307	277	277	246.5	245.5	245.5	243.5		7-890-1	ice 101,	RAL INF	APPLIC		TITLE	NUMBER	CORRES	; w	0	<i>a</i> O	23	COMPUT	. 0	0 0	CURREN	4 , 1	40	PRIOR	E24	at II	4	24
13	14	16	17	13	20	22	533	5 7 7 7	26	27	7 7	30	31	33	34	25	37	38	9.0	4.4	42	43	4.4		RESULT 1 US-10-127-890-101	; Sequer	; GENE		. •										•- :	- •-							••

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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GQLAEIAIDVISVYVVGYQVRNRSYFFXDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studmika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 251;
         PRIOR APPLICATION DATA:

APPLICATION DATE: 18-NOV-2003

RIGHLING DATE: 115-NOV-2003

PRIOR APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/981,707

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: MCNicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELEPHONE: 312/707-8889

TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1277; DB 17; Best Local Similarity 100.0%; Pred. No. 1.1e-115; Matches 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECTLE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-717-243-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ALLKFVDKDPK
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Studnika, Gary M.
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 251; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPACTION
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
             FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8189
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-127-890-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-17-243-101
Sequence 101, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                               TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
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61 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                        ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.7%; Score 1273; DB 14; 99.6%; Pred. No. 2.7e-115; tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REGISPERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 100: US-10-127-890-100
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                                                                                                                                                                                                                                                   ZIP: 60661
COMPUTER READABLE FORM:
                                                                                                   CORRESPONDENCE ADDRESS
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Best Local Similarity 99.6
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.7%; Score 1273; DB 14; Length 251; 99.6%; Pred. No. 2.7e-115; 1ve 0; Mismatches 1; Indels 0
                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13.4MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12.4MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12.4MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFRERNCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                              APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 99: US-10-127-890-99
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US-10-127-890-100
US-10-127-890-100
; Sequence 100, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFHONE: 312/707-8889
TELEFAX: 312/707-9155
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INFORMATION FOR SEQ ID NO: 99
SEQUENCE CHARACTERISTICS
                          ZIP: 60661
COMPUTER READABLE FORM:
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Matches 250; Conservative
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                                                                                                                                                                                                               Sequence 100, Application US/10717243
Publication No. US20050054035A1
GENERAL INPORMATION:
CATACLI, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                          181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDOVKPKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMULCATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.7%; Score 1273; DB 17; Best Local Similarity 99.6%; Pred. No. 2.7e-115; Matches 250; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/10/717,243

PILING DATE: 18-NOV-2003

CLASSIFICATION NUMBER: US/08/839,765

PILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/64,691

FILING DATE: 10-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 19-DEC-1992

APPLICATION NUMBER: US 07/981,707

FILING DATE: 19-UNC-1992

APPLICATION NUMBER: US 07/981,707

FILING DATE: 19-NUM-1992

APPLICATION NUMBER: US 07/91,707

FILING DATE: 19-UN-1992

APPLICATION NUMBER: US 07/91,707

FILING DATE: 19-UN-1992
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; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-717-243-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Illinois
COUNTRY: USA
ZIP: 6061
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 312/707-9155
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INFORMATION FOR SEQ ID NO: 100
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                 241 ALLKFVDKDPK 251
                                                                                                                                                                                                  241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                     US-10-717-243-100
                                                                                                                                                                                                                                                                                RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                          Sequence 99, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 16-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS: LENGTH: 251 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.7%;
Best Local Similarity 99.6%;
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-717-243-99
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10127890
; Sequence 2, Application US/10127890
; Publication No. US20030166196A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWYSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLIUM TITES: FLODEY GLIBA
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION TURER: US/08/646,360
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: US/08/64,691
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEB: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111nois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60661
COMPUTER READABLE FORM:
                                                                                                                                                                                                                           241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                       241 ALLKFVDKDPK 251
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                                         61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                  61 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                121 AYRETTOLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                          181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 247, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 99.4%; Score 1269; DB 9; Best Local Similarity 99.2%; Pred. No. 6.7e-115; Matches 249; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <URKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, MIChael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
PLING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: procein SEQUENCE DESCRIPTION: SEQ ID NO: 247: US-09-765-527-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ 1D NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLDTVSFSTCGATYITYVNPLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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                                                                                                                                                                                                                                                                               Length 251;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                         tch 99.4%; Score 1269; DB 14; al Similarity 99.6%; Pred. No. 6.7e-115; 250; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION: 330
PRIOR APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APP-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
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                            | LENGTH: 251 amino acids | TYPE: amino acidd | TYPE: amino acidd | TYPE: TOPOLOGY: linear | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 110: US-10-127-890-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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   INFORMATION FOR SEQ ID NO: 110:
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STATE: Illinois
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Matches
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                                                                                                                                                                                                                                               GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKWTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                        AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proceins
                                                                                                                         1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                               Gaps
                                                               .
0
   Length 251;
                                                               Indels
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COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <university control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the c
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STREET: 500 West Madison Street, 34th floor
CITY: Chicago
   DB 14;
                                                                   7
                            6.7e-115;
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APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/988,430
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/97,567
FILING DATE: 04-NOV-1991
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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: U9/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
                            Pred. No. 6.7e
0; Mismatches
   Score 1269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 110, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION: APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
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Query Match
Best Local Similarity 99.2%;
Matches 249; Conservative
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COMPUTER READABLE FORM:
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COUNTRY: USA
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61 GQLAEIAIDVISVYVVGYQVQRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Sequence 108, Application No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxing Comprising Ribosome-Inactivating
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                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
  FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-717-243-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 251 amino acids TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
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Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1269; DB 17; Length 251;
Pred. No. 6.7e-115;
0; Mismatches 2; Indels 0
ATTORNEY/AGENT INFORMATION:
NAME: MCNICADLAB. Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 110, Application US/10717243 Publication No. US20050054835A1 GENERAL INFORMATION:
                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins
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Best Local Similarity 99.2%;
Matches 249; Conservative
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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Best Local Similarity
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US-10-717-243-110
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ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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TELEFAX: 312/707-9155
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INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.8
Matches 248; Conservative
                                      CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-10-127-890-103
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Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLDTVSFSTKGATYITTVVFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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Pred. No. 2e-114;
0; Mismatches 3; Indels
                    PatentIn Release #1.0, Version #1.25
              CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/989,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/989,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/981,707
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/91,707
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 251 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 98.8°
Matches 248; Conservative
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61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                         CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 18-Nov-2003

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1995

APPLICATION NUMBER: US 08/04,691

FILING DATE: 12-APR-1995

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-APR-1993

APPLICATION NUMBER: US 08/064,691

FILING DATE: 19-APR-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/981,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/991,707

FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-717-243-108
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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61 GQLAEJAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                        Sequence 104, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxing Comprising Ribosome-Inactivating Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY.

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

^^TWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STRETT: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; 4e-114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
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FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 104: US-10-127-890-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: MCNicholas, Janet M.
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                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                  241 ALLKFVDCDPK 251
                                 241 ALLKFVDKDPK 251
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nes 248; Conserv
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US-10-127-890-104
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Best Local S
Matches 248
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                                              APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
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                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
PPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-MAY-1993
PELLING DATE: 09-DEC. 1992
FILING DATE: 09-DEC. 1992
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/127,890
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-127-890-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
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MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
Publication No. US20030166196A1 GENERAL INFORMATION:
                                                                                                                                                                      NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMYSEAARPTFIENQIRNN 180
61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
8686868
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180	181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKFKI 240	181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPCI 240

²⁴¹ ALLKFVDKDPK 251 |||||||||| 241 ALLKFVDKDPK 251

Search completed: June 20, 2005, 10:05:45 Job time: 104.5 secs

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TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 110, App
Sequence 2, Appli
                                                              June 20, 2005, 09:10:06.; Search time 30 Seconds (without alignments) 624.564 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                   1 GLDTVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-488-113B-101
US-08-477-484B-101
US-08-839-765-101
US-09-136-389-101
US-09-136-389-101
US-09-711-485-101
US-08-425-336-99
US-08-425-336-99
US-08-488-113B-99
US-08-488-113B-99
US-08-446-360-99
US-08-446-360-100
US-08-646-360-100
US-08-839-765-100
US-08-839-765-100
US-08-839-765-100
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US-08-839-765-100
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                                                                                                                                                                                            513545 seqs, 74649064 residues
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                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1277
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                             OM protein -
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                                                                                                                                     Sequence:
                                                                                                                                                                                              Searched:
                                                                 Run on:
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No.
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	Seguence 110, App	Sequence 2, Appli	Sequence 110, App	Seguence 2, Appli	Sequence 110, App	Sequence 247, App	Seguence 2, Appli	Sequence 110, App	Sequence 2, Appli	Sequence 110, App	Sequence 247, App	Sequence 2, Appli	Sequence 110, App	Sequence 2, Appli	Sequence 110, App	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	
	US-08-488-113B-110	US-08-477-484B-2	US-08-477-484B-110	US-08-646-360-2	US-08-646-360-110	US-08-621-803-247	US-08-839-765-2	US-08-839-765-110	US-09-136-389-2	US-09-136-389-110	US-09-217-352-247	US-09-610-838-2	US-09-610-838-110	US-09-711-485-2	US-09-711-485-110	US-09-645-603B-2	US-07-901-707-2	US-07-988-430-2	
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;	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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US-08-425-36-101
Sequence 101, Application US/08425336
Parent No. 5621083
GERREAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll Marker, 233 South Wacker Drive CORRESPONDERS: 100 Sears Tower, 233 South Wacker Drive CORRESPONDERS: 101 Sears Tower, 233 South Wacker Drive CORRESPONDERS: 103 Sears Tower, 233 South Wacker Drive CORPERS: 103 Sears Tower, 233 South Wacker Drive Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Companies Compa
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-000-1995
                                                                                                                                                                                                                                                  100.0%; Score 1277; DB 1; 100.0%; Pred. No. 6.8e-119;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
PILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
TELEFAX: 312//v/----
TELEFAX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 101
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ALLKFVDKDPK 251
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                                                                                                                                                                                                                                                                                                                                               121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENQIRNN 180
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                                                                                                              1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFYLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
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                 100.0%; Score 1277; DB 1; Length 251; 100.0%; Pred. No. 6.8e-119; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-08-488-113B-101
Sequence 101, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
                                       Best Local Similarity 100. Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 ALLKFVDKDPK 251
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                      Query Match
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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                          61 GQLAEIAIDVTSVYVVGYQVRNRSYFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Patent No. 5/56599

GENERAL INPORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studiaka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS: 169

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                   1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                       1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                    Gaps
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Length 251;
                                               Indels
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61 GQLAEIAIDVISVYVVGYQVRNRSYFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinks, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1277; DB 2; Length 251; Best Local Similarity 100.0%; Pred. No. 6.8e-119; Matches 251; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
              PRIOR AFFLICATION NUMBER:
PLICATION NUMBER:
FILING DATE: 12-NAY-1994
PRIOR APPLICATION NUMBER:
PRILING DATE: 12-NAY-1994
PRICR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-NAY-1993
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/98,430
FILING DATE: 09-DEC-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRICR APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAMME: MCANICADIAES, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHX: 312/707-989
TELEPHX: 312/707-989
TELEPHX: 312/707-989
TELEPHX: 312/707-989
TELEPHX: 312/707-989
TELEPHX: 550 389-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
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US-08-839-765-101
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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Batent No. 5837491

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATE: 09-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NCV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCANICATION: NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9889
TELEFAX: 312/707-9155
TELEFX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FLING DATE: 13-MAY-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1277; DB 1; Best Local Similarity 100.0%; Pred. No. 6.8e-119; Matches 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein.
US-08-477-484B-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 4
US-08-646-360-101
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Gaps

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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS: 173
CORRESPONDENCE ADDRESS: Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Best Local Similarity 100.0%; Pred. No. 6.8e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 10-DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1991
ATTONEY/AGERT INFORMATION:
ANAMER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INCORMATION
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-136-389-101
                                                                                                                                                                                                                                         ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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          COMPUTER: PORDAIL
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 18-APR-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
RILING DATE: 12-APR-1995
RILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 31,707-8889
TELEPHONE: 312/707-8889
TELEFRAX: 312/707-8889
TELEFRAX: 312/707-8889
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US-09-136-389-101
; Sequence 101, Application US/09136389
; Patent No. 6146850
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 251 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLKFVDKDPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGGK 120
                                                                                                                                                                                                                                                                          181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
  1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
                                                  61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                                            181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11022US09/200-70.P3.C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/711,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 500 West Madison Street, 34th floor CITY: Chicago
CITY: Chicago
CITY: Chicago
CITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PLORS APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-WAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-WOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 101, Application US/09711485
Patent No. 6649742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                     241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                            241 ALLKFVDKDPK 251
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                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>;</u>
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ZIP: 60661

COMPUTER BEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838

**TING DATE: 06-UUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1277; DB 3; Best Local Similarity 100.0%; Pred. No. 6.8e-119; Matches 251; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             3: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-A0G-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INPORMATION:
NAME: MCALCALON NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECPHONE: 312/707-8899
                                                                                                                                                                 Sequence 101, Application US/09610838 Patent No. 6376217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
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amino acid
                                     241 ALLKFVDKDPK 251
241 ALLKFVDKDPK 251
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STREET: Suc
CITY: Chicago
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                                                                                                                   RESULT 7
US-09-610-838-101
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GLDTVSFSTKGATYITTVVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60

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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-425-336-100
                                        TYPE: ami
TOPOLOGY:
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US-08-425-336-99
                   LENGTH:
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                                                                                                                                                                                                                                                                                                                                                         121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWYSEAARPTFIENQIRNN 180
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                                                                                                                          Gaps
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6100 Sears Tower, 233 South Wacker Drive
                                                                                                                        ö
                                                                               Query Match 100.0%; Score 1277; DB 4; Length 251; Best Local Similarity 100.0%; Pred. No. 6.8e-119; Matches 251; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPY disk
MEDIUM TYPE: RIOPY disk
COMPUTER: IBM PC Compatible
COMPTITE: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
PILING DATE: 18-APR-1995
CLASSIFICATION NAMBER: 08/064,691
FILING DATE: 12-ANY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATYONINY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 99, Application US/08425336 Patent No. 5621083 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 3139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 99:
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                 MOLECULE TYPE: protein
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Illinois
COUNTRY: USA
                   ; MOLECULE TYPE
US-09-711-485-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
TELEX: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           °,
                                                                                                                                                  Query Match 99.7%; Score 1273; DB 1; Length 251; Best Local Similarity 99.6%; Pred. No. 1.7e-118; Matches 250; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIORA APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-36,989
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: 251 amino acids
amino acid
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                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                    Gaps
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Sequence 99, Application US/08488113B
PREENT NO. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                         Length 251;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-ARR-1995
PRIOR APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DBC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                         Score 1273; DB 1;
Pred. No. 1.7e-118;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                         99.7%;
                                                                                                                                                                                                                                                Matches 250; Conservative
312/474-0448
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MOLECULE TYPE: protein
US-08-425-336-100
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                                                                                                                                                                                                         Query Match
Best Local Similarity
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TELEFAX:
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61 GQLAEIAIDVŢSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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i Sequence 100, Application US/08488113B

j Patent No. 5744580

j GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Carroll, Stephen F.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

YUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN
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ZIP: 60661

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,1138

TITING DATE: 07-UNN-1995
                                                                                                                                                  11022US07/200-70.P3.C2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1273; DB 1;
Pred. No. 1.7e-118;
0; Mismatches 1;
                                US 07/787,567
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022
TELECOMMUNICATION INFORMATION:
TELEFAK: 312/707-8889
TELEFAK: 650 388-1244
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6
Matches 250; Conservative
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MOLECULE TYPE: protein
US-08-488-113B-99
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COMPUTER READABLE FORM:
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Patent No. 575669

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studika, Gary M.
APPLICANT: Studika, Gary M.
TITLE OF INVENTION: Proteins
INUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 251;
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                                                                                                                                                                                                                                                                                                                                                                           11022US07/200-70.P3.C2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1273; DB 1;
Pred. No. 1.7e-118;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1955
PRIOR APPLICATION DATA: 38-PR-1955
APPLICATION DATA: 18-APR-1953
FILING DATE: 12-MAY-1993
APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: 09-DEC-1992
PRIOR APPLICATION DATA: 09-DEC-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION: NAME: MANE: MANE: 32,918
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/2
TELLEPANS: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 100:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.7
Best Local Similarity 99.6
Matches 250; Conservative
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-08-477-484B-99
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                                                                       CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

CLASSIFICATION NUMBER: US/08/477,484B

FILING DATE: 07-JUN-1995

PILING APPLICATION DATA:

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

FILING APPLICATION DATA:

APPLICATION NUMBER: US 08/064,691

FILING APPLICATION NUMBER: US 07/988,430

FILING APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION NUMBER: US 07/787,567

FILING DATE: US-JUN-1991

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11022US07/200-70.P3.C2A
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US-08-477-484B-100
; Sequence 100, Application US/08477484B
; Patent No. 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McNicholas, Janet M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acida
TYPE: amino acid
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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    Immunotoxins Comprising Ribosome-Inactivating Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCMALCANION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               COUNTRY: 14110118

SIGNER: 11110118

ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-UN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MSY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1273; DB 1;
Pred. No. 1.7e-118;
0; Mismatches 1;
                                                                                          E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.7%;
TITLE OF INVENTION: Immuno
TITLE OF INVENTION: Protei:
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDEWB, He
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.6
Matches 250; Conservative
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                                                                                          ADDALL
STREET: Suc
CITY: Chicago
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61 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Sequence 99, Application US/08646360

Patent No. 5837491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-AAY-1996
CLASSIFICATION STO
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-WAY-1994
FILING DATE: 12-WAY-1994
PRIOR APPLICATION NUMBER: US 08/064,691
PRIOR APPLICATION NUMBER: US 08/064,691
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, JAHOET M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1273; DB 2;
Pred. No. 1.7e-118;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECISTRATION NUMBER: 32,916
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312/707-8889
TELEFAK: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.6%;
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-646-360-99
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Dp	121	121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180	180
ò	181	181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240	240
qq	181	181 FQCRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240	240
ò	241	241 ALLKFVDKDPK 251	
qa	241	241 ALLKFVDKDPK 251	

²⁴¹ ALLKFVDKDPK 251 |||||||||| 241 ALLKFVDKOPK 251

Search completed: June 20, 2005, 09:22:44 Job time : 31 secs

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June 20, 2005, 09:09:06; Search time 25.5 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                               OM protein - protein search, using sw model
                                                                                                                                              Run on:
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	(without alignments) 947.075 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-717-243-101 1277 1 GLDTVSFSTKGATYITYVNFAVDOVKPKIALLKFVDKDPK 251
Scoring table: BLOSUM62	BLOSUM62 Gapop 10.0 , Gapext 0.5

	283416
residues	parameters:
96216763	ng chosen
283416 segs, 96216763 residues	hits satisfyi
earched:	otal number of hits satisfying chosen parameters:
ea	o t

Searched:

parameters:	
ng chosen para	0
l number of hits satisfying	2000000000
hits s	length:
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ттре	88
Total nu	Minimum 1 Maximum 1

0% 100% 45 summaries	
Match Match first	* * * *
Minimum Maximum Listing	PIR 79:* 1: pir1: 2: pir2: 3: pir3: 4: pir4:
Post-processing:	Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	ricin D precursor	rRNA N-glycosidase	agglutinin precurs	abrin-b precursor	rRNA N-glycosidase	abrin (clone 7.2)	rRNA N-glycosidase	rRNA N-glycosidase	abrin-a precursor	karasurin - Mongol	karasurin C - Tric	antiviral protein	karasurin-B - Tric	rRNA N-glycosidase	mistletoe lectin I	abrin-d precursor	abrin-c precursor	rRNA N-glycosidase	agglutinin I precu	beta-luffin - smoo	luffin-b - smooth	rRNA N-glycosidase	betavulgin - beet	ribosome-inactivat		rRNA N-glycosidase
SUMMARIES	DI	1	JC4840	825560	RLCSD	JC4235	RLCSAG	S32430	S28421	C39761	S17757	RLTZT	TZLSA	JU0393	JC5606	JE0401	JC5032	S22494	PD0018	S32431	S16022	RLPUGG	S62627	S23519	JN0108	A39817	JC4811	S46239	S17574	S28542
	rth DB			286 2			564 1	27 2	94 2	51 2	113 2	289 1	28 1	47 2	89 2	61 2	47 2	277 2	254 2	28 2	62 2						72 2			
	Length																													6
de (Query	99.4	27.7	27.3	27.1	26.9	26.4	26.2	26.0	25.8	25.6	25.3	25.1	24.8	24.8	24.5	24.4	24.3	23.8	23.4	23.4	22.9	22.7	22.5	•	16.9	16.4	16.0	15.3	14.4
	Score	1269	353.5	348	346	343	337.5	334.5	332.5	330	327	323	321	317	317	313.5	312	310.5	304.5	299	299	292	290.5	287.5	274	215.5	210	204	195	184.5
,	ReBult No.	7	63	М	4	ß	9	7	ω	σ	10	11	12	13	14	. 15	16	17	18	19	50	21	22	23	24	25	56	27	28	53

rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	N conserved hypoth	abrin (clone 3.7)	tritin - wheat	rRNA N-glycosidase	hypothetical prote	30K ribosome inact	protein synthesis
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RLQHG2	T12573	805205	S17519	S28541	\$28539	829931	A58923	S17932	B69511	B39761	833631	RLBH	T05612	B38664	JC5848
1	~	~	7	~	~	~	~	~	~	~	~	-	7	~	7
292	289	283	293	253	253	253	253	236	1948	106	275	280	456	281	280
14.4	14.3	14.1	14.1	14.1	14.1	14.1	13.6	11.7	9.6	9.5	0.6	9.0	8.5	8.3	8.1
183.5	183	180.5	180	179.5	179.5	179.5	173.5	149	122.5	121	115.5	115.5	108.5	106.5	104
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

		· RESULT 1	
		-glycosidase (BC 3.2.2.22) rnate_names: gelonin; type	precursor - Gelonium multiflorum I ribosome-inactivating protein
		C;Species: Gelonium multillorum C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1	multilorum #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
		Ciaccession: 010/55; Siotes: Rivolan, P.A.; Garrison, D.A.; Better, M.	
	•	Gene 134, 223-227, 1993 A; Title: Cloning and expression of a gene encoding gelonin,	ing gelonin, a ribosome-inactivating prote
		A;Reterence number: JT0753; MUID:94085781; PMID A;Accession: JT0753	:7916721
		A;Molecule type: mRNA A:Residues: 1-316 <nol></nol>	
		A,Cross-references: UNIPROT: P33186; GB:L12243; NID:9388633;	
		k;Montecuccni, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, Int. J. Pept. Protein Res. 33, 263-267, 1989	L.; SCITPE, F.; SOTIA, M.; LADDI, U.
		A; Title: N-terminal sequence of some ribosome-inactivating proteins A; Reference number: \$16331; MUID:89326691; PMID:2753596	nactivating proteins. :2753596
		A; Accession: S16489	
		A;Molecule type: procein A;Residues: 47-89,'K',91-92,'D' <mon></mon>	
		C;Function:	
		A;Description; hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA there C;Superfamily: rRNA N-qlycosidase; rRNA N-qlycosidase homology	ot a specific adenosine in 285 rRNA there sidase homology
•		C; Keywords: glycosidase; hydrolase P:1-46/Domain: signal semience #status predicte	7010
		F:47-216/Product: ribosomal RNA N-glycosidase #status predicted P:53-294/Domain: rRNA N-glycosidase #status predicted	status predicted <mat></mat>
		The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon	
		Query Match 99.4%; Score 1269; DB 2; Best Local Similarity 99.2%; Pred. No. 1.1e-96; Matches 249; Conservative 0; Mismatches	DB 2; Length 316; e-96; 2; Indels 0; Gaps 0;
		Qy 1 GLDTVSFSTKGATY1TYVNFLNELRVKLKPEGNSHGI PLLRKKADDPGKAFVLVALSNDN	SHGIPLLRKKADDPGKAFVLVALSNDN 60
		Db 47 GLDTVSFSTKGATYITTYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN	
		Qy 61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	AYEGLEKNTIKTRLHFGGSYPSLEGEK 120
		Db 107 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK	AYEGLFKUTIKTRLHFGGSYPSLEGEK 166
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		Db 167 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN	ASSLLVVIQMVSEAARFTFIENQIRNN 226
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		Db 227 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI	FSEAVELERANGKKYYVTAVDQVKPKI 286
		Qy 241 ALLKFVDKDPK 251	

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**Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 12-75,'D',77-550,'R',552-576 <LAM>
A; Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078
R; Yoshitake, S.; Funateu, G.; Funateu, M.
Agrite: Biol. Chem. 42, 1267-1274, 1978
A; Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile challs. A; Reference number: A03372
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A)Residues: 36-97, 'Q', 99-109, 'S',111-269,'D', 272-283,'L',285-288,290-302 <YOS>
A)Rote: this paper cites the others in the series providing experimental details for the R,Araki, T.; Funatsu, G.
R,Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
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A; Mosidues: 1-576 cHAL>
A; Cross-references: 1-576 cHAL>
A; Cross-references: 1-576 cHAL>
A; Cross-references: J.W.; Roberts, L.M.
B; Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene A; Reference number: $20513; MUID:92163016; PMID:1371405
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C; Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
C; Accession: A24041; S20513; A24614; A03372; A24010; B.F.; Houston, L.L.; Weaver, R.F.
R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A; Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A; Reference number: A24041; MUID:86067214; PMID:2999712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 SVAIDVINVYVVAYRIRDVSYFFKESPPEAYNILFKGIRKITLPYTGNYENLQTAAHKIR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQ 183
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                                                                                                                                                                                                                                                                                                                                                                          5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLDLTSYAYETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 RIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI
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A; Residues: 1-576 <TRE>
A; Residues: 1-576 <TRE>
A; Residues: 1-576 <TRE>
A; Cross-references: EMBL: X52908; NID: 921084; PIDN: CAA37095.1; PID: 921085
B; Lamb, F.I.; Roberts, L.M.; Lord, J.M.
B; Lamb, F.I.; Roberts, L.M.; Lord, J.M.
A; Lien, F.I.; Roberts, L.M.; B55-270, 1985
A; Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A; Reference number: A24614; MUID: 85179479; PMID: 3838723
                                                                                                                                                         ; Score 348; DB 2; Length 28; Pred. No. 4e-21; 34; Mismatches 108; Indels
C;Keywords: glycosidase; hydrolase
F;27-264/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N, Contains: rRNA N-glycosidase (EC 3.2.2.22)
C, Species: Ricinus communis (castor bean)
                                                                                                                                                                    27.3%;
                                                                                                           ricin D precursor - castor bean
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C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
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R;Date: 25-Feb-1994 #text_change 09-Jul-2004
R;Date: 25-Feb-1994
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A; Residues: 1-132, 'S', 134-245 < CHO1>
A; Experimental source: source: sequence in Fig. 2 is inconsistent with the sequence data presented in Table R; Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
Bubmitted to JIPID, August 1995
A; Description: Amino acid sequence of trichoanguina, a ribosomal-inactvating protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from the protein from
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                                                                                                                                                                                                                                                   rRNA N-glycosidase (EC 3.2.2.22) trichoanguina - snake gourd
C;Species: Trichosanthes anguina (snake gourd)
C;Species: Trichosanthes anguina (snake gourd)
C;Date: 15-Aug-1996 #sequence revision 24-Oct-1997 #text_change 05-Dec-1997
C;Accession: JC4840; JT0010; JT0677
R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
Bichow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.
A;Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from A;Reference number: JC4840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-50, I.', 52-245 <CHO2>
A; Residues: 1-50, I.', 52-245 <CHO2>
C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase; phosphoprotein; seed C; Reywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed F; 4-242/Domain: rRNA N-glycosidase homology <RNG>
F; 51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental F; 70,158,161/Active site: Tyr, Glu, Arg #status predicted F; 155/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
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Best Local Similarity
Matches 90; Conserv
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A;Rutenber, E.; Robertus, J.D.
A;Contents: annotation; Active site
A;Rutenber, E.; Robertus, J.D.
A;Rutenber, E.; Robertus, J.D.
A;Rutenber, Structure of ricin B-chain at 2.5 angstroms
A;Reference number: A40238; MUID:91322005; PMID:1881882
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
R;Reference number: A40239; MUID:91322004; PMID:1881881
A;Reference number: A40239; MUID:9132004; PMID:1881881
A;Reference number: A40239; MUID:9132004; PMID:1881881
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains at C;Comment: The A chain; B chains are also responsible for cell agglutination (1cti) C;Comment: The A chain; B chains are also responsible for cell agglutination (1cti) C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is equence #status experimental <AH>F;145,000<br/>F;145,000<br/>F;145,409,449/Bainding site: carbohydrate (Asn) (covalent) #status experimental F;115,158,243,244|Bainding site: carbohydrate (Asn) (covalent) #status experimental F;115,158,243,244|Bainding site: carbohydrate (Asn) (covalent) #status experimental F;215/Active site: Ang #status experimental F;215/Active site: Ang #status experimental Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Apple Ap
                                                                                                                                             A Accession: A03374
Apolecule type: protein: A03374
A; Rosidues: 315-335, 'W', 337-342,'NH', 345-362,364-383,'PS',386-399,'T',401,'D',403,'E',40
527,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
A; Note: this paper, one of a series, summarizes the experimental details for the determing R; Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991 antagenesis of ricin A-chain and implications for the mechanism of A; Reference number: A48237; MUID: 91352006; PMID:1881883
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1548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental
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JC4235
rRNA N-glycosidase (EC 3.2.2.22) map30 precursor - balsam pear
N;Alternate names: ant1-HIV 30K protein
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Punatsu, G.; Kimura, M.; Punatsu, M.
gric. Biol. Chem. 43, 2221-2224, 1979
Title: Primary structure of Ala chain of ricin D.
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VSILIPIIALMVY 292
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                                      Agric. Biol. Chem. 43, 222.
A,Title: Primary structure
A,Reference number: A03374
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Best Local Similarity
Matches 93; Conserva
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Kung
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A,Molecule type: protein
A,Residues: 24-36,'T',38-66,'P' <LEW>
C;Comment: This plant protein has anti-HIV activity. It possesses antiviral action, antiactivation activities. It is capable of acting against multiple stages of the viral life C;Comment: This protein has conserved unique residues Trp-213 and Met-277.
                                                                                                                                                                                                                                                                                                                                                                  for residue 16
                                                                                                                                                                                                                                                                                                                                                                                             Huang, H.I.; h
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Molecule type: mRNA
A;Residues: 1-564 cROB>
A;Cross-references: UNIPROT:P06750; GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701
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N;Contains: rRNA N-glycosidase (EC 3.2.2.2.2)

C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A24261; A24210
C;Accession: A24261; A24210
C;Accession: A24261; A24210
J. Biol. Chem. 260, 15682-15686, 1995
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin. A;Reference number: A24261; MUID:86059449; PMID:2999130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :24-286/Product: TRNA N-glycosidase (EC 3.2.2.22) map30 #status predicted <MAT>:27-264/Domain: rRNA N-glycosidase homology <RNG>
:77-264/Domain: rRNA N-glycosidase homology <RNG>
:74/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 RIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 BIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLNLTSYAYETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: map30
C;Superfamily: rRNA N-glycosidase, rRNA N-glycosidase homology
C;Superfamily: rRNA N-glycosidase, rgycosidase, hydrolase
C;Keywords: antiviral; glycoprotein; glycosidase, hydrolase
F;1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;93,181,184/Active site: Tyr, Glu, Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 26.9%; Score 343; DB 2; Similarity 37.0%; Pred. No. 1e-20; 90; Conservative 34; Mismatches 109;
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234 DOVKPKIALLKFVDKDP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 HOSVAVLALMLFVCNPP 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.2%
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                        A; Reterence number: A24210
A; Reterence number: A24210
A; Resession: A24210
A; Resession: A24210
A; Resession: A24210
A; Resession: A24210
A; Residues: 30.325; F; 327-330, T', 332-361, D', 363-373, G', 375-403, T', 405-551, V', 553-67, C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compared c; Superfamily: ricin; rRNA N-glycosidase homology
C; Superfamily: ricin; rRNA N-glycosidase homology cs Cs G'G's
F; 1-24/Domain: RNA N-glycosidase homology cs Cs G'G's
F; 35-280/Product: agglutinin chain A #status predicted cACH>
F; 319-361/Jonain: rRNA N-glycosidase homology cs RNG>
F; 319-361/Jonain: rRNA N-glycosidase homology cs Cs G'G's
F; 319-361/Jonain: rRNA N-glycosidase homology cs RNG>
F; 319-361/Jonain: rRNA N-glycosidase homology cs RNG>
F; 319-361/Jonain: rRNA N-glycosidase homology cs RNG>
F; 319-361/Jonain: RNA N-glycosidase homology cs RNG>
F; 319-361/Jonainin chain B #status predicted
F; 319-361/Jonainin site: substrate (Asn) (covalent) #status predicted
F; 320,203/Active site: Glu, Arg #status predicted
F; 320,203/Active site: Glu, Arg #status predicted
F; 324,337,348/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F; 356,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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A; Residues: 1-527 < HUNA
A; Residues: 1-527 < HUNA
A; Residues: 1-527 < HUNA
A; Cross-references: UNIPROT: Q06077; GB: M98345; NID: g166296; PIDN: AAA32625.1; PID: g166297
R; Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A; Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A; Reference number: UC1399; MUID: 93169023; PMID: 7763422
R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti
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A;Residues: 260-281, D', 283-290, N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-436
A;Residues: 260-281, D', 286-666
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p
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C;Species: Abrus precatorius (Indian licorice)
C;Species: 30-8ep-1993 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S32430; JC1399
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 253-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. A;Reference number: S32429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVTLALDVTNAYVVGCRAGNSAYFFH--PDNQEDAEAITHLFTDVQNSFTFAFGGNYDRI 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGEKAYRETTDIGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 IRN--NFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAEIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKT-RLHFGGSYPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 VSFSTKGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.4%; Score 337.5; DB 1; Length 564; 36.3%; Pred. No. 7.2e-20; tive 42; Mismatches 105; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abrin-b precursor - Indian licorice (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVKPKIALLKF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 ILIPITALMVY 280
                                                                                            Reference number: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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Nylternate names: antiviral protein alpha-PAP
C;Species: Phytolacca americana (Virginian pokeweed)
C;Species: Phytolacca americana (Virginian pokeweed)
C;Species: Phytolacca americana (Virginian pokeweed)
C;Species: Phytolacca americana (Virginian pokeweed)
C;Species: Phytolacca americana (Virginian pokeweed)
C;Species: Sp413
R;Kataoka, J; Habuka, N; Masuta, C; Miyano, M; Koiwai, A.
B;Ant Mol. Biol. 20, 879-886; 1992
A;Tile: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein.
A;Reference number: S28421; MUID: 9309240; PMID:1281438
A;Reference number: S28421; MUID: 9309240; PMID:1281438
A;Residues: 1-294 <KAT>
A;Cross-references: UNIPROT: 003464; EMBL: D10600; NID: 9218010; PIDN: BAA01451.1; PID: 921801
C;Superfeanily: TRNA N-91ycosidase; rRNA N-91ycosidase homology <RNG>
F;30-278/Domain: rRNA N-91ycosidase homology <RNG>
F:1-250/Product: abrin-b chain A #status predicted <ACH>
F;7-245/Domain: rRNA N-glycosidase homology <RNG>
F;260-527/Product: abrin-b chain B #status experimental <BCH>
F;282-334,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F;7/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;7/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;7/Modified site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;7/Modified site: carbohydrate (Ann) (covalent) #status predicted
F;10,360,400/Binding site: carbohydrate (Ann) (covalent) #status predicted
F;181,166/Active site: Glu, Arg #status predicted
F;262-268,285-304,328-345,416-429,455-412/Disulfide bonds: #status predicted
F;287,311/Binding site: N-acetylgalactosamine (Asp. Ann) #sratus predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 ARQTRQQIPLGLQALRHAISFLQSGTDDQ----BIARTLIVIIQMASBAARYRFISYRVG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 VSEAARFTFIENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --IRNNFQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV- 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 LKTITLMLKRNNLYVMGYADTYNGKCRYHIFKDISNTTE----RNDVMTTLCPNPSSRVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRKKRADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---HFGGSYPSLEGEKAY-RETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                 P;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP----GKAFVLVALSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.2%; Score 334.5; DB 2; Length 527; Best Local Similarity 37.7%; Pred. No. 1.2e-19; Matches 97; Conservative 34; Mismatches 103; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
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A; Molecule type: DNA
A; Residues: 1-313 <LIN>
A; Molecule type: DNA
A; Residues: 1-313 <LIN>
A; Residues: 1-313 <LIN>
A; Residues: 1-313 <LIN>
A; Residues: 1-313 <LIN>
A; Residues: 1-313 <LIN>
A; Residues: UNIPROT: P10297; EMBL: X55383; NID: g20421; PIDN: CAA39054.1; PID: g20422
B; Barbieri, L.; Bolognesi, A.; Cenini, P.; Falasca, A.I.; Minghetti, A.; Garofano, L.; G
B; Biochem. J. 257, 801-807, 1989
A; Ricession: S02792
A; Rocession: S02792
A; Mulc. Biophys: Acresion: S02792
A; Molecule type: protein
A; Residues: 23-55, X, 57-65 < BAR>
B; Ribolognesi, A.; Barbieri, L.; Abbondanza, A.; Falasca, A.I.; Carnicelli, D.; Battelli, A. Biochim. Biophys. Acra 1087, 293-302, 1990
A; Ribolognesi, A.; Barbieri, L.; Abbondanza, A.; Falasca, A.I.; Carnicelli, D.; Battelli, A. Biochim. Biophys. Acra 1087, 293-302, 1990
A; Ribolognesi, A.; Barbieri, Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. B
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Bjochim. Biophys. Acta 790, 154-163, 1984
A,Title: Characterization of translational inhibitors from Phytolacca americana. Amino-te
A,Reference number: S32610; MUID:85023392; PMID:6091760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N'Alternate names: alpha-TCS; type I ribosome-inactivating protein of Species: Trichosanthes Krillohii (Mongolian snake-gourd)
Sypecies: Trichosanthes Krillohii (Mongolian snake-gourd)
Sypecies: Trichosanthes Krillohii (Mongolian snake-gourd)
C;Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text_change 09-Jul-2004
C;Accession: UT0566; A36274; \(\tilde{J}\)C1093; A36273; \(\tilde{J}\)T0003
R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
Gene 97, 267-272, 1991
A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
A;Reference number: JT0566; MUID:91153657; PMID:1999291
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A;Experimental source: tuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEXMINEDSRYPTLESKAGVKSRSQVQLGIQILDSNIGKI--SGVMSFTEKTEAEFLLVA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 IQMVSEAARFTFIENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVEL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 IQMVSEAARFKYIENQVKTNFNRAFNPNPKVLNLQETWGKISTAIH-DAKNGVLPKPLEL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Keywords: glycosidase; hydrolase
1-22/Domain: signal sequence #status predicted <SIG>
; 23-313/Product: rRNA N-glycosidase PAP #status experimental <MAT>
; 28-277/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 313;
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A;Reference number: S17757; MUID:92003676; PMID:1912488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.6%; Score 327; DB 2; Le 31.6%; Pred. No. 2.4e-19; tive 49; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 ERANGKKYYVTAVDQVKPKIALLKFV 246
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252 VDASGAKWIVLRVDEIKPDVALLNYV 277
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nes 84; Conservative
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A, Molecule type: protein
A, Residues: 23-54 <BJO>
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R, Bjorn, M.J.; Larrick,
Biochim. Biophys. Acta 7
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A; Molecule type: mRNA
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N;Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-ins
C;Species: Bytolacca americana (Virginian pokeweed)
C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S17757; S02792; $13469; S32611
C;Accession: C, C, Chan, J, Sold Abnoon, J, White, R.F.
Plant Mol. Biol. 17, 609-614, 1991
A;Title: Isolation and characterization of a cDNA clone encoding the anti-viral protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicontains: rRNA N-glycosidase (EC 3.2.2.2)
(Species: Abrus precatorius (Indian licorice)
(Cispecies: Abrus precatorius (Indian licorice)
(Cibate: 21-Feb-1992 #sequence_revision 31-bec-1993 #text_change 09-Jul-2004
(Cibate: 21-Feb-1992 #sequence_revision 31-bec-1993 #text_change 09-Jul-2004
(Cibate: 21-Feb-1992 #sequence_revision 31-bec-1993 #text_change 09-Jul-2004
(Cibate Symposium Cibate Symposium A. Biol. Chem. 266, 6848-6852, 1991
(A) Fitch: Direct molecular cloning and expression of two distinct abrin A-chains.

A) Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 'M',1-251 <EV2>
A,Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
A,Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C,Superfamily: ricin; rRNA N-glycosidase homology
C,Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F;1-251/Product: abrin (clone 7.2) chain A #setuus predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q38760
R;Evensen, G; Mathesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
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; Pred. No. 1e-19;
40; Mismatches 104; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                         C39761
abrin (clone 7.2) precursor - Indian licorice (fragment)
                                                                                                                                                                     NGKKYYVTAVDQVKPKIALLKFVD 247
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1 Similarity 36.5%;
93; Conservative 4
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Best Local Similarity
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Residues: 1-251 <EVE>
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                                           197
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Ny Contains rRNA N-giycosidase (RC 1.2.2.2)
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Cypectes abrus a Bool 1203, 263-267, 1993
Ayritic: Primary structure of three distinct isoabrins determined by CDNA sequencing. Cor Apacession: 512429
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Ayritic: Primary structure of three distinct isoabrins determined by CDNA sequencing (Indian ilcoring a Apacession in Structure of the Abrus and Apacession in Structure of the Abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus abrus a
121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                 143 KIRENIPLGLPALDSAI----TTLFYYNANSAASALMVLIOSTSEAARYKFIEQOIGKR 197
                                                                                                                                                                                                                                                 181 FOORIRPANNTISLENKWGKLSFOIR-TSGANGMFSEAVELERANGKKYYVTAVDQ--VK 237
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A; Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>A; Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>A; Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>A; Residues: 0. Mathiesen, A.; Sundan, A.
B; Evensen, G.; Mathiesen, A.; Sundan, A.
B; Description: Direct molecular cloning of two distinct abrin A-chains.
A; Reference number: S14471
A; Residues: Preliminary
A; Residues: ME', 2-251 < KV2>
A; Residues: ME', 2-251 < KV2>
A; Residues: ME', 2-251 < KV2>
A; Residues: ME', 2-251 < KV2>
A; Residues: ME', 2-251 < KV2>
A; Residues: ME', 2-251 < KV2>
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A; Residues: ME', 2-251 < KV2>
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A,Reference number: S24133, MUID:92371656, PMID:1505674
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A; Cross-references: GB:305444; NID:9170534; PIDN:AAA34206.1; PID:9170535
A; Cross-references: GB:305444; NID:9170534; PIDN:AAA34206.1; PID:9170535
A; Cross-references: GB:305444; NID:9170534; PIDN:AAA34206.1; PID:9170535
A; Aritle: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A; Reference number: JC1093; MUID:94271613; PMID:8003348
A; Reference number: JC1093; MUID:94271613; PMID:8003348
A; Residues: 1-72, 7V', 74-90', S', 92-233, 77', 235-267, D', 269-289 < ZHE>
A; Rocasion: DNA
A; Residues: L-72, 7V', 74-90', S', 92-233, 77', 235-267, D', 269-289 < ZHE>
A; Rocalins: B.J; Robertue, JD: Lobresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
J. Biol. Chem. 265, 8665-8669, 1990
A; Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abr
A; Residues: 24-270 < COLD.
A; Residues: 24-270 < COLD.
A; Residues: 24-270 < COLD.
A; Residues: 24-270 < COLD.
A; Residues: 24-250 < COLD.
A; Residues: 24-250 < COLD.
A; Residues: 24-250 < COLD.
A; Residues: 24-36, 1980
A; Title: Scientific evaluation of Tian Hua Pen (THP): history, chemistry and application
A; Recession: JT0003
A; Roll of the Brookhaven Protein Data Bank, July 1994
A; Residues: 24-56, 11, 58-59, 17', 61-71, 17, 73-81, 85-86, 12', 88-92, DAGLPRNAVL', 93-142, GL'
A; Residues: 24-56, 11, 58-59, 17', 61-71, 17, 73-81, 85-86, 12', 88-92, 1003
A; Roll of the Brookhaven Protein Data Bank, July 1994
A; Contents a annotation: A; Residues: A; Angerroe number: Afordy Protein Data Bank, July 1994
A; Contents a annotation: A; Residues: A; Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: Angerroe number: An
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A; Contents: annotation; X: x; Wang, Y:

R; Xiong, J.P.; Xia, Z.X.; Wang, Y:

Submitted to the Brookhaven Protein Data Bank, December 1994

A; Reference number: A66711; PDB: 1TCS

A; Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27

B; Xiong, J.P.; Xia, Z.X.; Wang, Y:

Nat. Struct. Biol. 1, 695-700, 1994

A; Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution red

A; Reference number: A56622; MUID: 95360714; PMID: 7634073

A; Contents: annotation; X-ray crystallography, 1.7 angstroms

C; Genetics:
A; Contents: annotation; X-ray crystallography, 1.7 angstroms

C; Genetics:
A; Contents: annotation; X-ray crystallography, 1.7 angstroms

C; Genetics:
A; Contents: annotation; X-ray crystallography, 1.7 angstroms

C; Genetics:
A; Comment: Alpha-trichosanthin has been used to induce abortions.
A; Description: hydrolyzes the N-glycosidase; hodrolase, root; toxin

C; Superfamily: RRNA N-glycosidase; Nath N-glycosidase; noot; toxin

B; 1-23/Domain: signal sequence #status predicted <SIG>
F; 27-266/Domain: rRNA N-glycosidase homology <RNG>
F; 27-266/Domain: rRNA N-glycosidase homology <RNG>
F; 27-266/Domain: rRNA N-glycosidase homology <RNG>
F; 271-286/Domain: rRNA N-glycosidase homology <RNG </br>
                                                  J. Biol. Chem. 265, 8670-8674, 1990
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rit
A;Reference number: A36274; MUID:90256790; PMID:2341400
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Pred. No. 4.5e-19;
      Feldman, R.A.; Lovett, M.; Piatak, M.
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Best Local Similarity
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Cispecies: Trichosanthes kirilowii var. japonica
Cispecies: Trichosanthes kirilowii var. japonica
Cibaccession: JC5606; JC5033
R;Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-289 <MIZ>
A; Residues: 1-289 <MIZ>
A; Residues: 1-289 <MIZ>
A; Residues: UNIPROT: P24478; DDBJ: AB000666; NID: g2329830; PIDN: BAA21786.1; PID: g2:
A; Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A; Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and kara; Reference number: JC5032; MUID: 97108848; PMID: 8951169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abortificomment: This protein belongs to type I ribosomal-inactivating proteins which catalytic Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
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                                                                                                                                                                                                                                           64 AEIAIDVTSVYVVGYQVRNRSYFFKDA-PDAAYEGLFKNT-IKTRLHFGGSYPSLE-GEK 120
                                                                                                                                                                                                                                                                                                                                                         121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENOIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                             181 FQQRIRPANNTISLENKWGKLSFQIR-TSGANGMFSEAVELERANGKKYYVTAVDQ--VK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 AEIAIDVTSVYVVGYQVRNRSYFFKDA-PDAAYEGLFKNT-IKTRLHFGGSYPSLE-GEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 KIRENIPLGLPALDSAI----TTLFYYNANSAASALMVLIOSTSEAARYKFIEQQIGKR 197
                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 VDKTFLPSLAIIŚLENSWSALSKQIQIASTNNGQFETPVVLINAQNQRVTITNVDAGVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPG-KAFVLVALSNDNGQL
                                                                                                                             5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPG-KAFVLVALSNDNGQL
                                                                                                                                                                                 2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTL--PGSQRYALIHLTNYADET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 VSFRLSGATSSSYGVFISNLRKALPYBRKLYDIPLLRSTL--PGSQRYALIHLTNYADET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 289;
                                                                   33; Mismatches 105; Indels
               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.8%; Score 317; DB 2; Lv 38.2%; Pred. No. 1.4e-18; ive 33; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122-270/Product: Karasurin C #status predicted cMAC>
124-270/Product: Karasurin A #status predicted cMAA>
127-266/Domain: rRNA N-glycosidase homology cRNG>
            24.8%; Score 317; DB 2; 38.2%; Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          karasurin C - Trichosanthes kirilowii var. japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 38.2 tes 94; Conservative
                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 22-270 < KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 PKIALL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 SNIALL 240
         Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contains: karasurin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: JC5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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                                                                                                                                                                                                                                                                                  Caracteria: Trichosanthes Kirilowii (Mongolian snake-gourd)
C;Species: Trichosanthes Kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Dates: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: U0333; PS0163
Chem. Pharm. Bull. 39, 1244-1249, 1991
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A;Reference number: JU0393; MUID:92005921; PMID:1914000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 DTESIEVGIDVTNAYVVAYRAGTOSYFLRDAPSSASDYLFTGTDOHSLPFYGTYGDLERW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 AHOSRQOIPLGLQALTHGISFFRSGGNDN---EEKARTLIVIIQMVAEAARFRYISNRVR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 VSIQTGTAFQPDAAMISLENNWDNLSRGVQES-VQDTFPNQVTLTNIRNEPVIVDSLSHP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-----GKAFVLVALSND 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;361,401/Binding site: carbohydrate (ABD) (covalent) #status caparater F;500,521/Binding site: N-acetylgalactosamine (ABD, ABD) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F;361,401/Binding site: carbohydrate (Asn) (covalent) #status experimental
A;Residues: 262-297, Y', 299-426, 'L', 428-466,'P', 468-482,'L', 484-528 < CHE>
R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Biochem. 240, 564-569, 1996
A;Title: Probing the domain structure of abrin-a by tryptic digestion.
A;Reference number: S74110; MUID:97008945; PMID:8856055
A;Accession: S74110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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A;Note: a sequence which lacks Ala-247 is also shown in this publication
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.1%; Score 321; DB 1; Length 528; 35.7%; Pred. No. 1.5e-18; Live 39; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Kerwords: abortifacient
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKPKIALLKFVDKDP 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         karasurin - Mongolian snake-gourd
                                                                                                                                                                              Molecule type: protein
*Residues: 89-108;154-172 <LIN>
*Experimental source: seed
*Accession: S74111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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A.Residues: 17.61 cKUN>
A.Cross-references: UNIPROT:P23339
A.Cross-references: UNIPROT:P23339
A.Experimental source: seed
C.Comment: This protein prevents the replication of a number of plant viruses, and inhib C.Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C.Superfamily: rRNA N-glycosidase homology cRNOs
F.6-254/Domain: rRNA N-glycosidase homology cRNOs
F.10,44,255/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.34-258,84-105/Disulfide bonds: #status experimental
                                                                                                                                                                                                             antiviral protein - Virginian pokeweed
Cispecies: Phytolacca americana (Virginian pokeweed)
Cipate: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
CiAccession: JEG401
R;Kung, S.S.; Kimura, M.; Funatsu, G.
A;Title: The complete amino acid sequence of antiviral protein from the seeds of pokewee
A;Reference number: JEG401; MUID:91242096; PMID:1368643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGSYPSLEGEKA---YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EAARFTFIENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 VDKTFLPSLAIISLENSWSALSKQIQIASTNNGQFETPVVLINAQNQRVTITNVDAGVVT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRKKADDPGKAFVLVALSNDN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.5%; Score 313.5; DB 2; Length 261; Best Local Similarity 32.4%; Pred. No. 2.4e-18; Matches 85; Conservative 49; Mismatches 105; Indels 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: June 20, 2005, 09:21:38 Job time : 26.5 secs
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TKWIVLRVDEIKPDVGLLNYVN 255
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                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: JE0401
A;Molecule type: protein
                                               238 PKIALL 243
                                                                                            SNIALL 263
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 20, 2005, 09:00:50 ; Search time 114.5 Seconds (without alignments) 1122.549 Million cell updates/sec Run on:

US-10-717-243-101 1277 1-GLDTVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Q8gv09 gynostemma Q41216 trichosanth Q8h1y4 jqrnostemma Q88452 jatropha cu G66267 viscum albu Q8gv11 gynostemma P09989 trichosanth Q9484 trichosanth Q9484 trichosanth Q9481 sambucus ni Q4071 sambucus ni Q4611 sambucus ni Q4611 sabrus preca Q138761 abrus preca Q11140 abrus preca P11140 abrus preca
Q8CV09 Q41216 Q41216 Q814124 Q8S452 Q6GV11 RIPT_TRIKI Q94KE4 Q04071 Q70M12 Q73761 ABRA_ABRPR
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277 289 289 289 289 289 252 252 253
8 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
326.5 325.5 325.5 325.5 325.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5 323.5
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## ALIGNMENTS

STANDARD; (Rel. 27, Creat	01-NOV-1995 (Rel. 32, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Ribosome-inactivating protein gelonin precursor (EC 3.2.2.22) (rRNA N-glycosidase) Name=GEL;	ta; Te euddeae; deae;	Lonning and expression of a gene encoding genomin, a ribosome-inactivating protein from Gelonium multiflorum.";  Gene 134:223-227(1993).  Gene 134:223-227(1993).  SEQUENCE OF 47-93.  SEQUENCE OF 47-93.  MEDLINE-899326691; PubMed=2753596;  MEDLINE-899326691; PubMed=2753596;  MEDLINE-899326691; PubMed=2753596;  MEDLINE-899326691; PubMed=2753596;  MACHEURINE SEQUENCE OF SOME ribosome-inactivating proteins.";  "N-terminal sequence of some ribosome-inactivating proteins.";  "N-terminal Reguence of Some ribosome-inactivating proteins.";	X.FAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  X.FAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).  MEDLINE=95333189; PubMed=7608981;  Mesur M.V., Nair B., Satyamurthy P., Misquith S., Surolia A.,  Kannan K.K.;  Xray structure of gelonin at 1.8-A resolution.";  J. Mol. Biol. 250:368-380(1995).  -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S rRNA.  -!- SUBDNIT: Homodimer.  -!- SUBDNIT: Homodimer.  -!- SUBLIMARITY: Belongs to the ribosome-inactivating protein family Type 1 RIP subfamily.	ight f Bi stit ons not reem	* * * * * * * * * * * * * * * * * * *
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WEDLINE=2188635; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;

X Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;

Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;

RT "Studies of three genes encoding Cinnamomin (a type II RIP) isolated

RT "Studies of camphor tree and their expression patterns.";

Gene 284:215-223(2002).

The CATALIYIT ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

C. -: AMILARITY: Belongs to the ribosome-inactivating protein family.

ENEL; AY039801; AAR82458.1; -.

DR ROSS; PO2879; ZAAI.

GO; GO:0006782; F:hydrolase activity; IEA.

GO; GO:0006922; Piedfense response; IEA.

GO; GO:0006929; F:rRNA N-glycosylase activity; IEA.

GO; GO:0006929; Piedfense response; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR000972; Ricin B like.

InterPro; IPR000772; Ricin B lectin.

PEam; PF00062; Ricin B lectin.

PEam; PF00065; RIP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 IENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GQLABIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTI-----KTRLHFGGS 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 YPSLEGEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTF 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKNPLLFGGKTRLHFGGS
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PROSITE; PSS0231; RICIN B_LECTIN; 2.
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
1 32 Potential.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, magnoliids, Laurales, Lauraceae;
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                                                                                                                                                                                                                                                       Query Match

96.8%; Score 1235.5; DB 2; Length 258;
Best Local Similarity 95.4%; Pred. No. 2.4e-92;
Matches 247; Conservative 1; Mismatches 2; Indels 9;
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;
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01-067-2003 (TrEMBLrel. 25, Last annotation update)
17pe 2 ribosome-inactivating protein cinnamomin I precursor.
Cinnamomum camphora (Camphor tree)
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Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
Rosenblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
Toman P.D., Cheung L.;
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                                      InterPro; IPR001574; RIP.
PREM; PR00161; RIP; 1.
PRINTS; PR00196; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN; FALSE NEG.
Direct protein sequencing; Glycoprotein; Hydrolase; Plant defense;
Protein synthesis inhibitor; Signal; Toxin.
SIGNAL
SIGNAL
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Ribosome-inactivating protei
316
Removed in mature form.
96
N-linked (GlCNAc. . .).
212
C -> K (in Ref. 2).
93
P -> D (in Ref. 2).
93
P -> D (in Ref. 2).
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P -> D (in Ref. 2).
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P -> D (in Ref. 2).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
TRNA -glycosidase (EC 3.2.2.22) (TRNA N-glycosidase)
Gelonium multiflorum (Euphorbiaceae himalaya)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1269; DB 1;
Pred. No. 5.8e-95;
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0; Mismatches
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298
235
212
90
90
93
316 AA;
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       HSSP; P09989; 1MRJ
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DISULFID
CARBOHYD
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CONFLICT
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Q9S9E4

RESULT 2

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234 -DOVKPKIALLKFV 246
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269 SDRVISGLAIMLFI 282
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Matches 100; Conservative
                         101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
Best Local Similarity
Matches 101; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   153 VAGERREIILLGMDPLENAISALWISNINQQR--ALARSLIVVIQMVAEAVRFRFIEYRV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 RGSISRAEMFRPDPAMLSLENKWSALSNAVQQSNQGVFSSPVELRSISNKPVYVGSVSD 270
                                                                                                                                                                                                                                                                    60 NGQLABIAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLEG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 RNNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV-D 234
                                                                                                                                                                                                                                                                                                                                                                    119 EKA-YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQI 177
                                                                                                                                                                                                                      94
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-I. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.

-I. SIMILARITY: Belongs to the ribosome-inactivating protein family. HSSP; P02879; 2AAI.
                                                                                                                                                                                                    4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-GKAFVLVALSN---D
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231, RICINB BLECTIN; 2.
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
                                                                                                                           Gaps
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GO; GO:0030598; FirkNA N-glycosylase activity; IEA.
GO; GO:00006952; Pidefense response; IEA.
GO; GO:0017148; Pinegative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Type 2 ribosome-inactivating protein cinnamomin III precursor. Cinnamomum camphora (Camphor tree). Subtryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              type 2 ribosome-inactivating protein
                                                                                                                         13;
                                                                     Query Match 31.2%; Score 398.5; DB 2; Length 581; Best Local Similarity 39.7%; Pred. No. 7.8e-24; Matches 100; Conservative 46; Mismatches 93; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 580;
cinnamomin I.
6E8F5FB8FBA3D196 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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InterPro; IPR000972; RicinB like.
InterPro; IPR000174; RicinB_lectin.
Pfam; PF00052; Ricin B_lectin; 6.
Pfam; PF00161; RIP; I.
                         64215 MW;
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271 RVISGLAIMLFI 282
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                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 QIRNNF--QQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV 233
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALXTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNN.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AF259548; AAF68978.2; -.
HSSP; P02879; 2AAI.
                                                                                                                                   3 TVIFITEKKATKISYIQFIEALRAQLASGEEPHGIPVWRERSIVPDSKRFILVELSNWAAD
                                                                                              4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDP-GKAFVLVALSN---D
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GO; GO:0030558; F:rRNA N-glycosylase activity; IEA.
GO; GO:000592; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008997; RicinB_like.
InterPro; IPR000772; RicinB_like.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
Cinnamomum.
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Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SW00458; RICIN, 2.
PROSITE; PS50231; RICIN B LECTIN, 2.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type II ribosome-inactivating protein cinnamomin (Fragment).
39.8%; Pred. No. 9.4e-24; ive 47; Mismatches 89; Indels
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SP--VALAVDVTNAYVVAYRTGSQSFFLREDNPDPAIENLLPDTKRYTFPPSGSYTDLER 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3; Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.; "Studies of three genes encoding Cinnamomin (a type II RIP) isolated from the seeds of camphor tree and their expression patterns."; Gene 284:215-223(2002).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
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PRINTS; PR0036; SHIGHZIN.
SMART; SM0458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
Pydrolase; Plant defense; Protein Synthesis inhibitor; Signal; Toxin.
   179 NNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKP
                                      203 NNLLDEYKPKNDTISYENNWEKLSEQIQLSGTDGKFKKPVTLLYANGTDKIVSTVAQVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific adenosine on the 28S rRNA.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
HSSP; P02879; 2AAI.
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GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0010598; F:rRNA N-glycosylase activity; IEA.

GO; GO:0010598; F:rRNA N-glycosylase activity; IEA.

GO; GO:0006952; P:defense response; IEA.

GO; GO:0007408; P:negative regulation of protein biosynthesis; IEA.

GO; GO:0009405; P:pathogenesis; IEA.

InterPro; IPR008997; RicinB_like.

InterPro; IPR001574; RIP.

InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
11-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin II precursor.
Cinnamomum camphora (Camphor tree).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type 2 ribosome-inactivating protein cinnamomin II.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.6%; Score 390.5; DB 2 39.8%; Pred. No. 3.5e-23;
                                                                                                                                                                                                                                                                                                                                                                         580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                     239 KIALLKF 245
                                                                                                                                                                               |::| :
263 DISILLY 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101;
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                                                               234
                                                                                                                                                                                                                                       LA-EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKA 121
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SP--VTLAVDVTNAYVVAYRTGSQSFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLEG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Girbes T., Arias F.J., Benvenuto E.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| | : | | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                    RNNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Malpighiales, Euphorbiaceae, Euphorbioideae, Euphorbieae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO; GO:00030598; F:RTRNA N-giycosylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:001148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the ribosome-inactivating protein family EMBL; AF457875; AA015531.1; -. HSSP; Q9AVR2; 1HWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosome inactivating protein Buserratin 2 precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 AA; 33115 MW; DE791872B9CE2A7D CRC64;
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RVISGLAIMLFI 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euphorbia serrata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=196589;
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88 KRIVILALIVLNVÝVIGÝKSGIKSFFLKDAPSDAKTLLFTDŤIPKTLEVDINÝNNĽ-GD- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AYRETTDLGIEPLRIGIKKLDENAIDNYK-PTEIASSLLVVIOMVSEAARFTFIENQIRN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 NFQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GLLTQYLPKPDTISYQNNWSALSKSIQLADANGRLSESVTLKYEDGKDRVVFWVEQVQRD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKAD--DPGKAFVLVALSN-DN 60
                                                                                                                                                                                                                                                                                Girbes T., Arias F.J., Benvenuto E.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- CARALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AF457874; AAO15530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RSKVGLGIPALKNAINIL--NQFDGVSTDQDFKHSLLIVIQMVSEAARFKFIQLKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 TVKFTTHLASVGSYQTLMSALRVNLESKLESHNIPLLRKPSDITDQNK-YLLVELTNYDT
                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Malpighiales, Euphorbiaceae, Euphorbioideae, Euphorbieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosome inactivating protein Euserratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P33183; P33184; P93542;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Nigrin b precursor (Agglutinin V) (SNAV) (Contains: Nigrin b A chain (EC 3.2.22) (rRNA N-91ycosidase); Nigrin b B chain].
Sambucus nigra (European elder).
                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P33185; 1BRY.
GO; GO:0015798; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005952; P:defense response; IEA.
GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 AA; 33146 MW; A5269E1DDB91287A CRC64;
  1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1bosome inactivating protein Euserratin 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.2%; Score 359.5; DB 2
39.8%; Pred. No. 4.9e-21;
tive 40; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 39.8
Hes 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 İSLLLY 267
                                                                                                               Euphorbia serrata.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                   NCBI_TaxID=196589;
                                                                                        Name=Eus1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LE-GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       our-mak-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Type 2 ribosome-inactivating protein Nigrin 1 (EC 3.2.2.22).
Sambucus nigra (Buropean elder).
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, asterids, campanulids, Dipsacales, Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Girbes T., Arias F.J., Antolin P.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AF249280; AAN86130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLD--TVSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKADDPGKA-FVLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO; GO:0005958; F:rRNA N-glycosylase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0005975; P:defense response; IEA.
GO; GO:001448; P:negative response; IEA.
GO; GO:000405; P:pathogenesis; IEA.
InterPro; IPR000977; RicinB like.
InterPro; IPR000977; RicinB like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 28.6%; Score 365.5; DB 2; Length 563; l Similarity 41.0%; Pred. No. 3.6e-21; 94; Conservative 38; Mismatches 80; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 NOIRNNFQO--RIRPANNTISLENKWGKLSFQIRTSGAN-GMFSEAVEL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563 AA; 62173 MW; 0EB236421FC5E04F CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)
-DQVKPKIALLKFV 246
                        |:| :|:|
|SDRVISGLAIMLFI 282
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                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE

Query Match

Matches

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Q8GZP0

RESULT 9
Q8GZP0
ID Q8GZI
AC Q8GZI
DT 01-M

7;

11; Gaps

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TISSUE=Leaf
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CARBOHYD
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CARBOHYD
CARBOHYD
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                        DISULFID
                                               DISULFID
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                                                                                                                  TISSUE=Bark;
MEDLINE=96215449; PubMed=8647092;
Wan Damme B.J.; Barre A., Rouge P., Van Leuven F., Peumans W.J.;
Van Damme E.J.; Barre A., Rouge P., Van Sambucus nigra agglutinin V
"Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GalNAG-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
Eur. J. Biochem. 237:505-513(1996).
                                                                                                                                                                                                                                                                                                                                                                                 Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.; "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus nigra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Direct protein sequencing; Glycoprotein; Hydrolase; Lectin;
Plant defense; Protein synthesis inhibitor; Repeat; Signal; Toxin.
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Interchain (By similarity).
By similarity.
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Nigrin b B chain.
Ricin B-type lectin 1.
Ricin B-type lectin 2.
                      campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-alpha.
2-beta.
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1-beta.
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InterPro; IPRO00772; Ricin B lectin.
InterPro; IPR008997; RicinB like.
InterPro; IPR001574; Ricin B lectin; 6.
Pfam; PF00161; RIC; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2-gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. 22:1181-1186(1993).
                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94003077; PubMed=8400135;
                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 26-49 AND 298-321.
TISSUE=Bark;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S37382; S37382.
PIR; S37383; S37383.
                                                                                              SEQUENCE FROM N.A.
                                     NCBI_TaxID=4202;
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298
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DISÜLFID
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116 LE-GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 LSNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                        1 GLD--TVSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKADDPGKA-FVLVA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Damme E.J.M.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- CARTALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AF409135; AAL04123.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sambucus nigra (European elder).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophya, Magnoliophyta, eudicotyledons, core eudicots, asterids;
campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGTYEVNGLPVLRRESEVQVKSRFVLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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G0; G0:0015787; FirMA.

G0; G0:0015787; FirMA N-Glycosylase activity; IEA.

G0; G0:00150598; F:RRA N-Glycosylase activity; IEA.

G0; G0:00150598; F:RRA N-Glycosylase activity; IEA.

G0; G0:0015148; P:negative regulation of protein biosynthesis; IEA.

G0; G0:0017148; P:negative regulation of protein biosynthesis; IEA.

InterPro; IPR008997; RicinB like.

InterPro; IPR00172; RicinB like.

InterPro; IPR00157; RicinB like.

Pfam; PF00152; Ricin B lectin; 6.

Pfam; PF00161; RIP; I
                                                  By Similarity.
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                      77; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0231; RICIN_B_LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
SEQUENCE 563 AA; 62242 MW; 07P7CBEDCF33BF10 CRC64;
                                                                                                                                                                                                                                                                                              Length 563;
                                                                                                                                                                                                                                            F250CBE24621BF14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 NQIRNNFQQ--RIRPANNTISLENKWGKLSFQIRTSGAN 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosome-inactivating protein.
                                                                                                                                                                                                                                                                                                 27.9%; Score 356; DB 1;
41.1%; Pred. No. 2.1e-20;
                                                                                                                                                                                                                   -> V (in Ref. 2)
                                                                                                                                                                                                                                                                                                                                                      36; Mismatches
                              similarity
                                                                                                                                                                                                                                                  62300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS, PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                             41.1%;
                                                                                                                                                                                                                                                                                                                                                   90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             Similarity
360
4448
489
321
376
483
537
537
539
563 AA;
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144 116

84

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62 SVAIDVTNVYVVAXRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIR 121
                                                                                                                                   117 E-GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIEN 175
                                                                                                                                                      122 ENIDLGLPALSSAI----TTLFYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSILVVIQMVSEAARFTFIENQIRNNFQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 RIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI
                                                                    SNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSL
     GLD--TVSFSTKGATY1TYVNFLNELR-VKLKPEGNSHGIPLLRKKADDPGK-AFVLVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                Momordica charantia (Bitter gourd) (Balsam pear).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.

NCBI_TaxID=3673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Potential.
264 type I ribosome inactivating protein.
29775 MW; AD9E1175B70521AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,

Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,

Tran Thi Phuong L., Nong Van H.;

"Expression of a gene encoding ribosome inactivating protein from bitter melon (Momordica charantia).",

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10,
                                                                                                                                                                                                                     198 EVRRSLQQTAGFTPNALMLSMENNWSSMSLEVQQSGDNVSPFTGTVQLQ 246
                                                                                                                                                                                                  176 QIRNNFQQR--IRPANNTISLENKWGKLSFQIRTSGAN-GMFSEAVELE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Type I ribosome inactivating protein precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patch 27.3%; Score 348; DB 2; Local Similarity 37.4%; Pred. No. 3.7e-20; Les 91; Conservative 34; Mismatches 108.
                                                                                                                                                                                                                                                                                                                   264 AA
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                    57
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Matches
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Q684J5
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                                                                                                                                 S6 LSNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
                                                                                                                                                    116 LE-GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIE 174
                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; plant 7. 12:125(1126)(11997).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family. EMBL; U76524; AAC15886.1; -.
HSSP; Q9AVR2; 1HWM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosome inactivating protein precursor.
Sambucus nigra (European elder).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Dipaacales; Adoxaceae; Sambucus.
                                                                                       25 GIDYPSVSFNLDGAKSATYRDFLSNLR-KTVATGTYEVNGLPVLRRESEVQVKSRFVLVP
                                                                    1 GLD--TVSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKADDPGKA-FVLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RĪCIN; 1.
Hydrolase; Plant defensē; Protein synthesis inhibitor; Signal; Toxin.
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chain.
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                                       Gaps
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GO; GO: 0016787; F: hydrolase activity; IEA.
GO; GO: 0016787; F: hydrolase activity; IEA.
GO; GO: 0006559; F: F: RNA N-glycosylase activity; IEA.
GO; GO: 0006552; P: defense response; IEA.
GO; GO: 0017148; P: negative response; IEA.
GO; GO: 0004905; P: pathogenesis; IEA.
InterPro; IPR001473; Clathrin propl N.
InterPro; IPR00197; Ricin B. lectin.
InterPro; IPR00172; Ricin B. lectin.
Pfem; PF00652; Ricin B. lectin; 6.
Pfem; PF00161; RIP; I.
                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosome inactivating protein, A s63 ribosome inactivating protein, B 62336 MW, 3ED2B6C08E796205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.6%; Score 352.5; DB 2; Length 563; 39.7%; Pred. No. 4.1e-20; ive 37; Mismatches 86; Indels 15
   ; Score 356; DB 2; Length 563; Pred. No. 2.1e-20; 36; Mismatches 77; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
                                                                                                                                                                                                                                                                                      197 QEVRRSLQQATSFTPNALMLSMENNWSSMSLEIQQAGNN 235
                                                                                                                                                                                                                                                                 175 NQIRNNFQQ--RIRPANNTISLENKWGKLSFQIRTSGAN 211
                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=98112023; PubMed=9450339;
     27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 27.6%;
Best Local Similarity 39.7%;
Matches 91; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00458; RICIN; 2.
                                  90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 :
563 AA;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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AC P24817; Q1257; Q9FSH2; Q9FUV7;
DT 01-MAR-1992 (Rel. 21, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-GCT-2004 (Rel. 44, Last sequence update)
DT 25-GCT-2004 (Rel. 45, Last annotation update)
DE Ribosome-inactivating protein beta-momorcharin precursor (EC 3.2.2.2)
DE (TRNA N-G1YCOSidase) (MAP 30) (B-MMC).

GN Name=MAP30; Synonyms=RIP;
SN Momordica charantis (Bitter gourd) (Balsam pear).
Charantophyra; Magnoliophyta; Embryophyta; Tracheophyta;
C Spermatophyra; Magnoliophyta; eudicotyledons; core eudicots; rosids;
N NCBI TaxID=3673;
N 11
    PubMed=10571185; DOI=10.1016/S0092-8674(00)81529-9;
PubMed=10571185; DOI=10.1016/S0092-8674(00)81529-9;
Wang Y.-X., Neamati N., Jacob J., Palmer I., Stahl S.J., Kaufman J.D., Huang P.L., Huang P.L., Winslow H.E., Pommier Y., Wingfield P.T., Lee-Huang S., Bax A., Torchia D.A.;
"Solution structure of anti-HIV-1 and anti-tumor protein MAP30: structural insights into its multiple functions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acta Crystallogr. D 55:1144-1151(1999).
-!- FUNCTION: Possesses anti-HIV and anti-tumor activities. Inhibits
HIV-1 integrase, irreversibly relax supercoiled DNA and catalyzes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 23-286 FROM N.A.
Wei Y.-F., Cai L.-B., Zhuang W.;
"Cloning rip gene and identification of its resistance to Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A; Lee-Huang P.L., Huang P.L., Chen H.-C., Huang P.L., Bourinbaiar A., Huang H.I., Kung H.-F.; "Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91032105; PubMed=1699801; DOI=10.1016/0014-5793(90)80438-0; Lee-Huang S., Huang P.L., Nara P.L., Chen H.-C., Kung H.-F., Huang P.L.; Huang P.L.; Huang P.L.; Rins H.-F., Huang B.L.; Huang B.L.; Huang B.L.; Huang B.L.; Hawang B.L.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; The max B.C.; Th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=10329776; DOI=10.1107/S0907444999003297;
Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X.;
"Three-dimensional structure of beta-momorcharin at 2.55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quanhong Y., Rihe P., Aisheng X.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A., AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 161:151-156(1995).
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                                                                                                                                  243
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                                                                                                                                  241 ALL
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                                                                                                                                                                                                                                                                                                                                         RESULT 15
RIP3 MOMCH
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123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQ 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 RIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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"Momordin II, a ribosome inactivating protein from Momordica
"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologous to other plant proteins.";
Nucleic Acids Res. 20.4662-4662(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
Type I RIP subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA
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PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Momordica balsamina (Bitter gourd) (Balsam apple).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosome-inactivating protein momordin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Ribosome-inactivating protein momordin II precursor (EC 3.2.2.22)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ii.
By similarity.
; 3B89FF1AE6B25986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93027170; PubMed=1408771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 24, Created)
(Rel. 24, Last seq
(Rel. 44, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (rRNA N-glycosidase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                             241 ALL 243
                                                                                                                                                                                                                237 KLL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                MOMBA
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ID RIP2 MOMBA
DT 01-DBC: DD 01-DBC: DD 01-DBC: DD 00-DBC: DD 00
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                                 CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                              specific adenosine on the 28S rRNA.

PIT: Bound to a branched hexasaccharide.

MINGCELLANBOUS: Manganese or zinc required for enhancing substrate binding rather than catalysis.

MINGCELLANBOUS: The oligosaccharide does not influence the fold of the polypeptide chain and probably does not play a role in the enzymatic function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00275; SHIGA RICIN; 1.
3D-structure; Antiviral; Direct protein sequencing; Glycoprotein;
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
1 23
SIGNAL 1 24 286
Ribosome-inactivating protein beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                      SIMILARITY: Belongs to the ribosome-inactivating protein family. Type 1 RIP subfamily.
double-stranded breakage. Acts also as a ribosome inactivating
                                                                                                                                                          MISCELLANEOUS: Is not toxic to uninfected normal cells as it cannot enter into them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribosome-inactivating protein beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 348; DB 1; Length 286;
; Pred. No. 4.1e-20;
34; Mismatches 108; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6B2DF55A41D8F921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 -> M (in Ref. 35 -> T (in Ref. 55 -> P (in Ref. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D -> E (in Ref.
I -> T (in Ref.
G -> A (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
By similarity.
By similarity.
N-linked (GlcNA/G -> M (in Ref.
Y -> T (in Ref.
                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                   EMBL, S79450; AAB35194.2; -.
EMBL, AF264811; AAG33028.1; -.
EMBL, AX523412; AAS17014.1; -.
EMBL, AJ294541; CAC08217.1; -.
PIR, B61318; B61118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 G
32030 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 27.3%;
1 Similarity 37.4%;
91; Conservative 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1CF5; X-ray; A/B=-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1D8V; NMR; A=-
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Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 AA;
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CONFLICT
SEQUENCE
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CARBOHYD
CONFLICT
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84 SVAIDVTNVYVVAXRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIR 143

65 EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123

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5 VSFSTKGATYITYVNFLNBLRVKLKPBGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA

124 ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQ 183

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Db 259 KLL 261
Search completed: June 20, 2005,
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241 ALL 243

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Search completed: June 20, 2005, 09:20:41 Job time : 114.5 secs loiqzu MnDl8 9009 zinr

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AAW21699
AAW25136
AAP70097
                                                           AAP70838
AAP95639
AAR70827
AAP90079
(without alignments)
829.717 Million cell updates/sec
                                                           GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK
                               June 20, 2005, 09:00:05; Search time 117 Seconds
    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                      OM protein - protein search, using sw model
                                                                         Gapop 10.0 , Gapext 0.5
                                                 US-10-717-243-101
1277
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Sequence Ricin A-c Ricin A-c Ricin A.

Aap50166
Aap70320
Aar30022
Aar30022
Aar30022
Aar3902
Aab19265
Aac24288
Aav21699
Aaw25136
Aap70838
Aap70838
Aag78304
Aag78304
Aag78304
Aag78304
Aaw25583

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Ricin

Sequence Ricin A f Ricin A c Ricin A-c Amino aci aci

Sequence Ricin A e Anti-cata

Castorbea Ricin D. Modified Sequence

## ALIGNMENTS

AAG78304 AAP70326 AAW25787

2105692

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*

Database

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:*

geneseqp2004s:*

2105692 segs, 386760381 residues

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

AAR63914 standard; protein; 251 AA AAR63914; RESULT 1 AAR6391 

Type I RIP gelonin analog Gel (A44/A50)

Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.

WO9426910-A1

24-NOV-1994.

93US-00064691. 12-MAY-1993;

Better MD, Carroll SF, Studnicka GM;

which Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents. AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is tragetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 251 AA;

(revised)
(first entry) 25-MAR-2003 27-JUL-1995

Gelonium multiflorum

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

94WO-US005348 12-MAY-1994;

(XOMA ) XOMA CORP

Aar63914 Type I RI Aar63912 Type I RI Aar63903 Type I ri Aar63915 Type I RI

Description

Length DB

Query Match

Result ġ 100.0

WPI; 1995-006804/01

Example 3; Page 181-182; 221pp; English.

Aar63903 Type I ri Aar63915 Type I RI Abg71551 G. multif Abg71551 G. multif Abw29300 BPI pepti Aar29303 BPI pepti Aar63921 Type I RI Aar63921 Type I RI Aar63920 Type I RI Aar63920 Type I RI Aar63920 Type I RI Aar63920 Type I RI Aar63917 Type I RI Aar63917 Type I RI Aar63917 Type I RI Aar63917 Type I RI Aar63917 Type I RI Aar63917 Type I RI Aar63913 Type I RI Aar63913 Type I RI Aar63913 Type I RI Aar63913 Type I RI Aar63913 Type I RI Aar63913 Type I RI Aar63913 Type I RI Aar63913 Type I RI

AAR63918 AAR63920

AAR63915 ADG63044 ABG71551 ABG71552 AAW29303 AAW29303 AAW292943 AAR63923 AAR63923

AAR63919 AAR63924 AAR63922 AAR63916

AAR63905 AAR74179

Gaps

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Indels

Score 1273; DB 2; Pred. No. 1.1e-119; 0; Mismatches 1;

99.7%;

Conservative

Length 251;

120

9

180

240

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61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                      AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                         181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                   1 GLDTVSFSTKGATYITYVNFLNBLRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN
                                                                                                                                            GOLABIAIDVTSVYVVGYQVRNRSYFFXDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                    1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                             FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                       241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                         241 ALLKFVDKOPK 251
                                        Similarity
Sequence 251 AA;
                                                    Matches 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR63903;
                                                                                                                                            61
                                                                                                                                                                                                                                                             181
                            Query Match
                                           Local
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                                                                                                                                                                                                                                                240
                                                                                                                                                           120
                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                            GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.
                                                                       9
                                                                                                9
                                                                                                                                            AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWVSEAARFTFIENQIRNN
                                                                                       GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                      AYRETTDLGI EPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFI ENQIRNN
                                                                     GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                           Gaps
                                          ö
               Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                          Indels
            100.0%; Score 1277; DB 2;
100.0%; Pred. No. 4.2e-120;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 179-180; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type I RIP gelonin analog Gel (A50/C44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                          AAR63912 standard; protein; 251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US005348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                         Local Similairy
nes 251; Conservative
                                                                                                                                                                                                                                                                                                      ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                        Carroll SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gelonium multiflorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-006804/01.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1993;
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            Query Match
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Matches
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AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cyctoxic therapeutic agents (CTA91), which include gene fusion products and immunoconjugates. CTA9 may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                             Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                                                                                                Type I ribosome-inactivating protein gelonin.
                                                                                                                                                                                                                                                                                                                                                                                                                 Studnicka GM;
AAR63903 standard; protein; 251 AA.
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                                                                                                                                                                                                                                                                                                                 94WO-US005348
                                                                                                                                                                                                                                                                                                                                                  93US-00064691
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Better MD, Carroll SF,
                                                                 (revised)
                                                                                                                                                                                                                  Gelonium multiflorum
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                                                                                                                                                                                                                                                                                                                                                                                 (XOMA ) XOMA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ75532
                                                                                                                                                                                                                                                                                                                12-MAY-1994;
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                                                               25-MAR-2003
27-JUL-1995
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The invention describes an isolated peptide or polypeptide having an antitumour and antiviral activity. Also described is a composition comprising the isolated peptide or polypeptide, and a carrier, excipient or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or polypeptide. The peptide or polypeptide is useful for treating HIV infection, and tumour. This is the amino acid sequence of Gelonium anti-HIV protein 30kDa (MAP30).
                                                                                                                                                                                         61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                     121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTEIENQIRNN
                                                                                                                                                                                                                                                                          121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWVSEAARFTFIENQIRNN
                                                                                                                                               1 GLDTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                        61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKAYIKTRLHPGGSYPSLEGEK
                                                                                                                           1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30; GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and antiviral activity, useful for treating human immunodeficiency virus infection or tumor.
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                                                             Length 251,
                                                                                            Indels
                                                            Score 1269; DB 2;
Pred. No. 2.7e-119;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gelonium anti-HIV protein 31kDa (GAP31).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADG63044 standard; protein; 251
                                                            99.4%;
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                                                                            Best Local Similarity 99.6 Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         241 ALLKFVDKDPK 251
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correct PN field.)
                               Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                   181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYYTAVDQVKPKI 240
                                                                                                                                                                                           61 GQLAEIAIDVTSVYVVGYQVRNRSYFFXDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                     AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                         240
                                                                                                                                                                       GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                           1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                         1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                         181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                            Gaps
                                                                            ;
0
                                           Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                                                            Indels
                                         99.4%; Score 1269; DB 2;
99.2%; Pred. No. 2.7e-119;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Type I RIP gelonin analog Gel(C10/A44/A50).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                       Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                      ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                  241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carroll SF,
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                                                          Best Local Similarity
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             Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9426910-A1
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27-JUL-1995
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                                                                                                                                                                       61
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                                             Query Match
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                                                                                                                               120
                                                                                                                                                             120
                                                                                                                                                                                           180
                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                         181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified protein, reduced antigenicity, modified toxin, gelonin, designer toxin, immunotoxin, proteinaceous compound, cancer, microbial pathogenesis; acquired immunodeficiency syndrome; AIDS; autoimmune disease, hyperproliferative disorder; leukaemia; arthritis; inflammatory disease, cardiovascular disease, diabetes; pathogenic disease, cytostatic, antiarthritic; antiinflammatory; cardiant; antidiabetic; virucide; protozoacide; funglicide; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method of generating a modified protein with reduced antigenicity while maintaining its biological activity. The method comprises identifying a region of the protein that is antigenic in a first subject using antiserum from either the first
                                                                                                                                               GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLIRKKCDDFGKCFVLVALSNDN
                                                                                                                                GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                           AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                        121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENOIRNN
                                                                                                                                                                                                                                                        FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                    GLDTVSFSTKGATY1TYVNFLNELRVKLKPEGNSHG1PLLRKKADDPGKAFVLVALSNDN
                                       ;
0
       Length 251;
                                      2; Indels
                      2.7e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G. multiflorum recombinant gelonin (rGel) toxin.
           Score 1269; DB 8;
99.2%; Score 99.2%; Pred. No. 2.7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 63; Page 169-170; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABG71551 standard; protein; 316 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2001; 2001US-0268402P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recombinant gelonin; rGel
                                      Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                    ALLKFVDKDPK 251
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N-PSDB; ABS56021.
                         Local Similarity
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           Query Match
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c subject or a second subject of the same species as the first subject. In particular the invention discloses modified toxin compounds, for example galonin toxin derived from Gelonium multiflorum, that are truncated condoni toxin derived from Gelonium multiflorum, that are truncated and/or possess reduced antigenicity. Such designar toxins have therapeutic, diagnostic, and preventative benefits, particularly as immunotoxins. The method of the invention is useful for generating proteinaceous compounds with less antigenicity. The immunotoxin and gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic, bone, bone marrow, head and neck, cervical, oesophagus, eye, gall consistions of the invention are also useful for treating microbial pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune diseases, hyperproliferative disorders including cancer, leukaemias, arthritis, inflammatory diseases, cardiovascular diseases, pathogenic arthritis, inflammatory diseases, which are more effective than prior art. The peptides and polypeptides, which are more effective than prior art. The present sequence represents G. multiflorum recombinant gelonin (rGel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.4%; Score 1269; DB 5; Length 316; 99.2%; Pred. No. 3.8e-119; ive 0; Mismatches 2; Indels
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Best Local Similarity 99.2
Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ALLKFVDKDPK 251
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Synthetic.
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The present invention relates to a method of generating a modified protein with reduced antigenicity while maintaining its biological activity. The method comprises identifying a region of the protein that is antigenic in a first subject using antiserum from either the first cubject or a second subject using antiserum from either the first subject. In particular the invention discloses modified toxin compounds, for example gelonin toxin derived from Gelonium multiflorum, that are truncated and/or possess reduced antigenicity. Such designer toxins have therapeutic, diagnostic, and preventative benefits, particularly as immunotoxins. The method of the invention is useful for generating proteinaceous compounds with less antigenicity. The immunotoxin and gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain, contended and neck, cervical, oseophagus, eye, gall chone, bone marrow, head and neck, cervical, oseophagus, eye, gall chance, bone marrow, head and neck, cervical, oseophagus, eye, gall charder, kidney, adrenal glands, heart, colon, or blood cancer. The pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune diseases, hyperproliferative disorders including cancer, leukaemias, arthritis, inflammatory diseases, cardiovascular diseases, pathogenic diseases, and diabetes. The method provides less antigenic proteins, peptides and polypeptides, which are more effective than prior art. The present sequence represents murine single-chain ZME-018 antibody/G. comultiflorum recombinant gelonin (rGel) (scfWMEL/rGel) fusion protein
                                                                                                                                                                                                                                                                                                                     Generating a modified protein with reduced antigenicity for treating cancer, AIDS, autoimmune diseases, comprises identifying a protein region antigenic in the first subject using antiserum from either the first or a
                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 174-176; 176pp; English.
                                                   12-FEB-2002; 2002WO-US004195
                                                                                             12-FEB-2001; 2001US-0268402P
                                                                                                                                                                                             Rosenblum MG, Cheung L;
                                                                                                                                                 (RERE-) RES DEV FOUND.
                                                                                                                                                                                                                                              WPI; 2002-750431/81.
N-PSDB; ABS56029.
                                                                                                                                                                                                                                                                                                                                                                                                   second subject
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Sequence 507 AA;

240 496 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 316 GOLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120 317 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 376 121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180 377 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 436 9 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 437 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI Gaps ö Query Match 99.4%; Score 1269; DB 5; Length 507; Best Local Similarity 99.2%; Pred. No. 7.3e-119; Matches 249; Conservative 0; Mismatches 2; Indels ALLKFVDKDPK 251 257 Н 241 497 61 181 ઠ <del>a</del> ò 셤 ò g ò d ò 셤

RESULT 8

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A new recombinant DNA vector construct has been developed which encodes a fusion protein and is suitable for introduction into a bacterial host.

The vector comprises: (a) DNA encoding at least one cationic bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site coarded between (a) and (b). The present sequence represents the protein from the pING3797 vector construct which codes for a BPI fusion protein. The peptides have many uses including the treatment of bacterial and contralising their effects. The peptides also bind to endotoxins and heparin, neutralising their effects. The peptides save further been shown to inhibit anglogenesis (partly due to heparin-binding activity). The fusion proteins have been found to be expressed in large amounts without significant proteolysis, and in some cases are actually secreted from the coeffides in microbial hosts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant production of bactericidal/permeability increasing protein - by expression as a fusion protein in microbial host cells, then cleaving the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                       Bactericidal/permeability increasing peptide; BPI; fusion protein;
bacterial infection; fungal infection; endotoxin; heparin; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GLDTVSFSTKGATY1TYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
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                                                                                                       BPI peptide fusion protein pING3797 vector construct protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 160-161; 186pp; English.
                                                                                                                                                                            fungicidal; recombinant DNA; vector.
AAW29300 standard; protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                             97WO-US005287.
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                                                                                                                                                                                                                                   carotovorum
                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-480215/44.
N-PSDB; AAT86336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 293 AA;
                                                                                                                                                                                                                               Pectobacterium
                                                                                                                                                                                                                                                   sapiens.
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                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1996;
                                                                     20-APR-1998
                                                                                                                                                                                                                                                                                                                                          5-SEP-1997.
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                                                                                                                                                                                                              Synthetic
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GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

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AAW29294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            significant proteolysis, and in some cases are actually secreted from the host cells. This allows the indirect production of anti-microbial BPI peptides in microbial hosts
203 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 262
                                                                                                                                                                                                                                                                                         Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant production of bactericidal/permeability increasing protein - by expression as a fusion protein in microbial host cells, then cleaving the BPI peptide from the carrier.
                                                                                                                                                                                                                                                            BPI peptide fusion protein pING3795 vector construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.1%; Score 1266; DB 2; 98.8%; Pred. No. 7.3e-119; ive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 152-153; 186pp; English.
                                                                                                                                                               AAW29303 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US005287.
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                                                                                                                                                                                                                                                                                                                                                                           Pectobacterium carotovorum.
                                                                                                                                                                                                                            20-APR-1998 (first entry)
                                                                   ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-480215/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT86341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9735009-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Better MD;
                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                               AAW29303;
                                                241
                                                                               263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric.
                                                                                                                                                  AAW29303
                                                                                                                               RESULT
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The vector comprises: (a) DNA encoding at least one cationic carrier protein and is suitable for introduction into a bacterial host.

The vector comprises: (a) DNA encoding at least one cationic carrier protein, and (c) DNA encoding an amino acid (as) cleavage site located between (a) and (b). The present sequence represents the protein from the plusion protein. The peptides have many uses including the treatment of bacterial and fungal infections. BPI peptides also bind to endotoxins and heparin, neutralising their effects. The peptides have further been shown to proteins have been found to be expressed in large amounts without significant proteolysis, and in some cases are actually secreted from the peptides in microbial hosts
                                                  180
                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      new recombinant DNA vector construct has been developed which encodes a
                                                                                    202
                                                                                                                                                           262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant production of bactericidal/permeability increasing protein -
by expression as a fusion protein in microbial host cells, then cleaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA; vector.
83 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK
                                                                                                                        181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                  121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                         143 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWVSEAARFTFIENQIRNN
                                                                                                                                           203 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                    BPI peptide fusion protein pING3793 vector construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 148-150; 186pp; English.
                                                                                                                                                                                                                                                                                                                           AAW29294 standard; protein; 332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US005287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pectobacterium carotovorum
                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                               241 ALLKFVDKDPK 251
                                                                                                                                                                                                                               263 ALLKFVDKDPK 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                             AAW29294;
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23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN

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Studnicka GM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Type I RIP gelonin analog Gel(C10)
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                                                99.0%;
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                                            Query Match
Best Local Similarity 98.8°
Matches 248; Conservative
                                                                                                                                                                                                                                                                                              241 ALLKFVDKDPK 251
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                                                                                                                                                                                                                                                                                                                     241 ALLKFVOKOPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gelonium multiflorum.
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correct PN field.)
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                        Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9426910-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1994;
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27-JUL-1995
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                                                                                                                                               83 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKIRLHFGGTYPSLEGEK 142
                                                                                                                                                                                121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                               143 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 202
                                                                                                                                                                                                                                181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                              FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDOVKPKI 262
                                                                                                                               61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                              23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.
                                                                                 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                            Gaps
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                                  Length 332;
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                                                         Indels
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                                  Score 1266; DB 2;
Pred. No. 8.1e-119;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 187-188; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Studnicka GM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type I RIP gelonin analog Gel (C103)
                                                                                                                                                                                                                                                                                                                                                                   AAR63923 standard; protein; 251 AA.
                               Ouery Match 99.1%;
Best Local Similarity 98.8%;
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                   ALLKFVDKDPK 273
                                                                                                                                                                                                                                                                                 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll SF,
                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gelonium multiflorum.
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          Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9426910-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1994;
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27-JUL-1995
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                                                                                                                                                                                                                                                                                                            61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                        61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTCKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune
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                                                                                                                                                                                                    1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDFGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
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                                                                                                                                                        1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                    Gaps
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    Length 251;
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                                                                            Indels
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Score 1264; DB 2;
Pred. No. 8.7e-119;
0; Mismatches 3;
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Gaps ; 9 9 180 240 240

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elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAB), which include gene fusion products and immunoconjugates. CTAB may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of
                                                                                                                                                                                                            61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                      121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                                                  1 GLDTVSFSTKGATYITYVNPLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                      FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                  1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                          Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                                                                                                    3; Indels
                                                                                         Score 1261; DB 2;
Pred. No. 1.7e-118;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR63920 standard; protein; 251 AA.
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                                                                                          98.7%;
98.8%;
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                                                                                       Query Match 98.7
Best Local Similarity 98.8
Matches 248; Conservative
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                                                               Sequence 251 AA;
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27-JUL-1995
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                                                                                                                                                                                                          121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDOVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelboin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytchcoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the
   cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
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                                                                                                                                                     GLDTVSFSTCGATYITYVNFINELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                    GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                        Gaps
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                                                                            Length 251;
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                                                                                                        Indels
                                                                           Score 1261; DB 2;
Pred. No. 1.7e-118;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type I RIP gelonin analog Gel(C248).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR63918 standard; protein; 251 AA.
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                                                                         Query Match
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                correct PN field.)
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                                              Sequence 251 AA;
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the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 correct PN field.)
                                                                                                                                                            GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                           Length 251;
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                                                                                          Score 1261; DB 2;
Pred. No. 1.7e-118;
0; Mismatches 3;
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targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 correct PN field.)
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12 6/ptodata/2/pubpaa/USO6_NEW PUB.ppp.*

13 6/ptodata/2/pubpaa/USO6_PUBGOMB.ppp.*

14 6/ptodata/2/pubpaa/USO7_NEW PUB.ppp.*

15 6/ptodata/2/pubpaa/PCTUS PUBGOMB.ppp.*

16 6/ptodata/2/pubpaa/USO8_NEW PUB.ppp.*

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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* Query Match Length DB ID	251	251	251	251	251	251	251	251	251	251	251
ery	0.0	0.0	7.6	7.6	7.6	7.6	4.6	99.4	4.6	4.6	4.6
* 2 g	10	2	σ	0	σ	σ	Q	σ	σ	σ	σ
Score	1277	1277	1273	1273	1273	1273	1269	1269	1269	1269	1269
Result No.		7	m	4	ഹ	9	7	80	6	10	11

Seguence 1, Appli	Н	259,	253,	equence 251,	100	e 108	103	104	100	106	100	Sequence 103, App	104	105	106	100	102	101	11	100	10	111	4	4,	H	Ä	-	H	H	'n	39,	e 39,	4
US-10-074-596-1	-10-074	-09-765-527-25	527-	-09-765-527-	-10-127-890-1	US-10-717-243-108	-890-	-10-127-890-	7	US-10-127-890-106	-10-127-890-	10-717-2	US-10-717-243-104	_	US-10-717-243-106	US-10-717-243-109	2	10-127-8	0 - 127 - 89	-10-717-24	-10-717-24	US-10-717-243-111	US-10-127-890-4	0 - 717 - 24	10-282-93	-10 - 127 - 89	US-10-440-796-1	US-10-717-243-1	-10	-46	792-7	-10-375-	US-10-280-679B-4
14	14	σ	σ	σ	14	17	14	14	14	14	14	17	17	17	17	17	14	14	14	17	11	17	14	17	14	14	15	17	14	16	δ	15	14
316	507	293	309	332	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	251	263	263	267	267	267	267	576	312	247	247	289
99.4	99.4	99.1	99.1	99.1		99.0		98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	98.7	27.3	27.3	27.1	27.1	27.1	27.1	27.1	25.6	25.3	25.3	25.3
1269	1269	1266	1266	1266	1264	1264	1261	1261	1261	1261	1261	1261	1261	1261	1261	1261	1260	1260	1260	1260	1260	1260	348	4	346	346	346	346	4	326.5	N	a	323
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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RESULT 1
US-10-127-890-101
US-10-127-890-101
Sequence 10., Application US/10127890
Sequence 10., Application US/10127890
Publication No. US20301066196A1
GENERAL INFORMATION:
CEATEOL! Stephen F.
Studnika, Gary M.
Froteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STREET: 111inois
COMPITER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPITER: Patentin Release #1.0, Version #1.25
COMPITER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/127, 890
FILING DATE: 23-Apr-2002
CLASSIFCATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1994
FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carroll, Stephen F. Studnika, Gary M. TITLE OF INVENTION: Immunocoxins Comprising Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1277; DB 17; Length 251; 100.0%; Pred. No. 1.1e-115; tive 0; Mismatches 0; Indels 0;
                                                            APPLICATION NUMBER: US 08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1993
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-000-1991
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 1102ZUS09/200-70.P3.C3
TELEPRAN: 312/707-8889
TELEPRAN: 312/707-9155
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 99, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Better, Marc D.
                         CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 251; Conservative
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Best Local Similarity
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US-10-717-243-101
15 Gequence 101, Application US/10717243
17 Publication No. US20050054835A1
17 GENERAL INFORMATION:
18 APPLICANT: Better, Marc D.
19 APPLICANT: Better, Marc D.
19 Studnika, Gary M.
17 TILE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1277; DB 14; Length 251; 100.0%; Pred. No. 1.1e-115; Artive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTATION TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/10/717,243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
          FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/91,707
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: MCMICACLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHONE: 312/707-9155
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: procein SEQUENCE DESCRIPTION: SEQ ID NO: 101: US-10-127-890-101
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                           TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 251; Conservative
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STATE: Illinois
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181 PQQRIRPANNTISLENKWGKLSFQIRTSGANGWFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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     oxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                  ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1273; DB 14;
Pred. No. 2.7e-115;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890
CLASSIFICATION NUMBER: US/10/127,890
CLASSIFICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/989,430
FILING DATE: 19-UN-1993
APPLICATION NUMBER: US 07/981,787
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/981,787
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/97,787,567
FILING DATE: 04-NOW.1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MCNIcholas, Janet M.
REGISTRATION NUMBER: 32, 918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
TOPOLOGY: linear
;
MOLECULE TYPE: procein
; SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-127-890-100
                                                                                                                                                                                                                          ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                               Proteins
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INFORMATION FOR SEQ ID NO: 100:
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                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.6
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.7%; Score 1273; DB 14; Length 251; 99.6%; Pred. No. 2.7e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                   APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-127-890-99
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Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 99
SEQUENCE CHARACTERISTICS
ZIP: 60661
COMPUTER READABLE FORM:
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Best Local Similarity 99.6
Matches 250; Conservative
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                                                                                                                                                                                                                  Sequence 100, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                               181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
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COMPUTER: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATE: 18-NOv-2003

CLASSIFICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 12-APR-1995

APPLICATION NUMBER: US 08/64,691

FILING DATE: 12-APR-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/988,430

FILING DATE: 19-UN-1992

APPLICATION NUMBER: US 07/988,430

FILING DATE: 19-UN-1992

APPLICATION NUMBER: US 07/988,567

FILING DATE: 19-UN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMULCATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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99.6%; Pred. No. 2.7e-115;
tive 0; Mismatches 1;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-10-717-243-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 251 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                              241 ALLKFVDKDPK 251
                                                                                                                                                                             CITY: Chicago
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                                                                                                                                                                                     Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MCNIcholas, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 99:
                                                                                           Sequence 99, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 99,
SEQUENCE CHARACTERISTICS,
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60661
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-717-243-99
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Gaps

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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGWFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                            121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                      121 AYRETTÖLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURSNY APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 13-MAY-1996

PILING DATE: 12-MAY-1996

PILING DATE: 12-MAY-1994

APPLICATION NUMBER: PCT/US94/05348

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: MONICHOLAS, JANGER: 200-70.P4

TELECOMMUNICATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                               241 ALLKFVDKDPK 251
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                                                                                                61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYFGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                         121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                   121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWYSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                             181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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TITLE OF INVENTION: Methods for Recombinant Microbial Production of FITLE OF INVENTION: Methods for Recombinant Microbial Production of FITLE OF INVENTION.
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                       GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKCFVLVALSNDN
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 251;
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COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.4%; Score 1269; DB 9; Best Local Similarity 99.2%; Pred. No. 6.7e-115; Matches 249; Conservative 0; Mismatches 2;
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APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 247:
US-09-765-527-247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR AFFLICATION NUMBER: 08/621,803
APPLICATION NUMBER: 08/621,803
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 247, Application US/09765527
Patent No. US20020006638A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 251 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
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US-09-765-527-247
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                          99.4%; Score 1269; DB 14;
ilarity 99.6%; Pred. No. 6.7e-115;
Conservative 0; Mismatches 1;
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APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APP-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
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FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
                                                                         ;
**MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-10-127-890-110
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                       SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
    INFORMATION FOR SEQ ID NO: 110:
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STATE: Illinois
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Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                    1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                                             Gaps
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  Score 1269; DB 14; Length 251; Pred. No. 6.7e-115;
                                           Indels
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COMPUTER: IBM PC compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <UNKNOWD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/97,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: MCMICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 110, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
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99.4%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                           249; Conservative
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                     Local Similarity
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    Query Match
                                           Matches
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us-10-717-243-101.open.rapb

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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Sequence 1, Application US/10074596;
Publication No. US20030176331A1
GENERAL INFORMATION:
APPLICANT: ROSEMBLUM, MICHAEL G.
APPLICANT: CHEUNG, LAWRENCE
TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
TITLE OF INVENTION: MAKING THEEOF
FILE REFERENCE: CLFR:007US
CURRENT APPLICATION NUMBER: US/10/074,596
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/268,402
PRIOR FILING:DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN OF: 2.1
SOFTWARE: PATENTIN OF: 2.1
SOFTWARE: PATENTIN OF: 2.1
SOFTWARE: PATENTIN OF: 2.1
SOFTWARE: PATENTIN OF: 3.1
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                                                                                                             | FILING DATE: 12-MAY-1993 | PILING DATE: 12-MAY-1993 | PILING DATE: 12-MAY-1993 | PILING DATE: 12-MAY-1993 | PILING DATE: 09-DEC-1992 | PILING DATE: 09-DEC-1992 | PILING DATE: 09-DEC-1992 | PILING DATE: 09-DEC-1992 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING DATE: 04-MY-1991 | PILING D
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                                                                                 APPLICATION NUMBER: US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 251;
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COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: Patentin Release #1.0, Version #1.25
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/10/717,243
    FILING DATE: 18-Nov-2003
    CLASSIFICATION: 530
                                                                     NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFA: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Pred. No. 6.7e-115;
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APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Publication No. US20050054835A1
GENERAL INFORMATION:
FILING DATE: 04-NOV-1991
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TYPE: amino acid
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Matches 249; Conservative
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US-10-717-243-110
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61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                               TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GLDIVSPSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                                                                                                                                                                                                 CITEL: 0500 Sects fower, 233 South macket Direct CUNTY: Chicago STATE: 111inois COUNTY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPEATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%; Score 1266; DB 9;
98.8%; Pred. No. 1.6e-114;
tive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION NUMBER: 08/621,803
ATTORNEY/AGENT INFORMATION:
NAME: BOYUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 25,447
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 259:
US-09-765-527-259
                                                                   Sequence 259, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 265
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Matches 248; Conservative
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US-09-765-527-253
                                                US-09-765-527-259
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                                                                                                                                                                                                                                                                                     180
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                                                                                                                                         47 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 106
                                                                                                                                                                                         GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                  Gaps
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Sequence 11, Application US/10074596

Sequence 11, Application US/10074596

Sequence 11, Application US/10074596

Sequence 11, Application US/10074596

GENERAL INFORMATION: MICHAEL G.

APPLICANT: CHEUNG, LAWRENCE

TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF TITLE OF INVENTION: MAKING THEEOF

TITLE OF INVENTION: MAKING THEEOF

TITLE OF INVENTION: MAKING THEEOF

CURRENT APPLICATION NUMBER: US/10/074,596

CURRENT FILING DATE: 2002-02-12

PRIOR APPLICATION NUMBER: 60/268,402

PRIOR APPLICATION NUMBER: 60/268,402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-074-596-11
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  Length 316;
                                                Indels
  Score 1269; DB 14;
Pred. No. 9.2e-115;
                                                0; Mismatches
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 507
TYPE: PRT
ORGANISM: Artificial Sequence
  99.4%;
Query Match
Best Local Similarity 99.2
Matches 249; Conservative
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Matches 249; Conservative
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Sequence 253, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of NUMBER OF SEQUENCES: 265
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                                                                                                                           NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 6666-6402

COMPUTER: ERDABLE FORM:
MEDIUM TYPE: PLORDY disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION NUMBER: 08/621,803
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F
REGISTRATION NUMBER: 25,447

REGISTRATION NUMBER: 25,447

RELEPRANS: 312/474-6300
TELEPRANS: 312/474-6300
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MOLECULE TYPE: procein
; SEQUENCE DESCRIPTION: SEQ ID NO: 253:
US-09-765-527-253
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INFORMATION FOR SEQ ID NO: 253:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acid
TYPE: amino acid
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-425-336-59

US-08-488-113B-59

US-08-843-55

US-08-136-389-59

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US-09-136-389-59

US-09-136-389-59

US-09-110-488-59

US-09-111-485-59

US-09-396-196G-105925

US-09-396-196G-114261

US-09-396-196G-114261

US-09-396-196G-114261

US-09-38-130-18

US-09-38-130-18

US-09-38-130-18

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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Sequence 122538, Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 55, Appl Sequence 57, Appl Sequence 51, Appl Sequence 51, Appl Sequence 51, Appl Sequence 52, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, Appl Sequence 67604, App		s of 5-Inactivating Proteins	
25 4 US-09-396-196G-122538 24 1 US-08-489-548-55 24 1 US-08-48-56-58-55 24 1 US-08-452-654-55 24 3 US-08-452-658-55 24 3 US-08-450-658-55 24 4 US-09-396-196G-37209 25 4 US-09-396-196G-58823 20 4 US-09-396-196G-58823 20 4 US-09-422-978-11795 23 3 US-09-396-196G-58823 24 US-09-396-196G-58823 25 4 US-09-396-196G-58823 25 4 US-09-396-196G-58823 25 4 US-09-396-196G-58866 25 4 US-09-396-196G-58866 25 4 US-09-396-196G-58866 25 4 US-09-396-196G-57606 25 4 US-09-396-196G-67666 25 4 US-09-396-196G-67666		SULT 1 Sequence 61, Application US/07988430 Patent No. 5416202 GENERAL INFORMATION: APPLICANT: Bernhard, Susan L. APPLICANT: Bernhard, Susan L. APPLICANT: Lane, Warc D. APPLICANT: Lane, Usle A. APPLICANT: Lane, Usle A. APPLICANT: Lane, Usle A. APPLICANT: Lane, Shau-Ping TITLE OF INVENTION: Materials Comprising and Methods TITLE OF INVENTION: Preparation and Use for Ribosome NUMBER OF SEQUENCES: 101 CORRESPONDENCE ADDRESS: ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & ADDRESSEE: Micknell; O'Toole, Gerstein, Murray & STREET: Street CITY: Chicago STATE: Illinois COMPUTER READABLE FORM: MEDLUM TYPE: PatentIn Release #1.0, Version #1.25 COMPUTER: DATENTION NUMBER: US/07/988,430 FILING DATE: 19921209 CLASSIFICATION NUMBER: US 07/901,707 FILING DATE: 19-100 DATA: APPLICATION NUMBER: US 07/901,707	APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991 ATORNEY/AGENT INFORMATION: NAME: No. 5416202and, Greta E. REGISTRATION NUMBER: 35302 REGISTRATION NUMBER: 31133 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 346-5750 TELEFAX: 25-3856 TELEX: 25-3856 TELEX: 25-3856 TELEX: 25-3856 TELEX: 28-3856 TELEX: 38-3856 T
13.2 13.2 4.4 13.3 4.6 4.6 4.6 4.6 4.6 4.6 4.6 4.6	:	T 1  -988-430-61  uence 61, Application U ent No. 5445202  APPLICANT: Bernhard, S APPLICANT: Berter, Mar APPLICANT: Carroll, St APPLICANT: Lane, Julie APPLICANT: Lane, Julie APPLICANT: Lei, Shau-P TITLE OF INVENTION: Ma TITLE OF INVENTION: Ma APPLICANT: Lei, Shau-P TITLE OF INVENTION: Ma APPLICANT: Lei, Shau-P TITLE OF INVENTION: Ma ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Marshall, ADDRESSEE: Bicknell, STREET: Street CITY: Chicago STATE: Illinois COMPUTRY: USA ZIP: 60603  COMPUTER: PatentIn R CUMPUTR: BatentIn R CUMPUTR: PatentIn R CUMPUTR: Data APPLICATION NUMBER: FILING DATE: 192120 CLASSIFICATION NUMBER: FILING DATE: 19210N	APPLICATION NUMBER: US 07/ PILING DATE: 04-NOV-1991 ATTORNEY SEE: 04-NOV-1991 NAME: No. 5416202and, Grec. REGISTRATION NUMBER: 33302 REPERNCE/DOCKET NUMBER: 33302 RELECOMMUNICATION INFORMATION TELEPHONE: (312) 944-9740 TELEFAX: (312) 944-9740 TELEX: 25-3856 INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS: LENGTH: 28 base pairs TYPE: NUCLEIC ACID
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STRANDEDNESS: single

Sequence 27, Appl Sequence 3846, Ap Sequence 163, App Sequence 1783, Ap Sequence 125558, Sequence 74, Appl Sequence 74, Appl

-09-396-196G-5918 -09-396-196G-21250 -09-396-196G-36903

Sequence Sequence

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Sequence 59, Application US/08488113B
Fatent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOWBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NUMBER: MEDICATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
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100.0%; Score 28; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 28; Conservative 0; Mismatches
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; Patent No. 5756699
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REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION
TELEPHONE: 312/707-8889
TELEPAX: 312/707-9155
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
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STRANDEDNESS: single
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STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 59, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                 Query Match 100.0%; Score 28; DB 1; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0031; Matches 28; Conservative 0; Mismatches 0; Indels
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COUNTEY.

COUNTEY.

ZIP: 6066-6402

COMPUTER READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/425,336

FILING DATE: 18-APR-1995

CLASSIFICATION: 530
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APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: 08/07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-MOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAYERS, Thomas C.
REGISTRATION NUMBER: P-36,989
REGISTRATION NUMBER: P-36,989
REGISTRATION NUMBER: B-36,989
REGISTRATION NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/44-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312/474-0448
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TOPOLOGY: linear
                     , MOLECULE TYPE: DNA
US-07-988-430-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-425-336-59
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Inmunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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Pred. No. 0.0031;
                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
                 TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
CITY: Chicago
CITY: Chicago
CITY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 28; DE Best Local Similarity 100.0%; Pred. No. 0.0 Matches 28; Conservative 0; Mismatches
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APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/08839765
Patent No. 6146631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 312/707-8889
312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA
US-08-646-360-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: I 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDITEWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor CITY: Chicago STATE: Illinois COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-646-360-59
US-08-646-360-59
Sequence 59, Application US/08646360
Patent No. 583741
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 28; DB 1; Length 28; 100.0%; Pred. No. 0.0031; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            OUREAUTION SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,404B
FILING DATE: U-JUN-1995
CLASSIFICATION NUMBER: US/08/477,404B
FILING DATE: U-JUN-1995
RIGHT APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
RIGHT APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
RIGHT APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
RIGHT APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DEC-1992
RIGHT APPLICATION NUMBER: US 07/901,707
FILING DATE: US-DEC-1992
RIGHT APPLICATION NUMBER: US 07/901,707
FILING DATE: US-JUN-1992
RIGHT APPLICATION NUMBER: US 07/787,567
FILING DATE: US-JUN-1992
RIGHT APPLICATION NUMBER: US 07/787,567
FILING DATE: US-DEC-1991
ATTCANEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERRICE/OMCHUNICATION INFORMATION:
TELEPRAK: 312/707-8889
TELEFRAK: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11022US07/200-70.P3.C2A
                                                                                                                                                                                                                                                                                                                     ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity
                   GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:

ADDRESSEE: MANdrews, Held & Malloy, Ltd.

STREET: 500 west Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 28; DB 3; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0031; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                    Patentin Release #1.0, Version #1.25
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                                                                                                                                    SOFIWARE: Factorial Release #1.0, vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-MAY:
APPLICATION NUMBER: US 07/787,567
FILING DATE: OF-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MONICHOLSE, Janet M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Policy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 59, Application US/09610838
Patent No. 6376217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ 1D NO: 59: SEQUENCE CHARACTERISTICS: LENGTH: 28 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDREWS, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFPICATION: DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
FILING DATE: 18-APR-1995
FILING DATE: 12-APR-1995
FILING DATE: 12-APR-1995
FILING DATE: 10-MAY-1993
FILING DATE: 10-MAY-1993
FILING DATE: 10-MAY-1993
FILING DATE: 09-DEC-1992
FILING DATE: 09-DEC-1992
FILING DATE: 19-MAY-1993
FILING DATE: 19-MAY-1993
FILING DATE: 19-MAY-1993
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500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CACATGTAAAACAAGACTTCATTTTGGC 28
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Patent No. 6146850
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INPORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
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Best Local Similarity 100.
Matches 28; Conservative
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STRANDEDNESS: single
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COMPUTER READABLE FORM:
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STREET: buc
CITY: Chicago
STATE: Illinois
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                                                           Illinois
: USA
                       Chicago
                                                                                                                       60661
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APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
CORRESPONDENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 28; DB 4; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0031; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                          PFILING DATE:
PRIOR ADDITION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRILING DATE: 12-MAY-1993
PRILING DATE: 09-DEC-1992
PRILING DATE: 09-DEC-1992
PRILING DATE: 19-MAN-1992
PRILING DATE: 19-MAN-1992
PRILING DATE: 19-MAN-1992
PRICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MANICADAS, JANE M.
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 11022US09/200-70.P3.C3
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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STREET: Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                  US/09/711,485
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     08/839,765
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INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
CURRENT APPLICATION DATA
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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STATE: Illinois
CONNTRY: USA
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Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Beteer, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: MANDAGRAWS, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PIEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
PatentIn Release #1.0, Version #1.25
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500 West Madison Street, 34th floor
                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/989,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/991,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY, AGENT UNPERMENTION:
ANALY AGENT UNPORMATION:
ANALY ANALY AGENT UNPORMATION:
ANALY ANALY AGENT UNPORMATION:
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                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200
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TELEFAX: 312/707-9155
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INPORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
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                                                                                                           FILING DATE: 0
CLASSIFICATION:
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US-09-610-838-59
SOFTWARE:
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Wig-09-682-597A-3

| Sequence 3, Application US/09682597A |
| Sequence 3, Application US/09682597A |
| Sequence 3, Application US/09682597A |
| Sequence 3, Application US/09682597A |
| Patent No. 668980 |
| APPLICANT: Monsanto Technology LLC |
| APPLICANT: Applicant Meather and Methods |
| APPLICANT: Alou, Hua-Ping |
| APPLICANT: Alou, Hua-Ping |
| TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions and Methods |
| TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions and Methods |
| TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions and Methods |
| TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions and Methods |
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| TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions |
| TITLE OF INVENTION: Glyphosate Tolerant Wheat Plant 33391 and Compositions |
| TITLE OF INVENTION: Glypho
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APPLICANT: LAM, HON-MING
APPLICANT: LAM, HON-MING
APPLICANT: LAM, HON-MING
APPLICANT: HSIEH, MING-HSIUN
TITLE OF INVENTION: P-PII GENES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS:
                                    APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR PAPLICATION NUMBER: 60/100,678
PRIOR PILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FasteEQ for Windows Version 4.0
SEQ ID NO 114261
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ATGIAAAACAAGACTICAT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 ATCTTAAACAAGAGTTCAT 6
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David Lockhart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: mus musculus
US-09-396-196G-114261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
hes 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
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US-08-899-330-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 28; DB 5; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0031; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-396-196G-105925
; Sequence 105925, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Mitchael Mittmann
; APPLICANT: David Mack
APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 105925
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US-00-196-196G-114261/C
Sequence 114261, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittmann
APPLICANT: David Mack
                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-007-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IGTAAAACAAGACTICATITIG 26
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REGISTRATION NUMBER: 3113:
REFERENCE/DOCKET NUMBER: 3113:
TELEPHONE: (312) 346-5750
TELEPKX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Query Match 49.3%; Score 13.8; DB 4; Length 20; Best Local Similarity 88.2%; Pred. No. 5.9e+03; Matches 15; Conservative 0; Mismatches 2; Indels
        REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-042-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
                                                                                                                                                                                                                                  TOPOLOGY: linear

MOLECULE TYPE: Other
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-756-541-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June 21, 2005, 19:15:10 Job time : 125 secs
                                                                                     TELEFAX: (212)8699741
TELEX: 66141 PENVIE
INFORMATION FOR SEQ 1D 00: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        LENGTH: 20 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                          2 ACATGTAAAACAAGACT 18
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                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: singl
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Patent No. 6822079
GENERAL INFORMATION:
APPLICANT: CORUZZI, GLORIA
LAM, HON-MING
HSIEH, MING-HSIUN
TITLE OF INVENTION: PLANT NITROGEN REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13.8; DB 3;
Pred. No. 5.9e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 21 CLEDS
CORRESPONDENCE ADDRESS:
ADDRESSE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IEM COMPATIBLE
COMPUTER: IEM COMPATIBLE
SOFTHARE: FASTSEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,541
FILLING DATE: 08-Jan-2001
CLASSIFICATION: B00
PRIOR APPLICATION: DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.3%; Scc. V 88.2%; Pred. No. 5...
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOGTWARE: FASTESQ Version 2.0
SUGRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/899,330
FILING DATE: 23-UU-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/022,328
FILING DATE: 2-UU-1996
ATTORNEY AGENT INFORMATION:
NAME: COTUZZI, LAURA A
RECISTRATION NUMBER: 50/42
REFERENCE DOCKET NUMBER: 5914-042-999
TELEFRANC (212) 7909090
TELEFRANC (212) 7909090
TELEFRANC (212) 7909090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/899,330
FILING DATE: 23-4UL-1997
APPLICATION NUMBER: 60/022,328
FILING DATE: 24-VUL-1996
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NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                          IEDEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ACAGGTAAAACACGACT 19
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Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-899-330-18
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| cgn2_6/ptodata/1/pubpna/DCT_NEW PUB. seq:*
| cgn2_6/ptodata/1/pubpna/DCT_NEW PUB. seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/DCTUS_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_NEW PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US09_REW PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US108_PUBCOMB.seq:*

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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.eeg:
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.eeg:
                                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-717-243-59
28
1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6054689 seqs, 3103772919 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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                                                                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 59, Appl Sequence 89652, Sequence 17282, A Sequence 17282, A Sequence 16595, Sequence 93516, Sequence 231959,
\$ Query Match Length DB ID	US-10-127-890-59 US-10-717-243-59 US-10-719-900-839652 US-10-098-263B-17282 US-10-96-189-105925 US-10-956-157-93516 US-10-956-157-93516
DB	16 21 21 21 21 21
* Query ore Match Length DB II	28 2 2 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8
% Query Match	100.0 100.0 59.3 55.7 55.7 55.0
Score	116.28 115.6 115.6 115.6
Result No.	O 1004000

Sequence 265753 Sequence 342034 Sequence 898965 Sequence 292506 Sequence 463285 Sequence 333643 Sequence 333644 Sequence 273438 Sequence 19337, Sequence 19337, Sequence 19337, Sequence 19337, Sequence 19337, Sequence 697924 Sequence 697924 Sequence 687924	7214 Sequence 157214, 84754 Sequence 157214, 7755 Sequence 177735, 7715 Sequence 177735, 7715 Sequence 465260, 5260 Sequence 465261, 5390 Sequence 55230, 7711 Sequence 93519, 767 Sequence 170,47, 767 Sequence 170,47, 767 Sequence 170,67, 767 Sequence 170,67, 767 Sequence 170,67, 767 Sequence 170,67, 767 Sequence 270,623, 768 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,63, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 270,65, 769 Sequence 40,2444,	ising Ribosome-Inactivating oy, Ltd. 34th floor Version #1.25
US-10-95 US-10-71 US-10-71 US-10-71 US-10-95 US-10-95 US-10-95 US-10-99 US-10-99 US-10-99 US-10-99 US-10-71 US-10-71 US-10-71	21 US-10-956-157-157214 21 US-10-956-157-170735 21 US-10-956-157-244754 US-10-956-157-244754 US-10-719-900-107315 21 US-10-719-900-46526 21 US-10-719-900-46551 US-10-719-900-65539 21 US-10-719-900-86531 US-10-719-900-86531 21 US-10-719-900-844034 21 US-10-719-900-844034 22 US-10-956-157-93519 23 US-10-719-900-107507 US-10-719-900-13415 24 US-10-719-900-273465 25 US-10-719-900-273465 26 US-10-719-900-273465 27 US-10-719-900-273465 28 US-10-719-900-273465 29 US-10-719-900-273465 21 US-10-719-900-273465 21 US-10-719-900-273465 21 US-10-719-900-273465 21 US-10-719-900-273465	ALIGNMENTS  10127890 6A1 rc D. tephen F. anyoroxins Compr roceins 173 3ary M. munotoxins Compr roceins 173 6A2 Fews, Held & Mall Madison Street, Madison Street, Fec-Dos/Ars. In Release #1.0, Ars. Fec-Dos/Ars. Compatible Compatible RR: US/10/127,890 Ars. ER: US/10/127,890 Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Compatible Com
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	0 0 0 00 000 000 000 000 000 000 000 0	RESULT 1 US-10-127-890-5 Sequence 59, Publication N GENERAL INF GENERAL INF TITLE TITLE TOWNBER CORRES S S S S S S S S S S S S S S S S S S

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; Sequence 839652. Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOPTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 839652
; LENGTH: 25
; TURNET IN 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 28; DB 21; Length 28; 100.0%; Pred. No. 0.055;
                FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Squence 17282, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 31181.
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
APPLICATION NUMBER: US 07/901,707
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                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-717-243-59
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INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
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ilarity 82.6%;
Conservative
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Matches 28; Conservative
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CORGANISM: Mus musculus
US-10-719-900-839652
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nes 19; Conserv
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Matches
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TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
              FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/717,243 FILING DATE: 18-Nov-2003 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; BINGLE
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-127-890-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CACATGTAAAACAAGACTTCATTTTGGC 28
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US-10-717-243-59
Sequence 59, Application US/10717243
Publication No. US20050054835A1
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 231959, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wouts,
MOULES WIlliam
TITLE OF INVENTION: HUMAN OSTEORETHRITIS AND HUMAN PROTEASES

TITLE OF INVENTION: HUMAN OSTEORETHRITIS AND HUMAN PROTEASES

CURRENT APPLICATION NUMBER: US/10/956,157

CURRENT FILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 231959

LENGTH: 25
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Sequence 265753, Application US/10956157

Publication No. US20050118625A1

GENERAL INFORMATION:

APPLICANT: Wouth

APPLICANT: Wouth

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APPLICANT: Wouth

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APPLICANT: Wouth

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APPLICANT: Wouth

TITLE OF INVENTION: HUMAN OSTBOARTHRITIS AND HUMAN PROTEASES

FILE REPERBENCE: 031896-043000 (AM 101081)

CURRENT APPLICATION NUMBER: 02/10/956,157

CURRENT PILING DATE: 2004-10-04

NUMBER OF SEQ ID NOS: 319805

SOFTWARE: Patentin version 3.2

SEQ ID NO 265753

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 25;
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TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.
CURRENT APPLICATION NUMBER: US/10/719,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.1%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 1;
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
                                                    1 AIGTIATACTAGACTCCATIGICC
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Best Local Similarity 94.1%;
Matches 16; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Probe Sequence
US-10-956-157-265753
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US-10-719-900-342034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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US-10-956-157-93516
US-10-956-157-93516
Sequence 93516, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wouth
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
TITLE OF INVENTION: US-10-04
CURRENT PILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 319805
SEQ ID NO 93516
LENGTH: 25
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                                                                                                                                                           Length 25;
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 17282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                         Query Match 55.7%; Score 15.6; DB 15; Best Local Similarity 81.8%; Pred. No. 8.7e+03; Matches 18; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 105925, Application US/10809189; Publication No. US20050048531A1; GENERAL INFORMATION: APPLICANT: Michael Mittmann; APPLICANT: David Mack; APPLICANT: David Lockhart; APPLICANT: Affwertrix, Inc.; TITLE OF INVENTION: Methods of Genetic Analysis; FILE REFERENCE: 3101.1 CURRENT APPLICATION NUMBER: US/10/809,189; CURRENT APPLICATION NUMBER: US/09/396,196; PRIOR FILING DATE: 1999-09-15; PRIOR FILING DATE: 1999-09-15; PRIOR FILING DATE: 1998-09-17; NUMBER OF SEQ ID NOS: 127806; SOFTWARE: FBSESEQ for Windows Version 4.0; LENGTH: 25
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Pred. No. 8.7e+03;
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Best Local Similarity 81.8%;
Matches 18; Conservative
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CORGANISM: mus musculus
US-10-809-189-105925
                                                                TYPE: DNA
ORGANISM: Homo sapien
US-10-098-2638-17282
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Best Local Similarity
Matches 19; Conserv
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US-10-719-900-463285/c
; Sequence 463285, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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    12 CAAGACTICATITIG 26
                                            15 CAAGACTTCATTTTG 1
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Matches 18; Conservative
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; ORGANISM: Mus musculus
US-10-719-900-839653
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Mus musculus
US-10-719-900-463285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 898965, Application US/10719900
; bublication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; TITLE OF INVENTION: WHERE: US/10/719,900
; CURRENT APPLICATION NUMBER: 05/03-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11-20
; NUMBER OF SEQ ID NOS: 982914
; SEQ ID NO 898965
; LENGTH: 25
                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 15.2; DB 21; Length 25;
Pred. No. 1.3e+04;
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CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 342034
LENGTH: 25
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SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 292506
LENGTH: 25
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TITLE OF INVERTION: Methods of Genetic Analysis of Mouse
FILE REPERENCE: 35.28.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT PILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
                                                                                                                                                                                                                                         Query Match 54.3%; Score 15.2; DB 21;
Best Local Similarity 85.0%; Pred. No. 1.3e+04;
Matches 17; Conservative 0; Mismatches 3;
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
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Best Local Similarity 85.0%
....hes 17; Conservative
                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-342034
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US-10-719-900-898965
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US-10-719-900-292506
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US-10-719-900-292506/c
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US-10-719-900-898965
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US-10-719-900-839653, Application US/10719900

Publication No. US20050026164A1

GRNERAL INFORMATION:

GREEAL INFORMATION:

TITLE OF INVENTION: Methods of Genetic Analysis of Mouse

FILE REFERENCE: 3528.1

CURRENT PELLING DATE: 2003-11-20

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR APPLICATION NUMBER: 60/427,808

PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 982914

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

FERRIT OF 199653
TILE OF INVENTION: Methods of Genetic Analysis of Mouse FILE REFERENCE: 35201
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 00/427,808
PRIOR PILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 463285
LENGTH: 25
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78.3%; Pred. No. 1.6e+04;
ive 0; Mismatches 5; Indels
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; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Nue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
```

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APPLICANT: Mounts, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: 101896-043000 (AM 101081)
CURRENT APPLICATION NUMBER: US/10/956,157
CURRENT FILING DATE: 2004-10-04
NUMBER: PATENTIN VERSION 3.2
SEQ ID NO 93524
LEMGTH: 25
LEMGTH: 25
TYPE: DNA
TYPE: DNA
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PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 933648
LENGTH: 25
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US-10-956-157-93524
; Sequence 93524, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                   12 CAAGACTICATITIG 26
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Best Local Similarity 78.39
Matches 18; Conservative
                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-933648
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Search completed: June 21, 2005, 20:43:48 Job time : 530 secs

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us-10-717-243-59.open.rni

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pseudoce 61, Application US/07988430

patent No. 5416202

GENERAL INFORMATION:

APPLICANT: Bernhard, Susan L.

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Lai, Shau-Ping

TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marchall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell

STREET: Street

CITY: Chicago

STREET: Street

CITY: Chicago

STATE: Illinois

COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION UNDER: US 07/901,707
FILING DATE: 19921209
FRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UW-1992
PRIOR APPLICATION NUMBER: 3302
FRIOR APPLICATION NUMBER: 33302
FRIOR APPLICATION NUMBER: 33302
FRIOR APPLICATION NUMBER: 33302
FRIOR APPLICATION NUMBER: 3133
TELECOMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-576
TELEPHONE: CARRACTERISTICS:
TELEPHONE: CARRACTERISTICS:
TELEPHONE: CARRACTERISTICS:
TELERAX: 25-3856
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: NUCLEIC ACID
                         RESULT 1
US-07-988-430-61
June 21, 2005, 14:27:12 ; Search time 128 Seconds (without alignments) 357.936 Million cell updates/sec
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.: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
.: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-488-1138-59
US-08-646-360-59
US-08-136-389-59
US-09-136-389-59
US-09-136-389-59
US-09-11-485-59
PCT-US9-0948-61
US-07-901-707-11
US-07-901-707-11
US-07-901-707-11
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US-07-908-430-57
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US-08-646-360-11
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US-08-646-360-11
US-08-631-803-246
US-08-631-803-246
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US-08-621-803-258
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                                                                                                                                                                                                                                     1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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US-08-621-803-250
US-08-521-352-250
US-08-781-986A-329
US-08-71-986A-329
US-08-201-879A-2
US-08-103-663-31
US-09-103-663-31
US-09-949-016-11750
US-09-949-016-116934
US-08-115-106-9
US-08-115-106-9
US-08-115-106-9
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## ALIGNMENTS

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STRANDEDNESS:
TOPOLOGY: line
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Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                        Query Match 100.0%; Score 28; DB 1; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0031; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FLING DATE: 18-AFR-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PROR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
FILING DATE: 04-NOV-1991
ATTONEY/AGENT INPORMATION:
MAND: MANDER: US-MANDINERATION:
                                                                                                                                                                                1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                       1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 28 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
; TOPOLOGY: linear; MOLECULE TYPE: DNA US-07-988-430-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                          RESULT 2
US-08-425-336-59
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us-10-717-243-59.open.rni

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GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28; DB 2; Length 28; Pred. No. 0.0031; Mismatches 0; Indels
STREET: ANDRESS:
STREET: S00 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ZIP: 60661
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 cacargraaacaagacrrcarrrregc 28
                                                                                                                                                                                                                                                                                            PRICE APPLICATION 5730

PRICE APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12.MAY-1994

PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691

FILING DATE: 12.MAY-1993

PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY AGENT INFORMATION:
NAME: MCNicholas, Janet M.

REGISTATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-839-765-59
; Sequence 59, Application US/08839765
; Patent No. 6146631
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INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: DNA
US-08-646-360-59
        Sequence 59, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 28; DB 1; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0031; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-477-484B-59
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US-08-646-360-59
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1 CACATGTAAAACAAGACTTCATTTTGGC 28
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COMPUTER: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Pal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59, Application US/09610838
Patent No. 6376217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312/707-9155
TELEX: 650 389-1248
INFORMATION FOR SEQ ID NO: 59: SEGUENCE CHARACTERASICS: LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-610-838-59
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US-09-136-389-59
US-09-136-389-59
i Sequence 59, Application US/09136389
j Patent No. 6146850
j Patent No. 6146850
j GENERAL INFORMATION:
    APPLICANT: Better, Marc D.
    APPLICANT: Garroll, Stephen F.
    APPLICANT: Garroll, Stephen F.
    APPLICANT: Grudnika, Gary M.
    TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
    TITLE OF INVENTION: Proteins
    NUMBER OF SEQUENCES: 173
    CORRESPONDENCE ADDRESS:
    ADDRESSE: McAndrews, Held & Malloy, Ltd.
    STREET: 500 West Madison Street, 34th floor
    CITY: Chicago
    STATE: Illinois
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                      COMPUTER KEADLE FORM:
MEDIUW TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSITCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 19-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,918
REFERENCE/OWNUNICATION INFORMATION:
TELEPHONE: 312/707-8899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CACATGTAAAACAAGACTTCATTTTGGC 28
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TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60661
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-839-765-59
                     Chicago
                                                                        USA
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
INVERS OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STREET: 11inois
COUNTRY: USA
ZIP: 60661
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Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels
OPERATING STSTEM:
OPERATING STSTEM:
OPERATING STSTEM:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
CLASSIFICATION
FILING DATE:
APPLICATION NUMBER: US/09/136,389
FILING DATE:
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REFERENCE/OPERATION:
TELEPRAX: 312/707-8889
TELEFRAX: 312/707-8889
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APPLICANT: Bernhard, Susan L.
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lai, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michell
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                     APLICATION NUMBER: 08/839,/65
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
FILING DATE: 09-DEC-1992
FILING DATE: 09-DEC-1992
FILING DATE: 19-JUN-1992
FILING DATE: 19-JUN-1992
FILING DATE: 19-JUN-1992
FILING DATE: 19-JUN-1992
FILING DATE: 19-JUN-1991
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOY-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 31,918
RELEPHONE: 312/707-8889
TELEFRAKE: 09-0555
TELEFRAKE: 09-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 28; DE
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CACATGTAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US92/09487
                    US/09/711,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 61, Application PC/TUS9209487 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                 FILING DATE:
CLASSIFICATION:
RICR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: :60603
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Patent No. 649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studmika, Gary M.
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 28; DB 3; Length 28; 100.0%; Pred. No. 0.0031;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
CITY: 11inois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                 CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICADIAS JANCE N.
REGISTRATION NUMBER: 32,918
NAME: MCNICADIAS JANCE N.
REGISTRATION NUMBER: 32,918
                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 650 389-1248
INFORMATION FOR SEQ ID NO: 59:
SEGUIENCE CHARACTERIFICS:
LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 28; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: DNA US-09-610-838-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-711-485-59
SOFTWARE:
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APPLICANT: Bernhard, Susan i.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, July Steve F.
APPLICANT: Lane, July Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                         Query Match 88.6%; Score 24.8; DB 1; Length 813; Best Local Similarity 92.9%; Pred. No. 0.16; Matches 26; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILLING DATE: 19920619
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5376546and, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                         303 CACAATTAAAACAAGACTTCATTTTGGC 330
                                                                                                                                                                                                                                                                                                                                                         1 CACATGTAAAACAAGACTTCATTTTGGC 28
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Patent No. 5376546
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
(312) 984-5750
                                                                                        LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                 TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-07-901-707-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60603
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TELEFAX:
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APPLICANT: Bernhard, Susan L.
APPLICANT: Bernhard, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
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100.0%; Score 28; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two First National Plaza, 20 South Clark
STREET: Street
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APPLICATION NUMBER: US 07/787,567
FILING DATE: US 4NOV-1991
ATTORNEY,AGENT INFORMATION:
NAME: No. 5376546and, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37,129,30910
TELECOMMUNICATION INFORMATION:
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                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDRER:
FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNY/AGENT INFORMATION:
NAME: NOLLAND, Greta E.
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 11, Application US/07901707; Patent No. 5376546
                                                                                                                                                                                                                                                    REFERENCE DOCKET NUMBER: 3113:
TELECOMMUNICATION INFORMATION:
TELEFAX: (312) 344-5750
TELEFAX: (312) 944-9740
TELEFX: 25-3856
INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (312) 346-5750
19921104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: USA
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US-07-901-707-11
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 11, Application US/08425336
; Patent No. 5621083
Bernhard, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
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TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.93
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                     ZIP: 60603
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-988-430-57
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                                                                                                                                                                                                       APPLICANT: Bernhard, Susan L.
APPLICANT: Bernhard, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza, 20 South Clark STREET: Street CITY: Chicago STATE: 111inois COUNTRY: USA
                                  303 cacaarraaacaagacrrcarrriggc 330
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 946-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                 RESULT 13
US-07-988-430-11
; Sequence 11, Application US/07988430
; Detent No. 5416202
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57, Application US/07988430 Patent No. 5416202
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Best Local Similarity 92.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 813 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear // MOLECULE TYPE: cDNA US-07-988-430-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60603
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US-07-988-430-57
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/988,430

FLING DATE: 19921209

CLASSIFICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION NUMBER: US 07/901,707

FILING DATE: 19-JUN-1992

PRIOR APPLICATION NUMBER: US 07/787,567

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5416202and, Greta E.

REGISTRATION NUMBER: 35302
                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                   STREET: Two First National Plaza, 20 South Clark
STREET: Street
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
STREET: 6300 Sears To
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CUTY: Chicago
COUNTRY: Ullinois
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
COMPUTER: ENDOY disk
COMPUTER: FROME PER COMPATIBLE
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Search completed: June 21, 2005, 16:14:04 Job time : 130 secs

303 CACAATTAAACAAGACTTCATTTTGGC 330

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Title: Perfect score:

Sequence:

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Scoring table:

Searched:

Database

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AX430080 Sequence
AR125594 Sequence
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AX026369 Sequence
AX11379 Sequence
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AX17677 Sequence
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Better, M.D., Carroll, S.F. and Studnicka, G.M.
Immunotoxins comprising ribosome-inactivating proteins
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 5744580-A 59 28-APR-1998;
Location/Qualifiers
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Sequence 59 from patent US 5756699.
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AR010103.1 GI:3968908
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/wol_type="unassigned DNA"
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AR003767
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AR010103 Sequence
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AR430985 Sequence
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AR068695 Synthetic
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Copyright (c) 1993 - 2005 Compugen Ltd.
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PAT 04-DEC-1998

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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 6146631-A 59 14-NOV-2000;
Location/Qualifiers
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Polynucleotides encoding gelonin sequences
Patent: US 5837491-A 59 17-NOV-1998;
Location/Qualifiers
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Patent: US 5756699-A 59 26-MAY-1998;
Location/Qualifiers
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AR141238
AR141238.1 GI:15100755
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/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
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AR055309.1 GI:5980886
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Bernhard, S.L., Better, M.D., Carroll, S.F., Lane, J.A. and Lei, S.-P.
Materials comprising and methods of preparation and use for ribosome-inactivating proteins
Patent: US 5416202-A 61 16-MAY-1995;
Location/Qualifiers
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Better, M.D., Carroll, S.F. and Studnicka, G.M.
Immunotoxins comprising ribosome-inactivating proteins
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100.0%; Score 28; DB 6;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 28; Conservative 0; Mismatches 0;
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                                                                                                                                                                 Deter, M. D. and Carroll, S. F.
Proteins encoding galonin sequences
Patent: US 6146850-A 59 14-NOV-2000;
Location/Qualifiers
                 Seguence 59 from patent US 6146850.
AR141475
AR141475.1 GI:15100991
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 59 from patent US 5621083.
140520
140520.1 GI:2082812
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/mol_type="unassigned DNA"
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PAT 02-DEC-1993
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                                                                                                                                                                                                                  Lecocq,J.P.
Vectors for the expression of an antigenic rabies protein in eukaryotic cells, and their use in the preparation of a vaccine Patent: EP 0140762-A 19 08-MAY-1985;
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synthetic construct
other is artificial sequences.
1 (bases 1 to 28)
Lathe, R., Kieny, M.P., Lemoine, Y., Loison, G., Aigle, M. and
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                                         28 bp DNA linear
Nucleotide sequence 19 from patent number EP0140762.
A04644
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Pred. No. 6.3e+04;
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/mol_type="unassigned DNA"
/db xref="taxon:32630"
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Location/Qualifiers
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Sequence 147 from Patent WO0129262.
AX115024
AX115024.1 GI:14031966
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1 Similarity 74.1%;
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A34707
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Better,M.D. and Carroll,S.F.
Fusion proteins and polynucleotides encoding gelonin sequences
Patent: US 6376217-A 59 23-APR-2002;
Location/Qualifiers
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 6649742-A 59 18-NOV-2003;
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100.0%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 28; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 28; Conservative 0; Mismatches 0; Indels
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Patent: US 5621083-A 59 15-APR-1997;
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Sequence 59 from patent US 6376217.
AR368004
               Location/Qualifiers
1. .28 /organism="unknown"
/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 59 from patent US 6649742.
AR430985.1 GI:40192816
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/mol_type="genomic DNA"
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/mol_type="genomic DNA"
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AB068695 24 bp DNA linear SYN 21-MAY-2003
Synthetic construct DNA, reverse primer for human STS sts-SGC33042
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Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
                                                                                                                       12-MAR-2001 JP 2001068285
EIICHI SOEDA
C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566,
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Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Madicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8875, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8047)
Location/Qualifiers
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              Patent: JP 2001321190-A 212 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA GENOTECHS
OS Artificial Sequence
PN JP 2001321190-A/232
PD 20-NOV-2001
PF 12-NAR-2001 JP 2001068285
PI EIICHI SOEDN
PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/5
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A BAC-based STS-content map spanning a 35-Mb region of human
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/organism='Artificial Sequence'
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    forganism="synthetic construct"
/mol type="genomic DNA"
    /db_xref="taxon:32630"

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synthetic construct
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 method of arraying genome clone
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Genomics 74 (1), 55-70 (2001)
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Method for diagnosing non-small cell lung cancers
Patent: WO 20040314134 383 15-ARP-2004;
Oncotherapy Science, Inc. (JP); Japan as represented by the
president of the university of Tokyo (JP)
Location/Qualifiers
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                                                                 Picoult-Newburg, L. and Pohl, M. Genotyping reagents, kits and methods of use thereof Patent: WO 0129262-A 147 26-APR-2001; Orchid BioSchences, Inc. (US)
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54.3%; Score 15.2; DB 6;
Best Local Similarity 81.0%; Pred. No. 1.1e+05;
Matches 17; Conservative 0; Mismatches 4;
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Pred. No. 1.7e+05;
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1 (bases 1 to 24)
Soeda, E.
                                   other sequences; artificial sequences.
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Search completed: June 21, 2005, 18:22:42 Job time: 1807 secs

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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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28
1 CACATGTAAAACAAGACTTCATTTTGGC 28
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	AZ351302 1M0089I17	BZ665403 SALK 1114	BZ665404 SALK_1114	AL466420 T. brucei	AG202132 Pan trogl	BH863433 SALK 0938	BZ382660 SALK_1186	_	AI431201 Ba22£07.y	BQ590149 E012845-0		AZ804962 2M0066E10	AJ668296 AJ668296	AZ803453 2M0063D19	CD532369 26017 Ara	AJ593422 Arabidops	AU014317 AU014317	BQ589288 S014007-0	AJ591973 Arabidops	AU260224 AU260224	AG189325 Pan trogl	BQ584385 E011858-0	CD576873 25 H02 25	AZ759583 1M0552B21
SUMMARIES	f	ID	AZ351302	BZ665403	B2665404	TA140C03P	AG202132	BH863433	BZ382660	BZ763517	A1431201	BQ590149	AZ784713	AZ804962	AJ668296	AZ803453	CD532369	AJ593422	AU014317	BQ589288	AJ591973	AU260224	AG189325	BQ584385	CD576873	AZ759583
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de	Query	Match	45.7	45.7	45.7	45.0	44.3	44.3	44.3	44.3	44.3	43.6	43.6	43.6	42.9	42.9	42.1	42.1	41.4	41.4	41.4	41.4	41.4	40.7	40.7	40.7
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AJ666432 AU257173 AJ592989 AZ592489 BXS67143 BXS67743 BXS779804 CP298945 BH910951 AZ77815 AZ77815 AZ77815 AZ77815 AZ77815 AZ77815 AZ77815 AZ77815 AZ77815 AZ77815 AZ77815 AZ7786 AZ77815 AZ7788	ALIGNMENTS  AZ351302  Lone UUGCIM0089117 F, genomic sur AZ351302  AZ351302  AZ351302  AZ351302  AZ351302  AZ351302  Mus musculus  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Busaryota; Metazoa; Chordata; Cran  Reilly, M., Rose, R., Barber, M., Bose, R., Stoke  Wouse whole genome scaffolding wit  plasmid inserts  Unpublished (2000)  Contact: Robert B. Weiss  University of Utah  Email: Gunnedical Polymers Resea  84112, USA  Fax: 801 585 5606  Fax: 801 585 506  Fax: 801 585 5177  Email: ddunn@genetics.utah.edu  Insert Length: 10000 Std Error:  Location/Qualifiers  1. 24  Aligh quality sequence stop: 24.  Location/Qualifiers  // organia="CS7BL/67"  // organia="UUGCIMO089117"  // sex="Male"	E. Coli str "Mouse 10kb or: PWD42nv 7BL/6J (mal Mouse DNA F
44986644688644888	110 d	www.
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	AZ351302 IMO089117F Mouse 10kb clone UUGCIM0089117 F, AZ351302 GSS. Mus musculus (house mo musculus (house mo musculus (house mo musculus) Eukaryota; Metazoa; Ch Mammalia; Eutheria; Ro 1 (bases 1 to 24) Dunn,D., Aoyagi,A., Ro 1 (bases) I (bases 1 to 24) Dunn,D., Aoyagi,A., Ro 1 (bases) I (bases) I (bases) I (bases) I (bases) I (2000) Contact: Robert B. Wei University of Utah Gen University of Utah Gen University of Utah Gen University of Utah Gen University of Utah Gen University of Utah Gen Insert Length: 10000 Rea: 308, Biomedical Po 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics. Insert Length: 10000 Plate: 0089 row: I cast on I cacation/Qual I . 24 /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="Muchiculture"/ /organism="UUGCI"/ /ordow="UUGCI"/ /exa="Male"	lab hos clone l note="V nusculus aborato
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was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gol electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ665403 28 bp DNA linear GSS 31-JAN-2003 SALK 111481.23.75.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_111481.23.75.x, genomic
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/clone="SALK 111481.23.75.x"
/clone="SALK 111481.23.75.x"
/clone="lp="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of
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Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
The Salk Stale Stale Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Class: TDNA tagged
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BZ665403
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SOURCE

TITLE

COMMENT

ORIGIN

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TA140C03P 27 bp DNA linear GSS 13-DEC-2000
T. brucei sheared genomic DNA clone 140c03, forward sequence,
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                      BE665404 linear GSS 31-JAN-2003 SALK_111483.22.35.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_111483.22.35.x, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana Buratophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alonso, J.M., Leise, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
The Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Phines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Glome="SALK 11483.22.35.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines factored to contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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45.7%; Score 12.8; DB 8; Length 28; 87.5%; Pred. No. 9.1e+05; 1.ve 0; Mismatches 2; Indels
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/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:3702"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            BZ665404.1 GI:28183008
                                                                                                                  4 ATGTAAAACAAGACTT 19
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 survey sequence.
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of clone tracking errors.
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                         PRIMERS
                                                                LIBRARY
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KEYWORDS
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BH863433/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC), 52. Oun-dong, Yusong-gu, Daejeou 305-333, Korea (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/, Tel:B2-42-866-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                        Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                                                                                                                                                     Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kin, H., Joo, S., Kim, C., Song, W. and Yoo, H. Unpublished
                                                                                                                                              Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AG202132 22 bp DNA linear GSS 06
Pan troglodytes DNA, clone: RP43-085C03.TJ, genomic survey
                                                                                  sukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 1.1e+06;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="TREU927"
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/clone="140c03"
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                                       Trypanosoma brucei
Trypanosoma brucei
                                                                                                           frypanosoma.
1 (bases 1 to 27)
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                                                                                                                                                                                                                                                                                                        nh1@sanger.ac.uk
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AG202132
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Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Bcker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Order: Joseph R. Bcker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BH863433 27 bp DNA linear GSS 05-AUG-2002 SALK 093870 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_093870, genomic survey sequence.
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/clone="SALK_093870"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Engermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 27)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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0
                                                                                                                                                                                                                                                                                                                                   /sex="male"
/cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.3%; Score 12.4; DB 9; Length 22; 72.7%; Pred. No. 1.3e+06; ive 0; Mismatches 6; Indels
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/organism="Arabidopsis thaliana"
                                                                                                                                                                                                                /organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="RP43-085C03.TJ"
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/ecotype="Col-0"
                            JRAkı
Vector
Nector
R.Site 1: Econ.
R.Site 2: EcoRI.
Location/Qualifiers
.22 ...="Pan trog?" ...mc.
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Location/Qualifiers
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Sequencing: TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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Best Loca Matches

BZ382660/c

RESULT 7

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

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AI431201 28 bp mRNA linear EST 23-JUL-2004 sa22f07.y2 Gm-c1006 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1006-62 5' similar to SW:ATP6_TRYBB P24499 ATP SYNTHASE A CHAIN
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Shoemaker, X., Kain, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, X., Beila, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.,
Dublic Soybean EST project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
                               Arabidopsis thaliana
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 27)
Anoso, JM., Lesise, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
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/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used car be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At4g22800. Class: TDNA tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis Genome (2001)
Unpublished (2001)
Contact: 'Oscape Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
The Salk Institute for Biological Studies
Tollo N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
(201)
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   Length 27;
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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44.3%; Score 12.4; DB 8; 72.7%; Pred. No. 1.3e+06; ive 0; Mismatches 6;
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BZ763517
BZ763517.1 GI:28936070
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BZ763517/c DEFINITION

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RESULT 8

Matches

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/db_xref="taxon:10090"
/clone="UUGC2M0027K21"
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Unpublished (2000)
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Fax: 801 585 7177
                                                                                                                                                      line)"
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                                                                                                                                                             Figure 1: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTS on clone' field. Trace
considered overall poor quality Possible reversed clone: similarity
on wrong strand This clone is available through: Biogenetic
Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423'
Seq primer: T3 ET from Amersham
High quality sequence stop: 1
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Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TE1: 314 286 1800
Fax: 314 286 1810
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/clone="GENOME SYSTEMS CLONE ID: Gm-c1006-62"
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 18 Std Brror: 0.00
Plate: 19 row B column: 19
Seq primer: T7; GTAATACGACTCACTATAGGGC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Williams 82"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab host="XL10-Gold"
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BQ590149
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/clone lib="MPIZ-ADIS-024-storage root" force="Vector: pCMVSPORT6; Site 1: Sal1; Site 2: Not1; CDM library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Binbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  orientation:
SP6-Sall-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Notl-T7; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung: Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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2M0027K21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0027K21 R, genomic survey sequence.

    18
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KW82320 (double haploid, monogerm breeding

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Length: 10000 Std Brror: 0.00
0027 row: K column 31
                                                                                                                                                                        /db_xref="taxon:161934"
/clone="024-019-B19"
/tissue_type="storage root"
/lab_host="EMDH108"
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Class: plasmid ends
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University of Utah Genome Center
University of Utah
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/strain="C57BL/6J"
                                                                                                                                                  db_xref="GABI:189975"
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Location/Qualifiers
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                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gelectrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114[gb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XII.0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wniversity of Utah
84112, USA
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             /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42hv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
'lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
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Insert Length: 10000 Std Error: 0.00
Plate: 0066 row: E column: 10
Seg primer: CGTTGTPAPACGACGCCAGT
Class: plasmid ends
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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Location/Qualifiers
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/clone="UUGC2M0066E10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 14: Conserv
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
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В

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Laboracy yourse DNA kesource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch oritice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwM92 (giffa)2114 [gb](AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Single pass sequencing. Bases called and trimmed with phred
V0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
ECORI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institite,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of CDNA and EST resources for studying reproduction and embryo development in pigs and cattle
(Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organisme="Sus scrofa"
/mol_type="mRNA"
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/clone="C0000045 Jl2"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
Not1; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 24)
                            /clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PMD42In', Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-'
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AJ668296.1 GI:49352747
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Matches 14; Conserve
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Length 26;

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Query Match 42.9%; Score 12; DB 8; Length 26; Best Local Similarity 75.0%; Pred. No. 1.9e+06; Matches 15; Conservative 0; Mismatches 5; Indels
                                                                                                                           2 ACATGTAAAACAAGACTTCA 21
                                                                                                                                                        23 ATATAGAAAGAAGACTACA 4
                                                                                                                                                                                                                                                                                                                                                                                                        CD532369.1 GI:40452381
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Matches 16; Conserv
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CD532369/c
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                               26 bp DNA linear GSS 16-FEB-2001 200053D19R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZW0063D19 R, genomic survey sequence. AZ803453
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Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57bL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
84112, USA
                                                                         Gaps
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                     42.9%; Score 12; DB 1; Length 24; 75.0%; Pred. No. 1.9e+06; Live 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:10090"
/clone="UUGC2M0063D19"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
                                                                                                                         8 AAAACAAGACTTCATTTTGG 27
                                                                                                                                                                      24 AAAAAAAATTTTTTTGG 5
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Query Match
Best Local Similarity 75.0%
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Fax: 801 585 7177
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                                                                                                                                                                                                                                             RESULT 14
AZ803453/C
                                                                                                                                                                                                                                                                                                                       DEFINITION
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ORGANISM
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KEYWORDS
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FEATURES

TITLE

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/organisms="Arabidopsis thaliana"
/mol type="mRNA"
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/db_raxon:3702"
/tisue_type="Leaf"
/dev stage="Yellow Leaf With Greenish Base Area"
/dav stage="Yellow Leaf With Greenish Base Area"
/dav lab_host="R. coli"
/dlo_lib="Arabidopsis Leaf Senescence Library"
/dlo="Organ: Rosette Leaf; Vector: pBluscript SKII+;
/note="Organ: Rosette Leaf; Vector: 
                                                                                                                                                                                                                                                                                                                                                                                                                                              26017 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Horticulture
Cornell University
119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA
Tel: 607 254 5418
Fax: 607 255 0599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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1 Similarity 69.6%; Pred. No. 2.3e+06;
16; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guo,Y., Cai,Z. and Gan,S.
Transcriptome of Arabidopsis leaf senescence
Plant Cell Environ. 27 (5), 521-549 (2004)
Contact: Susheng Gan
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Insert Length: 25 Std Error: 0.00
Seg primer: T7
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Arabidopsis thaliana
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June 21, 2005, 16:11:58; Search time 417 Seconds (without alignments) 397.489 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                          US-10-717-243-59
28
1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                        4390206 segs, 2959870667 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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genesedn2000s:*
genesedn2001as:*
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geneseqn2003bs:*
                Copyright
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:* geneseqn2003ds:*

	Description	Aaq42253 PCR prime	Acf04990 Hair papi	Aan50399 Sequence	Aci17291 Human mic	Aah37351 SNP speci	Adn35702 Human NSC	Aci70121 Human mic	Aax10106 Human bia	Abl43188 Human chr	Aaz89383 A. thalia	Acil9346 Human mic	Adg31135 C-fos mRN	Adq31044 C-fos mRN	Adk72984 Chimeric	Adk72983 Chimeric	Adk73036 Chimeric	Adk73099 Chimeric	Adj51107 Human NOV	Adr20628 Human oes	Ack15826 Human mic
SUMMARIES	ID	AAQ42253	ACF04990	AAN50399	ACI17291	AAH37351	ADN35702	AC170121	AAX10106	ABL43188	AAZ89383	ACI19346	ADQ31135	ADQ31044	ADK72984	ADK72983	ADK73036	ADK73099	ADJ51107	ADR20628	ACK15826
	DB	8	10	нi	σ	4	12	σ	~	9	ო	σ	12	12	12	12	12	12	12	13	σ
	* Query Match Length DB	28	28	28	25	27	23	25	28	24	25	25	24	24	20	20	20	20	22	25	25
	% Query Match	100.0	9.3	6.4	5.7	4.3	5.9	2.9	2.9	2.1	2.1	2.1	1.4	51.4	0.7	50.7	0.7	0.7	0.7	0.7	0.0
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	Score	28	16.6	15.8	15.6	15.2	14.8	14.8	14.8	14.6	14.6	14.6	14.4	14.4	14.2	14.2	14.2	14.2	14.2	14.2	14
	Result No.		7 0	m	O 4	2	9 U	c 2	ю С	σ	c 10	11	c 12	c 13	c 14	c 15	c 16	c 17	c 18	19	c 20

Aci17290 Human mic Aad28022 A. tumefa	Aaf58586 Arabidops Adi19115 Arabidops	Aaa40065 Rice dise	Aas17875 FC-1 forw	Aci84703 Human mic	Aci42430 Human mic	Adg92070 Schizophr	Abz81587 PKA regul	Adh18270 2'-MOE ga	Adk72943 Chimeric	Adk72748 Chimeric	Adk72793 Chimeric	Adl58504 Human ESM	Adl58418 Human ESM	Ado32811 Antisense	Aas05019 Neurofibr	Aal47475 Human zin	Human	Aci77522 Human mic	Aci54916 Human mic	Aci85790 Human mic	Aac68513 Mitochond	Abx13209 DNA encod
ACI17290 AAD28022	AAF58586 ADI19115	AAA40065	AAS17875	ACI84703	ACI42430	ADG92070	ABZ81587	ADH18270	ADK72943	ADK72748	ADK72793	ADL58504	ADL58418	AD032811	AAS05019	AAL47475	ABA04869	ACI77522	ACI54916	AC185790	AAC68513	ABX13209
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50.0	49.3	49.3	49.3	49.3	49.3	49.3	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6	48.6
14	13.8 13.8	13.8	13.8	13.8	13.8	13.8	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6	13.6
22	23	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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## ALIGNMENTS

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Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; Mutagenic polymerase chain reaction; 88.
                                                     PCR primer GeloC-20 to replace Ile103 of gelonin with Cys.
                                                                                                                                                                                         SP;
                                                                                                                                                                                         Lei
                                                                                                                                                                                         Lane JA,
      BP.
                                                                                                                                                     91US-00787567.
92US-00901707.
                                                                                                                                        92WO-US009487.
     AAQ42253 standard; cDNA; 28
                                 (revised)
(first entry)
                                                                                                                                                                           (XOMA ) XOMA CORP.
                                                                                                                                        04-NOV-1992;
                                                                                                             WO9309130-A1
                                                                                                                                                      04-NOV-1991;
19-JUN-1992;
                                25-MAR-2003
13-SEP-1993
                                                                                                                          13-MAY-1993.
                                                                                                Synthetic.
                    AAQ42253;
AAQ42253
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Carroll SF, Better MD, Berhard SL,

WPI; 1993-167617/20.

Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.

Example 3; Page 35; 163pp; English.

Fifteen analogues of gelonin were constructed. Ten non-cysteine residues in surface positions and available for conjugation to a second protein were targeted for substin. In the other analogues, one or both of the native Cys residues present in gelonin were substd. Overlap extension PCR was used to construct the various analogues. Primer geloC-20 was used in

RESULT 2

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The inventors claim vectors which express a rabies virus antigenic protein in eucaryotic cells. AANS0399 is part of a vector designed for expression in yeast. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR Afield.) (Updated on 25-MAR-2003 to correct PR Afield.) (Updated on 25-MAR-2003 to correct PR Afield.) (Updated on 27-MAR-2003 to correct PR Afield.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression vector contg. DNA sequence for antigenic rabies protein - aviral or yeast expression elements, for transforming eucaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
                                                                             Sequence of the junction betwen yeast PGK gene promoter and rabies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.4%; Score 15.8; DB 1; Length 28; Best Local Similarity 74.1%; Pred. No. 6.2e+03; Matches 20; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                     /product= "rabies glycoprotein N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human microarray DNA oligonucleotide SEQ ID NO 17282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loison M, Aigle J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 28 BP; 14 A; 3 C; 4 G; 7 T; 0 U; 0 Other;
                                                                                                                                       Rabies antigen; vaccine; immunogen; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAATATAAAACAAGATCTAATATGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CACATGTAAAACAAGACTTCATTTTGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                   Location/Qualifiers
14. 19
/*tag= a
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/*tag= b
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84FR-00004754.
84FR-00015716.
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ID ACI17291 standard; DNA; 25
                                        (first entry)
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                                                                                                                                                                            Saccharomyces cerevisiae.
Rabies virus.
  (revised)
                      (revised)
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                                                                                                glycoprotein gene.
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27-MAR-1984;
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  27-AUG-2003
                  25-MAR-2003
16-OCT-1991
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                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                         Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hair growth tonics or hair stimulants containing hair papilla cell growth factors like Pochonia chlamydosporia-originated macrolide compounds capable of inhibiting function of WNT-5A, useful in drugs and cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; hair growth; stimulant; tonic; hair papilla cell growth; promoter; WNT-5A; endocrine-gen; PCR; primer; probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to hair papilla cell growth promoters which contain compounds with inhibitory activity on the function of WNT-5A. The hair growth tonics and hair stimulants are useful in drugs and cosmetics. The present sequence is a primer/probe shown in the exemplification of
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
of Ile103 of gelonin by Cys. (Updated on 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        Hair papilla cell growth promoter related probe SEQ ID NO: 55.
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Pred. No. 2.8e+03;
                                                                                            Query Match
100.0%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28 BP; 10 A; 5 C; 3 G; 10 T; 0 U; 0 Other;
                                                         Sequence 28 BP; 10 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kasai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                              1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                  1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 118; Opp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujimoto N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ACATGIAAAACAAGACTTCATTT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2003; 2003WO-JP004884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-2002; 2002JP-00115529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TAIS ) TAISHO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                 ACF04990 standard; DNA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shinonaga H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-845259/78
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the substn. of Ile correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003086334-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-2003
                                                                                                                                                                                                                                                                                                                                                          ACF04990;
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                                                                                                Query Match
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ACF04990/C
11D ACF0499
XX AC ACF0499
XX BY 12-FEBXX Human;
XX Human;
XX WNT-5A,
XX WO2003
XX WO2003
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Gaps

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cross-species comparison.

Homo sapiens

24-OCT-2003 (revised)

AAN50399;

RESULT 3
AAN50399
ID AAN5
XX
AC AAN5
XX
AC AAN5

Matches

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perfect match, perfect mismatch, antisense match or antisense mismatch.
Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library.
In analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring probes are attached to a solid support. The analysis comprises monitoring can expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid to the sequence or specific contaction to identify or detect the sequence or specific mutations of any gene, in mapping the 5' termin of mRNA molecules by primer extensions or in screening CDNA or genomic libraries or subclones
                                                                                                                                                                                                                                                                                                                                New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 17282; 9pp; English
                                                                                                         15-MAR-2002; .2002US-00098263
                                                                                                                                                     16-MAR-2001; 2001US-0276759P
                                                                                                                                                                                               (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                        WPI; 2003-567953/53.
                     US2003104410-A1
                                                                                                                                                                                                                                            Mittmann MP;
                                                            05-JUN-2003.
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primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been scolated and previously sequenced. The sequence presented is one of the nucleic acid probes incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic format directly from USPTO at sequata.uspto.goc/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                             55.7%; Score 15.6; DB 9; Length 25; 81.8%; Pred. No. 7.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                           Sequence 25 BP; 7 A; 3 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 81.8
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                             Query Match
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AAH37351 standard; DNA; 27 BP. AAH37351; 

14-AUG-2001 (first entry)

SNP specific SNPE primer SEQ ID 147.

Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; primer; ss.

Human NSCLC gene semi-quantitative PCR primer forward primer #191.

(first entry)

01-JUL-2004

ADN35702;

ВР

ADN35702 standard; DNA; 23

ADN35702/c

ss; primer; cytostatic; gene therapy; vaccine; non-small cell lung cancer; NSCLC; diagnosis; cancer; URLC1

Homo sapiens.

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Suppraction (SPRE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the colliquoucleotides of the invention. The PCR primers are used to amplify a cliquoucleotides of the invention. The PCR primers are used to amplify a cliquoucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The presence or identity of a SNP and for genotyping nucleic acid sample by colliquoucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of caused by one or more SNPs. Phenotypic traits include disease e.g. adjunctionally a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include disease e.g. osteogenesis imperfecta and acute intermittent porphyria. Phenotypic craits also includes symptoms of or susceptibility to multifactorial disease, including, rheumatoid arthritis, multiple sclerosis, craits also including, rheumatoid arthritis, multiple sclerosis, including, rheumatoid arthritis, multiple sclerosis, conference, nervous system diseases and infection by pathogenic conference expressing internity analysis. The present sequence represents a single nucleotide primer extension (SNPR) primer specific for a human SNP containing DNA
                                                                                                                                                                                                                                                                                                                                                           New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 50; 83pp; English
                                                                                                                                                                                                                          ORCH-) ORCHID BIOSCIENCES INC
                                                                                                                                 13-OCT-2000; 2000WO-US028436.
                                                                                                                                                                             99US-0160096P.
                                                                                                                                                                                                                                                                       Pohl M;
                                                                                                                                                                                                                                                                                                                 WPI; 2001-290930/30
                                                                                                                                                                                                                                                                       Picoult-Newburg L,
                                          WO200129262-A2.
                                                                                                                                                                             15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                        acid sample.
                                                                                      26-APR-2001
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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch.

Also disclosed is a method of gene expression analysis. The array is used in monitoring gene expression levels by hybridisation to a DNA library, in analysis of genetic variation or in hybridisation of tag-labelled compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms, or family members of a gene and a cross-species comparison. Each of the concleic acide further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid containing sequence. The array of nucleic acid containing sequence or specific or utations of any gene, in mapping the 5' termini of mRNA molecules by cylimer extensions or in screening obby or genomic libraries or subclones for additional subclones containing segments of DNA that have been consolic soldated and previously sequenced. The sequence presented is one of the complex acid probes incorporated in the microarray. Note: The sequence date for this patent can also be obtained in electronic format directly from user or used and procoperated in the microarray.
                                                            New array of nucleic acid probes, useful for in situ hybridization, in Southern, Northern or dot-blot hybridization to identify or detect the sequence or specific mutations of any gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 52.9%; Score 14.8; DB 9; Length 25; Il Similarity 88.9%; Pred. No. 1.6e+04; 16; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human biallelic polymorphic marker downstream primer #412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 5 A; 5 C; 5 G; 10 T; 0 U; 0 Other;
                                                                                                                                                          Claim 1; SEQ ID NO 70112; 9pp; English
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ID AAX10106 standard; DNA; 28 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                     WPI; 2003-567953/53.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of diagnosing non-small cell lung cancer (NSCLC) or a predisposition to developing NSCLC in a subject by determining the expression level of a NSCLC-associated gene in a biological sample derived from the subject, where an increase or decrease of the level compared to a normal control level of the gene indicates that the subject suffers from or is at risk of developing NSCLC. The method is useful in diagnosing NSCLC or a predisposition to developing NSCLC in a subject. The compound, polymucleotide and the encoded NSCLC in a subject or an eseful in treating or preventing NSCLC. This sequence corresponds to a primer for semi-quantitative PCR amplification of genes that are differentially expressed in NSCLC cells.
                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing, preventing and treating non-small cell lung cancer (NSCLC) comprises determining an expression level of an NSCLC-associated gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.9%; Score 14.8; DB 12; Length 23; 88.9%; Pred. No. 1.6e+04; tive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 383; 394pp; English.
                                                                                                                                                                                                                                                                                                       Nakatsuru S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CACATGTAAAACAAGACT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-2002; 2002US-0414673P.
28-FEB-2003; 2003US-0451374P.
28-APR-2003; 2003US-0466100P.
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                                                                                            22-SEP-2003; 2003WO-JP012072
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                                                                                                                                                                                                                                   (ONCO-) ONCOTHERAPY SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 88.9 tes 16; Conservative
                                                                                                                                                                                                                                                                                                     Nakamura Y, Daigo Y,
                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-330206/30
                                                                                                                                                                                                                                                       (UYTY ) UNIV TOKYO.
WO2004031413-A2
                                              15-APR-2004
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WPI; 1998-286974/25,
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AAX09121-X10268 are allele-specific oligonucleotide primers used in the isolation of various biallelic polymorphic markers found in the human genome (represented in AAX10569-X12937). These primers can be used in a method for determining polymorphic forms in an individual for use in e.g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyham syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Pabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary comparance for spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, cante intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease. Claim 16; Page 201; 310pp; English.

Sequence 28 BP; 12 A; 4 C; 4 G; 8 T; 0 U; 0 Other;

Gaps ö Score 14.8; DB 2; Length 28; Pred. No. 1.6e+04; 2; Indels 0; Mismatches 52.9%; 88.9%; Local Similarity 88.9 nes 16, Conservative Query Match Matches

56 18 AAACGATACTTCATTTTG

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ABL43188 standard; DNA; 24 RESULT 9

ABL43188;

BP.

11-APR-2002 (first entry)

Human chromosome 1p36-35 PCR primer SEQ ID NO:232.

Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome; PCR primer; ss.

Homo sapiens.

JP2001321190-A.

20-NOV-2001.

12-MAR-2001; 2001JP-00068285.

10-MAR-2000; 2000JP-00066716

(RIKA ) RIKAGAKU KENKYUSHO. (GENO-) GENOTEX YG.

WPI; 2002-144136/19.

Arraying genome clones.

Claim 4; Page 9; 528pp; Japanese.

The present invention describes a method of arraying genome clones. The method comprises: (a) clones of the genomic libraries contained in ABL43188

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cc multiwell plates numbered for discrimination are mixed in each of the multiwell plates; (b) a primer designed based on the chromosome marker sequence; is added to the mixture to carry out an amplification reaction; (c) a signal corresponding to the marker is detected from the resultant explains containing the clones having said marker sequence; (d) the order cof the markers is changed so that the same discrimination Nos. of the multiwell cof the maximum in the specified discrimination Nos. to array the multiwell plates; (e) the clones in the multiwell plates of the specified discrimination Nos. are mixed respectively in each wells of longitudinal and lateral directions; (f) the mixed clones are cultured and the constitutes are amplified broducts; (h) the clones in the multiwell care detected from the amplified products; (h) the clones in the multiwell corrected treated and the constituted as the positions on the chromosome and arrayed. The clones are necessary is useful for gene analysis. ABL43297 to ABL45322 represent concreases for human chromosome 21q22.1, which are greated for use in the present invention \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$

Sequence 24 BP; 7 A; 4 C; 4 G; 9 T; 0 U; 0 Other;

Gaps ö Ouery Match 52.1%; Score 14.6; DB 6; Length 24; Best Local Similarity 81.0%; Pred. No. 1.9e+04; Matches 17; Conservative 0; Mismatches 4; Indels

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RESULT 10

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1383/c AAZ89383 standard; DNA; 25 BP AAZ89383/ ID AAZ8

AAZ89383;

15-JUN-2000 (first entry)

A. thaliana ACW1 PCR primer 4.

ACW1; plant cell wall; digestion efficiency; crop; agriculture; PCR primer;

Arabidopsis thaliana.

JP2000041685-A. 

15-FEB-2000

99JP-00077502. 23-MAR-1999; 98JP-00166174. 29-MAY-1998;

(OJIP ) OJI PAPER CO. (KAZU-) ZH KAZUSA DNA

KENKYUSHO

WPI; 2000-274045/24.

Modification of the cell wall components of a plant - useful for improving digestion efficiency of crops and feed crops.

Example 1; Page 21; 24pp; Japanese.

This invention describes a novel nucleic acid used for modifying the cell wall components of a plant. The modification is used for the improvement in digestion efficiency of useful crops and feed crops. The DNA is useful in agriculture, industry and gardening. AASB3800-Z89385 represent PCR primers used in the amplification of the Arabidopsis thaliana ACWI protein which is described in the method of the invention

Sequence 25 BP; 8 A; 4 C; 5 G; 8 T; 0 U; 0 Other;

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Gaps

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The invention discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its perfect match, perfect mismatch, antisense match or antisense mismatch. Also disclosed is a method of gene expression analysis. The array is used in analysis of genetic variation or in hybridisation to a DNA library, compounds. The nucleic acid probes are specifically designed for analysis of at least one target sequence. The method of analysis comprises of at least one target sequence. The method of analysis comprises of hybridising at least one or more nucleic acid probes and detecting the hybridisation. The nucleic acid probes and detecting the hybridisation. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring gene expression levels, identifying biallelic markers or polymorphisms. Compainty members of a gene and a cross-species comparison. Each of the nucleic acids further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence. The array of nucleic acid further comprises a tag sequence or specific comparations of any gene, in mapping the 5' termini of mRNA molecules by primer extensions or in screening cDNA or genomic libraries or subclones for additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is one of the companion of the form of the microarray. Note: The sequence of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form of the form 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST; ss; probe; expressed sequence tag; microarray; gene expression; genetic variation; biallelic marker; polymorphism; human;
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52.1%; Score 14.6; DB 3; Length 25; 81.0%; Pred. No. 1.9e+04; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human microarray DNA oligonucleotide SEQ ID NO 19337.
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                                                                                                                                                                          5 TGTAAAACAAGACTTCATTTT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACI19346 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-2003 (first entry)
                                                                                     17; Conservative
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                                   Best Local Similarity
Matches 17; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mittmann MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACI19346;
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
ACI19346

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The present invention describes a method for detecting an analyte in a sample. The method comprises: (a) providing detection probes being labelled with a first reporter, where the detection probes are capable of binding to the analyte; (b) providing objuding to the analyte; (c) providing capture probes being bound or capable of binding to the solid support, (d) providing concentrating the analyte on the solid support and the capture probes; and concentrating the detection probes where (i) the detection of detection probes; and (e) detecting the detection probes where (i) the detection of detection concentrating the detection probes; and (c) surplus detection probes; and the first reporter of said capture probes; and of capture probes binding to anyplus detection probes; and/or (ii) the solid support is labelled with a second reporter different from the first reporter; imaging the sample at an emission wavelength of the second reporter; imaging the sample at the emission wavelength of the second reporter; conting the detection probes; and the present sequence represents an emission probes; the present sequence represents an entity of the sample at the present sequence represents an analysis of the present sequence represents an analysis of the present sequence represents and applying this mask to an image of the sample used for coligonucleotide used in the detection of c-fos mRNA, which is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting an analyte such as protein or nucleic acid, useful for screening drugs, comprises probe detection of captured analyte where surplus probe signal is quenched and/or differential emission wavelength
                                                                                                                                                                                                       analyte detection; detection; probe; detection probe; reporter; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.4%; Score 14.4; DB 12; Length 24; 75.0%; Pred. No. 2.4e+04; ive 0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24 BP; 5 A; 6 C; 4 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                 C-fos mRNA detection related oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jaeger S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Droege S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 4; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of labeled support is measured.
                                        ADQ31135 standard; DNA; 24 BP
                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-2003; 2003WO-EP014661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-DEC-2002; 2002EP-00028582.
13-JAN-2003; 2003US-0439439P.
                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 75.0
nes 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EVOT-) EVOTEC OAI AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hinnah S, Lambrue D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-543305/52.
                                                                                                                                                                                                                                                                                                                              WO2004057023-A1.
                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
                                                                                                                         23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                     08-JUL-2004.
                                                                                                                                                                                                                               c-fos; ss.
                                                                                ADQ31135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
RESULT 12
                     ADQ31135/
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4 ATGTAAAACAAGACTTCATTTGG 27

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Length 25;

Score 14.6; DB 9; Pred. No. 1.9e+04;

52.1%; 81.0%;

Query Match Best Local Similarity

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Gaps

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Indels

9

0; Mismatches

18; Conservative

Matches

RESULT 14

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Detecting an analyte such as protein or nucleic acid, useful for screening drugs, comprises probe detection of captured analyte where surplus probe signal is quenched and/or differential emission wavelength
                                                                                                                        analyte detection; detection; probe; detection probe; reporter;
                                                                                                                                                                                                       /mod_base= OTHER
/note= "5' labelled with rhodamine-6G (Rh6G)"
                                                                                                                                                                                                                                                                                                                                Gall K;
                                                                                                       C-fos mRNA detection capture oligonucleotide.
                                                                                                                                                                                                                                                                                                                                Jaeger S,
                                                                                                                                capture oligonucleotide; human; c-fos; ss.
24 AGGAAAACTAGAGTTCATCCTGG 1
                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 19; 61pp; English
                                                                                                                                                                                                                                                                                                                                Droege S,
                                                                                                                                                                                                                                                                                                                                                                                             labeled support is measured
                                                                                                                                                                                                                                                                   19-DEC-2003; 2003WO-EP014661
                                                                                                                                                                                                                                                                                    20-DEC-2002; 2002EP-00028582,
13-JAN-2003; 2003US-0439439P.
                                                    ADQ31044 standard; DNA; 24
                                                                                      23-SEP-2004 (first entry)
                                                                                                                                                                                                /*tag= a
                                                                                                                                                                                                                                                                                                                                Hinnah S, Lambrue D,
                                                                                                                                                                                                                                                                                                              (EVOT-) EVOTEC OAI AG.
                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-543305/52.
                                                                                                                                                                                                                                   WO2004057023-A1
                                                                                                                                                                             Key
modified_base
                                                                                                                                                  Homo sapiens.
Synthetic.
                                                                    ADQ31044;
                                   RESULT 13
ADQ31044/c
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The present invention describes a method for detecting an analyte in a sample. The method comprises: (a) providing detection probes being labelled with a first reporter, where the detection probes being binding to the analyte; (b) providing a capture probes being bound or capable of binding to the solid support; (c) providing capture probes being bound or capable of binding to the analyte, and so concentrating the analyte on the solid support; (d) contacting the sample with the detection probes, the solid support and the capture probes; and (e) detecting the detection probes where (i) the detection of detection probes in conducted in the presence of quenching probes binding to surplus detection probes and/or (ii) the solid support is labelled with a second reporter different from the first reporter of said surplus detection probes; and/or (ii) the solid support is labelled with a second reporter different from the first reporter; imaging the sample at the emission wavelength of the second reporter, generating a mask obtained from imaging this mask to an image of the sample used for reporter and applying this mask to an image of the sample used for detecting the detection of the present sequence represents a capture of obtained between the present sequence represents a capture of the sample and the present sequence represents a capture of the second reporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          example from the present invention.
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51.4%; Score 14.4; DB 12; Length 24; 75.0%; Pred. No. 2.4e+04;

Query Match Best Local Similarity

Sequence 24 BP; 5 A; 6 C; 4 G; 9 T; 0 U; 0 Other;

```
The present invention relates to an antisense compound targeted to a mucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate but not limited to neomatal or infantile epilepsy, or ataxia. The present sequence represents a chimeric phosphorothioate oligonuclectide with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense compound targeted to a nucleic acid molecule encoding Nav1.3, useful for useful for treating a disease or condition associated with Nav1.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                                                                                                           Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2'MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target different regions of the human Nav1.3 RNA.
                                                                                                                          Chimeric phosphorothioate oligonucleotide to target Navl.3 #318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20 BP; 5 A; 2 C; 2 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14.2; DB 12;
Pred. No. 2.8e+04;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 318; 417pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TAAAACAAGACTTCATTTT 25
                ВР.
                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2002; 2002US-0403416P.
                                                                                                                                                                                                                                                                                                                                              14-AUG-2003; 2003WO-US025465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 TAAAACAAGACATGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.2%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
ADK72983/c
ID ADK72983 standard; DNA; 20
               ADK72984 standard; DNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-203785/19.
                                                                                                                                                                                                                                                                        WO2004016754-A2.
                                                                                  20-MAY-2004
                                                                                                                                                                                                                                                                                                            6-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roberds SL;
                                                  ADK72984;
ADK72984/
                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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New antisense compound targeted to a nucleic acid molecule encoding aval.3, useful for useful for treating a disease or condition associated with Navl.3, e.g. pain, seizure disorder such as childhood seizure disorder, or ataxia.
                                                                  Navl.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia; diabetic neuropathy; arthritic pain; migraine headache; infantile epilepsy; ataxia; ss.
                                               Chimeric phosphorothioate oligonucleotide to target Navl.3 #317.
                                                                                                                                                                                                                                                                                                                    Claim 4; SEQ ID NO 317; 417pp; English.
                                                                                                                                                                   14-AUG-2003; 2003WO-US025465.
                                                                                                                                                                                      14-AUG-2002; 2002US-0403416P.
                           20-MAY-2004 (first entry)
                                                                                                                                                                                                           (PHAA ) PHARMACIA CORP
                                                                                                                                                                                                                                                 WPI; 2004-203785/19.
                                                                                                                            WO2004016754-A2.
                                                                                                                                                26-FEB-2004.
                                                                                                                                                                                                                              Roberds SL;
                                                                                                         Synthetic.
         ADK72983;
```

The present invention relates to an antisense compound targeted to a nucleic acid molecule encoding Nav1.3, where the antisense compound specifically hybridizes with and inhibits the expression of Nav1.3. The compound and composition are useful for treating a disease or condition associated with Nav1.3, e.g. pain including but not limited to neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain, diabetic neuropathy, trigeninal neuropathy, arthritic pain, acute pain, pain from burns, migraine headache, cluster headache, mild-to-moderate headache; seizure disorder such as childhood seizure disorder, including but not limited to neonatal or infantile epilepsy; or ataxia. The present sequence represents a chimeric phosphorothioate oligonucleotide with 2.MOE wings and a deoxy gap. Used during the antisense inhibition of human Nav1.3 expression, the oligonucleotides are designed to target Sequence 20 BP; 5 A; 2 C; 3 G; 10 T; 0 U; 0 Other; Query Match

Gaps ö 'Match 50.7%; Score 14.2; DB 12; Length 20; Local Similarity 84.2%; Pred. No. 2.8e+04; les 16; Conservative 0; Mismatches 3; Indels Best Loc Matches

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5 TGTAAAACAAGACTTCATT 23 

ઠે g Search completed: June 21, 2005, 17:52:28 Job time : 423 secs

Sequence 2, Applisequence 10, Applisequence 329, Applsequence 329, Applsequence 1295, Applsequence 1295, Applsequence 141534, Sequence 141534, Sequence 141534, Sequence 470, Applsequence 3, Applisequence 3, Applisequence 601, Applsequence 601, Applemence 601, Applsequence 601, Applsequence 601, Applemence 601,

Sequence 179264, Sequence 179264, Sequence 179264, Sequence 195566, Sequence 195566, Sequence 195566, Sequence 14159, A

Sequence 2185, Ap Sequence 13, Appl

Sequence

nucleic

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Run on:

Sequence:

Searched:

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Sequence 59, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTES: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATE:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY. Chicago
STATE: 111inois
                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 US-10-074-596-2

6 US-10-074-596-10

US-08-781-996A-329

US-10-329-624-329

US-10-329-624-329

US-10-329-624-329

US-10-027-632-141533

3 US-10-027-632-141534

1 US-10-027-632-141534

1 US-10-027-632-141534

1 US-10-027-632-141534

1 US-10-027-632-141534

1 US-10-027-632-141534

1 US-10-027-632-141534

1 US-10-027-632-141534

1 US-10-328-60-3

5 US-10-345-680-3

5 US-10-35-823-96

1 US-10-345-680-1

1 US-10-345-680-1

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1 US-10-348-680-1

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1 US-10-348-680-1

1 US-10-348-680-1

1 US-10-348-60-6909
                                                                                                                                                                                                                                                                                                                                                                                                                                13 US-10-027-632-179264
17 US-10-027-632-179264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1244
·5886
99090
290547
1503841
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2953
3149
3149
3149
3149
5799
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                                                                                                                 Appl
App
App
                                                                                                                                 (without alignments)
320.094 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, 2
Sequence 246, 3
Sequence 11, 3
Sequence 11, 3
Sequence 258, 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
                                                                                                                 June 21, 2005, 15:19:32 ; Search time 543 Seconds
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S US-10-127-890-59

1 US-10-117-243-59

US-10-117-243-59

US-10-127-890-11

1 US-10-117-243-11

US-10-765-527-258

US-09-765-527-258
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                           6054689 seqs, 3103772919 residues
                                                                                                                                                                                                                   1 CACATGTAAAACAAGACTTCATTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published_Applications_NA:
                                                                               nucleic search, using sw model
                                                                                                                                                                                                                                                     IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16
21
9
9
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                                                                                                                                                                                  US-10-717-243-59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match
                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
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Database :

Result ္ဌ

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APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Product
Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                     FILING DATE: 19-JUN-1992

APPLICATION WURBER: US 07/787,567

FILING DATE: 04-MOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECPHONE: 312/707-9155

TELEPHONE: 312/707-9155

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 28; DB 21; Length 28; 100.0%; Pred. No. 0.055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 8300 Sears lower, 233 South wacker Dilve COUTRY: United States of America COUTRY: United States of America COUTRY: United States of America COUTRY: United States of America COMPUTER READABLE FORM:

MEDIUM TYPE: R-OPPY disk COMPUTER: IBM PC COMPALIDE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
FILING DATE: 18-Jan-2001
PRIOR APPLICATION NUMBER: 08/621,803
FILING DATE: CURMOWN:
ATTORNEY/AGENT INFORMATION:
NAME: BOTUM, MICHAE! F.
REGISTRATION NUMBER: 25,447
REFERENCE/OCKET WUMBER: 27,447
REFERENCE/OCKET WUMBER: 212/474.6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-717-243-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 246, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 813 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 246: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-765-527-246
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; Publication No. US20050054835A1
; GENERAL INFORMATION:
; Carroll, Stephen F.
; Studnika, Gary M.
; TITLE OF INVENTION: Proteins
Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 28; DB 16; Length 28; Best Local Similarity 100.0%; Pred. No. 0.055; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

ONDERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/717,243

FILING DATE: 18-Nov-2003

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

APPLICATION NUMBER: US 08/425,336

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 10-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: MCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                  FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCANICATION:
NAME: MCANICATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
TELEPHONE: 312/707-9155
TELEPHONE: 312/707-9155
  APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: DNA SEQUENCE DESCRIPTION: SEQ ID NO: 59: US-10-127-890-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CACATGTAAAACAAGACTTCATTTTGGC 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 28 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 169
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US-10-717-243-59
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Query Match
Best Local Similarity
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US-10-717-243-11
                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10127890
Publication No. US20030166196A1
GENERAL INPORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                              Gaps
                                                                                                                                                                            ö
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/981,707
                                                                                                                                 DB
                                                                                                                            Score 24.8; DB Pred. No. 2.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/127,890
         NAWE/KEY: misc_feature;
;
GTHER INFORMATION: "gelonin"
;
SEQUENCE DESCRIPTION: SEQ ID NO: 246:
US-09-765-527-246
                                                                                                                                                                                                                                                              303 CACAATTAAAACAAGACTTCATTTTGGC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-127-890-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 11;
                                                                                                                            ch 88.6%; 1 Similarity 92.9%; 26; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60661
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                          Query Match
Best Local Similarity
  FEATURE:
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                                                                                                                                                                                                                                              Sequence 11, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 88.6%; Score 24.8; DB 21; Best Local Similarity 92.9%; Pred. No. 2.3; Matches 26; Conservative 0; Mismatches 2;
  Score 24.8; DB 16;
Pred. No. 2.3;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION UNDBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
                                                                                                                       303 CACAATTAAAACAAGACTTCATTTTGGC 330
                                                                                             1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
88.6%;
92.9%;
                                                 26; Conservative
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Gaps

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Sequence 252, Application US/09765527

Patent No. US20020006538A1

GENERAL INPORMATION:

APPLICANT: Better, Marc D.

TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
OTHER INFORMATION: /label= cleavage linker
/note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
                                                                                                                                                         CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6310 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
CONTY: United States of America
ZIP: 606-6402
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BARGALE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 955;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                        NAME/KEY: misc feature
LOCATION: AA 286-293
LOCATION: AA 286-293
/note="BPI-derived peptide."
                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT 108/621,803
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFRERENCE/DOCKET NUMBER: 25,447
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 112/474-6300
                                                                                                                                                                                                                                                                                                                                                                        'Match . 88.6%; Score 24.8; Di
Local Similarity 92.9%; Pred. No. 2.3;
les 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/765,527 FILING DATE: 18-Jan-2001 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: residues 1-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1003 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 252:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66..992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                Bite."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-765-527-252
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                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                                                US-09-765-527-258
; Sequence 258, Application US/09765527
; Sequence 258, Application US/09765527
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of
; TITLE OF INVENTION: Pusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="residues 1-65 comprise EcoRI site to beginning of pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: AA 1-22
OTHER INFORMATION: /label= pel B
/note="pel B is the leader sequence from the pectate lyase
gene of Erwinia caratovora."
                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6310 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
CORFUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
ATONNEY/AGENT INFORMATION:
NAME: BOLUM, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 21,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: AA 23-273
OTHER INFORMATION: /label= "gelonin"
/note="gelonin (see U.S. Patent No. 5,416,202)."
                                                                                                                                                                                                                                                                                                                                                                      STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: AA 274-275
OTHER INFORMATION: /label= EagI
/note="EagI cloning site."
  303 CACAATTAAAACAAGACTTCATTTTGGC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc feature
residues 1-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 955 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 258:
SEQUENCE CHARACTERISTICS:
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66..944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
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                                                                                             US-09-765-527-258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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Best Local Similarity 92.9
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
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NAME/KEY:
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Patent No. US20020006638A1
GENERAL INPORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: AA 276-279
OTHER INFORMATION: /label= cleavage linker
/note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
site."
OTHER INFORMATION: /label= EcoRI
/note="residues 1-65 comprise EcoRI site to beginning of pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: residues 993-1011
OTHER INFORMATION: /label= XhoI
/note="residues 993-1003 comprise stop codon and XhoI site."
SEQUENCE DESCRIPTION: SEQ ID NO: 252:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                              NAME/KEY: misc_feature
LOCATION: AN 1-22
OTHER INFORMATION: /label= pel B
/note="pel B is the leader sequence from the pectate lyase
gene of Erwinia caratovora."
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CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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STATE: Illinois
COUNTX: United States of America
COUNTX: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: AA 23-213
OTHER INFORMATION: /label= "gelonin"
/note="gelonin (see U.S. Patent No. 5,416,202)."
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LOCATION: AA 280-309
OTHER INFORMATION: /label= peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/765,527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 CACAATTAAAACAAGACTTCATTTTGGC 461
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="BPI-derived peptide."
                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: AA 274-275
OTHER INFORMATION: /lah
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Best Local Similarity 92.5.
Thes 26, Conservative
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US-09-765-527-250
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LOCATION: AA 299-302
OTHER INFORMATION: /label= cleavage linker
/note="Ala-Leu-Asp-Pro linking sequence with Asp-Pro cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: residues 1062-1072
OTHER INFORMATION: /label= XhoI
/note="residues 1062-1072 comprise stop codon and XhoI site."
SEQUENCE DESCRIPTION: SEQ ID NO: 250:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /label= ECORI
/note="residues 1-65 comprise EcoRI site to beginning of pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: AA 1-22
UNTER INFORMATION: \label= pel B
/note="pel B is the leader sequence from the pectate lyase
gene of Erwinia caratovora."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: AA 23-273
OTHER INFORMATION
/note="gelonin (see U.S. Patent No. 5,416,202)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: AA 303-33
OCHER INFORMATION: /label= peptide sequence
/note="BPI-derived peptide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: AA 277-296
OTHER INFORMATION: /label= SLT linker
/note="SLT from shiga-like-toxin gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= FspI/ScaI
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET UNBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPRAK: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="FspI and ScaI cloning sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: AA 274-276
OTHER INFORMATION: /label= Eagl
/note="Eagl cloning site."
                                                                                                                                            INFORMATION FOR SEQ ID NO: 250:
SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: residues 1-65
OTHER INFORMATION: /lal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: AA 297-298
OTHER INFORMATION: /lak
                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 329, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.6%; Score 20.6; DB 20; Length 38142;
85.2%; Pred. No. 2.7e+02;
tive 0; Mismatches 4; Indels 0;
                                                                                             APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001600
CURRENT APPLICATION NUMBER: US/10/417,375
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 38142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16568 cagarddaaaacaadacrrcagrgrgg 16594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CACATGTAAAACAAGACTTCATTTGG 27
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REGISTRATION NUMBER: 30,446
REGISTRATION NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                          Sequence 55, Application US/10417375
Publication No. US20040219528A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1).T.(38142)
OTHER INFORMATION: n = A,T,C or G
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PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
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LENGTH: 2187 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 85.2
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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TOPOLOGY:
US-08-781-986A-329
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US-08-781-986A-329
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US-10-417-375-55
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Publication No. US20030176331A1
GEBREAL INFORMATION:
APPLICANT: ROSENBLUW, MICHAEL G.
APPLICANT: CHEUNG, LAWRENCE
TITLE OF INVENTION: MACKING THEEOF
TITLE OF INVENTION: MAKING THEEOF
TITLE OF INVENTION: MAKING THEEOF
TITLE OF INVENTION: MAKING THEOF
FILE REPERENCE: CLFR:00708
CURRENT APPLICATION NUMBER: G602-02-12
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                                                                                    APPLICANT: ROSENBLUM, MICHAEL G.
APPLICANT: CHEUNG, LARRENCE
TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF
TITLE OF INVENTION: MAKING THEOF
FILE REFERENCE: CLFR:007US
CURRENT APPLICATION UNMBER: US/10/074,596
CURRENT FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/268,402
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VOS: 11
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US-10-074-596-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
88.6%; Score 24.8; D
Best Local Similarity 92.9%; Pred. No. 2.4;
Matches 26; Conservative 0; Mismatches
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88.6%; Score 24.8; I

Best Local Similarity 92.9%; Pred. No. 2.5;

Matches 26; Conservative 0; Mismatches
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                                                      464 CACAATTAAAACAAGACTTCATTTTGGC 491
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                            CACATGTAAAACAAGACTTCATTTTGGC 28
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                                                                                                                                                                                             Sequence 2, Application US/10074596; Publication No. US20030176331A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Gelonium multiflorum
US-10-074-596-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1176
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LENGTH: 1527
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Gaps

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APPLICANT: Munger, William E.
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplass:
TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplass:
TITLE OF INVENTION: Gene Expression Profiles
FILE REPERENCE: 44921-5029-01US
FILE REPERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: 02/09-960,706
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTHER INFORMATION: Genbank Accession No. US20030134280A1 M89796
NAME/KEY: unsure
LOCATION: (1)..(11298)
COTHER INFORMATION: n = a or c or g or t
US-09-960-705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.4%; Score 20; DB 10; Length 11298; Best Local Similarity 82.1%; Pred. No. 3.8e+02; Matches 23; Conservative 0; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                 Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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  Length 2187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                         3; Indels
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Query Match 72.1%; Score 20.2; DB 8; Best Local Similarity 88.0%; Pred. No. 2.3e+02; Matches 22; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/10/329,624
FILING DATE: 27-Dec-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,171
FILING DATE: October 20, 1997
APPLICATION NUMBER: 66/09,861
FILING DATE: 300,1997
APPLICATION NUMBER: 08/781,986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 329: US-10-329-624-329
                                                                                                                                       451 CAGACGTAAAACAAGATTTCATTTT 475
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                                                                                                         1 CACATGTAAAACAAGACTTCATTT 25
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                                                                                                                                                                                                                                                                                  Sequence 329, Application US/10329624
Publication No. US20040043037A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (240) 314-12:
TELEFAX: (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 329:
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Sequence 12953, Application US/10424599

Sequence 12953, Application US/10424599

Publication No. US2040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwai

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION NUMBER: US/10/424,599

CURRENT APPLICANT: 2003-04-28

URRENT FILING DATE: 2003-04-28

NUMBER OP SEQ ID NOS: 285684

SEQ ID NO 12953

LENGTH: 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Glycine max PEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_111702C.1 US-10-424-599-12953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 19.8; DB 18;
Pred. No. 2.4e+02;
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                          4423 CACATTGAAAACAAGAACTCATTGTGGC 4450
1 CACATGTAAAACAAGACTTCATTTTGGC 28
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Job time : 549 gec8
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Best Local Similarity 91.3%;
Matches 21; Conservative
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Sequence 705, Application US/09960706 Publication No. US20030134280A1

RESULT 14 US-09-960-706-705

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Aaf20938 Human hig Ab29632 Human hig Ab419031 Human hig Ab297129 Human rec Ab41795 Human rec Ab417968 Human rec Aad43751 Human AGT Aad43821 Human AGT Aad43821 Human AGT Aad43821 Human AGT Aad43821 Human AGT Ab40938 Human Eph Ab778119 Human Eph Ab778119 Human Eph Ab59938 Human Eph Ab59958 Human Eph Ab59958 Human Eph Ab59966 Coding se Aad58484 Human rec Aad58484 Human rec Aad58484 Human rec Aad58484 Human rec Ad58484 Human rec Ad58484 Human rec Ad58484 Human rec Ad58484 Human rec

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AAA34816
AAF20938
ABZ96632
ABD19051
AAF29337
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AAF21435
ABD17968
AAD43749
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ADB75272
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ABX09938
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AAQ34513
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                        21742
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                          04-NOV-1992;
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19-JUN-1992;
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13-SEP-1993
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AAQ42253;
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Aat86336 BPI pepti
Aat86331 BPI pepti
Abs56021 CNA enco
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389.091 Million cell updates/sec
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                                                                                                                                                                                                                                                                               8780412
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                  4390206 seqs, 2959870667 residues
                                                                                                                                                                              CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                    nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
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ABD32682
ACF73271
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AAT86341
AAT86332
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AAQ75532
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geneseqn2003ds:*
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Maximum DB seq length: 200000000
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Match
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Fifteen analogues of gelonin were constructed. Ten non-cysteine residues in surface positions and available for conjugation to a second protein were targeted for substin. In the other analogues, one or both of the native Cys residues present in gelonin were substd. Overlap extension PCR was used to construct the various analogues. Primer geloC-20 was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.
                                                                                                                                                                                                 Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; Mutagenic polymerase chain reaction; ss.
                                                                                                                                                                     PCR primer GeloC-20 to replace Ile103 of gelonin with Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lane JA,
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carroll SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 35; 163pp; English.
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Aav74640 Staphyloc Aat86756 Human hig Aav54661 Human bet Aaa34815 Human ade Aaf20937 Human hig Abz96611 Human lig Aba96611 Human hig Abd19056 Human hig

AAF92144 ABZ96631 ABD19056

112

AAV74640 AAT86756 AAV54661 AAA34815 AAF20937

2103 2187 11298 11298 11298 11298 11298 11298

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Matches

8 g RESULT 2 AAQ48033

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Proteolytic peptide fragments of native gelonin were sequenced. PCR primers were designed based on these peptide fragments. The primers were used to amplify segments c DNA covering the 5'-terminal, middle and 3'-terminal regions of the gelonin coding sequence. A composite gelonin gene sequence was assembled from the overlapping gelonin DNA fragments (see AAAQ42221). Having cloned the gelonin gene, the development of gelonin analogues and gene fusions is facilitated. See AAAQ37291 for gelonin amino acid sequence. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                    Type I ribosome-inactivating protein, ricin, momordin, immunoconjugate, autoimmune disease; cell killing; toxin, Euphorbiaceae family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analogues of type I ribosome inactivating protein - useful as cytotoxion agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.6%; Score 24.8; DB 2; Length 813; 92.9%; Pred. No. 1.4; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type I ribosome-inactivating protein gelonin cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carroll SF,
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                                                                                                                                                                              Encodes plant type I RIP Gelonin.
                                            AAQ42222 standard; cDNA; 813 BP.
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                                                                                                                                                                                                                                                                            Gelonium multiflorum
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                                                                                                                                                                                                                                                                                                                  WO9309130-A1
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                                                                                                                      25-MAR-2003
13-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berhard SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                        13-MAY-1993.
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                                                                                  AAQ42222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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        RESULT 3
                            AAQ4222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ75532
                                                                ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention covers analogues of Type I RIPs. Gelonin is a Type I RIP and the analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment. See AAR37291 for gelonin amino acid sequence. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                          Gaps
the substn. of Ile103 of gelonin by Cys. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type I ribosome-inactivating protein; ricin; immunoconjugate; autoimmune disease; cell killing; toxin; Euphorbiaceae family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24.8; DB 2; Length 813; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 813 BP; 266 A; 150 C; 182 G; 215 T; 0 U; 0 Other;
                                                                                                100.0%; Score 28; DB 2; Length 28; 100.0%; Pred. No. 0.046; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lei
                                                              Sequence 28 BP; 10 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carroll SF, Lane JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CACATGIAAAACAAGACTICATITIGGC 28
                                                                                                                                                                                                                    CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 85; Page 114; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Encodes plant type I RIP Gelonin.
                                                                                                                                                                                                                                                                                                                  AAQ48031 standard; cDNA; 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92WO-US009487.
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92.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-00901707
                                                                                                                                                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                    Local Similarity 100.
ses 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berhard SL, Better MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-167617/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9309130-A1
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                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
13-SEP-1993
                                                                                                                                                                                                                                                                                                                                                        AAQ48031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                  Query Match
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cytotoxic

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Gaps

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Gelonium multiflorum

Best Loca Matches

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Analogues of Type I RIP are defined as non-naturally occurring protein but differ in A sequence. Preferred analogues have a Cys available for disulfide bonding located at a posn. It its AA sequence troming activity of the natural corresp. to posn. 251 in ricin A-chain RTA to the carboxy craminus of the analogue. (AAR74176 is the sequence of ricin A-chain RTA, which is a Type II RIP). The primary AA sequence of ricin A-chain RTA, which is a Type II RIP). The primary AA sequence of the Type I RIPS gelonin, BRIP, mormordin II, luffin [see Islam et al. Agricultural is located. (AAR74176 is 1931), alphatrichosanthin ([see Chow et al., 26, 1343-45, 1991], alphatrichosanthin ([see Chow et al., 31.1-4 1991), Mirabilis antiviral protein [see Habuka et al., 5. Biol. Chem., 264, [12) 6629-37 1989], pokeweed antiviral protein isolated from seeds [see Kung et al., Agric. Biol. Chem., 54, 120, 1331-18 1990] and saporin [see Banatti et al., Eur. J. Biochem., 133, 465-70 1989] are individually aligned with the primary sequence of the ricin A-chain [see Halling et al., Nucleic Acids Res., 13, 8019-8033 1983] respectively in Figures 1-9. The AAs invariant among the ricin A-chain and the Type I RIPS are indicated in FT. Also indicated are the preferred sites of Cys substitution. It is also preferred that the gelonin cysteine residues at costitions 44 and 50 be replaced with alamine residues. The complete DNA sequence of the gelonin gene is set out in AA022342. (Updated on 25-MAR-
                                                                                                        Polynucleotide(s) encoding gelonin analogues - having a cysteine residue for intermolecular bonding for the prodn. of immuno-toxin(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA; vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= pel_B
/standard name= "Leader"
/note= "pel B is the leader sequence from the pectate
1398 gene of Erwinla caratovora"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                    Better MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BPI peptide fusion protein pING3797 vector construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24.8; DB
Pred. No. 1.4;
                    Bernhard SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 CACAATTAAAACAAGACTTCATTTTGGC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                     Example; Col 71-72; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/label= gelonin
                    Lane JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT86336 standard; DNA; 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pectobacterium carotovorum.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 92.9
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .22
/*tag=
                  Carroll SF,
                                                             WPI; 1995-193480/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT86336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric
                    Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cyctoxoic therapeutic agents (CTAS), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribosome inactivating protein; RIP; Type I; cytotoxin; immunotoxin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) encoding type I ribosome-inactivating proteins -- are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 88.6%; Score 24.8; DB 2; Length 813; 1. Similarity 92.9%; Pred. No. 1.4; 26; Conservative 0; Mismatches 2 7-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 813 BP; 267 A; 150 C; 180 G; 216 T; 0 U; 0 Other;
                                                               /*tag= a
/transl_except= pos:754. .810
/note= "no corresponding amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Type I ribosome-inactivating protein gelonin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 CACAATTAAAACAAGACTTCATTTTGGC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                     Studnicka GM;
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 155; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-00988430
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                   Carroll SF,
                                                             *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-006804/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                      (XOMA ) XOMA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR63903
                                                                                                                                                                                                                                                                             12-MAY-1993;
                                                                                                                                                                                                                                    12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
01-JAN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-1992;
                                                                                                                                                WO9426910-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5416202-A
                                        mat_peptide
                                                                                                                                                                                       24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                   Setter MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ92342;
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Matches

RESULT 5 AAQ92342

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8

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Gaps

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/*tag= a |Tabel= pel B |standard_name= "Leader" | Inote= "pel B is the leader sequence from the pectate |Yase gene of Erwinia caratovora"

Location/Qualifiers

*tag= b |Tabel= gelonin |note= "gelonin - see U.S. Patent No. 5,416,202"

56. .992 *tag=

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Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA; vector; ss.
                                                               Pectobacterium carotovorum.
Homo sapiens.
                                                                                                                                                                                      misc_feature
                                                                                                                        misc_signal
                                                        Synthetic.
                                                                                        Chimeric
                                                                                                                                                                                                                                    CDS
  A new recombinant DNA vector construct has been developed which encodes a fusion protein and is suitable for introduction into a bacterial host.

The vector comprises: (a) DNA encoding at least one cationic bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a carrier protein, and (c) DNA encoding an amino acid (a) cleavage site located between (a) and (b). The present sequence represents the pING3797 vector construct coding for a BPI fusion protein. The peptides have many uses including the treatment of bacterial and fungal infections. BPI peptides also bind to endotoxins and heparin, neutralising their effects. The peptides have further been shown to inhibit angiogenesis (partly due to heparin-binding activity). The fusion proteins have been found to be expressed in large amounts without significant proteclysis, and in some cases are actually secreted from the host cells. This allows the indirect
                                                                                                                                                                                                                                                                                                                                                          Recombinant production of bactericidal/permeability increasing protein - by expression as a fusion protein in microbial host cells, then cleaving
                                                                                       /*tag= g
/label= cleavage_linker
/note= "Ala-Leu-Āsp-Pro linking sequence with Asp-Pro
/note= "gelonin - see U.S. Patent No. 5,416,202"
66. .944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24.8; DB 2; Length 955;
Pred. No. 1.4;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of anti-microbial BPI peptides in microbial hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 955 BP; 307 A; 189 C; 216 G; 243 T; 0 U; 0 Other;
                                                                                                                                            /*tag= h
/label= peptide_sequence
/note= "BPI-derīved peptide"
                                          /*tag= d
/label= EagI
/note= "EagI cloning site"
276. .279
                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 160-161; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                the BPI peptide from the carrier.
                                                                                                                        cleavage site"
                                                                                                                                                                                                                                    97WO-US005287
                                                                                                                                                                                                                                                         96US-00621803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 88.6%;
Local Similarity 92.9%;
Hes 26; Conservative
           6. .
/*tag= .
.275
                                                                                                                                    280. .293
                                                                                                                                                                                                                                                                                                                           WPI; 1997-480215/44.
                                                                                                                                                                                                                                                                               (XOMA ) XOMA CORP
                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW29300
                                 misc_feature
                                                                                                                                                                                                                                    18-MAR-1997;
                                                                                                                                                                                                                                                          22-MAR-1996;
                                                                            misc feature
                                                                                                                                  misc_feature
                                                                                                                                                                                       WO9735009-A1
                                                                                                                                                                                                              25-SEP-1997.
                                                                                                                                                                                                                                                                                                      Better MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
            CDS
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A new recombinant DNA vector construct has been developed which encodes a fusion protein and is suitable for introduction into a bacterial host. The vector comprises: (a) DNA encoding at least one cationic bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site located between (a) and (b). The present sequence represents the pING3795 vector construct coding for a BPI fusion protein. The peptides have many uses including the treatment of bacterial and fungal infections. BPI peptides also bind to endotoxins and heparin, neutralising their effects. The peptides have further been shown to inhibit angiogenesis (partly due to heparin-binding activity). The fusion proteins have been found to be expressed in large amounts without significant proteolysis, and in some cases are actually secreted from the host cells. This allows the indirect production of anti-microbial BPI peptides in microbial hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant production of bactericidal/permeability increasing protein - by expression as a fusion protein in microbial host cells, then cleaving
                                                                                                                                                                                                         /*tag= g
/label= cleavage_linker
/note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
                                                                                                                                                                                                                                                                                                                                                                               /*tag= h
/label= peptide_sequence
/note= "BPI-derived peptide"
                                                                                             /label= EagI
/note= "EagI cloning site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 152-153; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                           cleavage site"
280. .309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US005287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-00621803
J= C
                                                                                                                                                                     76. .279
                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-480215/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW29303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9735009-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1997;
                                misc_feature
                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-1997
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Gaps

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Matches

ઠ 유 AAT86341 standard; DNA; 1003 BP

RESULT 7

BPI peptide fusion protein pING3795 vector construct.

20-APR-1998 (first entry)

AAT86341;

AAT86341
ID AAT8
XX
AC AAT8
XX
DT 20-P
XX
DE BPI

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Gelonium multiflorum.
                                                                   WPI; 1997-480215/44
   (XOMA ) XOMA CORP.
                                                                                   P-PSDB; AAW29294
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                                    Better MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABS56021;
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                                                                                                                                                                                                                                                                                                                                                   Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA; vector; ss.
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|abel= cleavage_linker
|note= "Ala-Leu-Asp-Pro linking sequence with Asp-Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_nāme= "Leader"
/note= "pel B is the leader sequence from the pectate
1978es gene of Brwinia caratovora"
23. .273
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
//label= gelonin
/note= "gelonin - see U.S. Patent No. 5,416,202"
66. .1064
                                                                 ö
                                Length 1003;
Sequence 1003 BP; 325 A; 194 C; 227 G; 257 T; 0 U; 0 Other;
                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= SLT_linker
/note= "SLT_from shiga-like-toxin gene"
297. .298
                                                                                                                                                                                                                                                                                                                    BPI peptide fusion protein pING3793 vector construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= f
|aabel= FspI/ScaI
note= "FspI and ScaI cloning sites"
                               Score 24.8; DB 2;
Pred. No. 1.4;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= peptide sequence
/note= "BPI-derived peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             434 CACAATTAAAACAAGACTTCATTTTGGC 461
                                                                                               1 CACATGTAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                 AAT86332 standard; DNA; 1072 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cleavage site"
303. .332
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/label= pel_B
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                               Match 88.6%;
Local Similarity 92.9%;
les 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pectobacterium carotovorum Homo sapiens.
                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .302
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/label= p
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
misc_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                  AAT86332;
                                Query Match
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                                                                Matches
                                                                                                                                                                                RESULT 8

AAT86332

BAT86332

AAT86332

AAT86332

BAT86332

BAT86332

BAT86332

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BAT86332

BAT86332

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The vector comprises: (a) DNA encoding at least one cationic bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a carrier protein, and (c) DNA encoding an amino acid (a) DNA encoding a located between (a) and (b). The present sequence represents the pING3793 vector construct coding for a BPI thason protein. The peptides have many uses including the treatment of bacterial and fungal infections. BPI peptides also bind to endotoxins and heparin, neutralising their effects. The peptides have further been shown to inhibit angiogenesis (partly due to heparin-binding activity). The fusion proteins have been found to be expressed in large amounts without significant proteolysis, and in some cases are actually secreted from the host cells. This allows the indirect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified protein; reduced antigenicity; modified toxin; gelonin; designer toxin; immunotoxin; proteinaceous compound; cancer; microbial pathogenesis; acquired immunodeficiency syndrome; AIDS; autoimmune disease; hyperproliferative disorder; leukaemia; arthritis; inflammatory disease; cardiovascular disease; diabetes; arthritis; cardioidiseses; cyrostatic; antiarthritic; antiinflammatory; cardiant; antidiabetic; virucid; protozoacide; fungicide; antibacterial; recombinant gelonin; rGel; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cases are actually secreted from the host cells. This allows the indirect production of anti-microbial BPI peptides in microbial hosts
Recombinant production of bactericidal/permeability increasing protein - by expression as a fusion protein in microbial host cells, then cleaving the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24.8; DB 2; Length 1072;
Pred. No. 1.4;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding G. multiflorum recombinant gelonin (rGel) toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1072 BP; 340 A; 210 C; 244 G; 278 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 CACAATTAAAACAAGACTTCATTTTGGC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                  Example 1; Page 148-150; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
24. .974
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABS56021 standard; cDNA; 1176 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 92.9%;
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L2-FEB-2002; 2002WO-US004195.
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/*tag= a /product= "scfvMEL/rGel fusion protein"

Location/Qualifiers

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The present invention relates to a method of generating a modified protein with reduced antigenicity while maintaining its biological activity. The method comprises identifying a region of the protein that is antigenic in a first subject using antiserum from either the first subject or a second subject of the same species as the first subject. In particular the invention discloses modified toxin compounds, for example cand/or possess reduced antigenicity. Such designer toxins have therapeutic, diagnostic, and preventative benefits, particularly as immunotoxins. The method of the invention is useful for generating proteinaceous compounds with less antigenicity. The immunotoxin and gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain, skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic, bone, bone marrow, head and neck, cervical, oseophagus, eye, gall bladder, kidney, adrenal glands, heart, colon, or blood cancer. The compositions of the invention are also useful for treating microbial pathogensis, acquired immunodeficiency syndrome (AIDS), autoimmune diseases, hyperproliferative disorders including cancer, leukaemias, arthiraminotory diseases, cardiovascular diseases, pathogenic consent sequence encodes murities single-chain syndrome than prior art. The petides and polypeptides, which are more effective than prior art. The mitisform recommendes murities single-chain successions and diabetes shown in a more single consent sequence encodes murities single-chain are more effective than prior art. The mitisform recomminant engages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generating a modified protein with reduced antigenicity for treating cancer, AIDS, autoimmune diseases, comprises identifying a protein region antigenic in the first subject using antiserum from either the first or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Fig 5; 176pp; English.
                                                                                                                                                                                                                                                                                12-FEB-2001; 2001US-0268402P.
                                                                                                                                                                                                                              12-FEB-2002; 2002WO-US004195
                                                                                                                                                                                                                                                                                                                                                                                   Rosenblum MG, Cheung L;
                                                                                                                                                                                                                                                                                                                                  (RERE-) RES DEV FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-750431/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABG71552
                                                                                                                           WO200269886-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        second subject
                                                                                                                                                                            12-SEP-2002
  Key
  The present invention relates to a method of generating a modified protein with reduced antigenicity while maintaining its biological activity. The method comprises identifying a region of the protein that is antigenic in a first subject using antiserum from either the first subject or a second subject of the same species as the first subject. In particular the invention discloses modified toxin compounds, for example and/or possess reduced antigenicity. Such designer toxins have therefore and/or possess reduced antigenicity. Such designer toxins have therepeutic, diagnostic, and preventative benefits, particularly as immunotoxins. The method of the invention is useful for generating proteinaceous compounds with less antigenicity. The immunocxin and genome compounds with less antigenicity. The immunocxin and genome compounds with less antigenicity. The immunocxin and skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic, bone, bone marrow, head and neck, cervical, oesophagus, eye, gall bladder, kidney, adrenal glands, heart, colon, or blood cancer. The compositions of the invention are also useful for treating microbial pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune diseases, hyperproliferative disorders including cancer, leukaemias, arthiris, inflammantory diseases, cardiovascular diseases, pathogenic diseases, and diabetes. The method provides less antigenic proteins, peptides and polypeptides, which are more effective than prior art. The present sequence encodes G. multiflorum recombinant gelonin (rdel)
                                                                                                                                                                                                    cancer, AIDS, autoimmune diseases, comprises identifying a protein region antigenic in the first subject using antiserum from either the first or a
                                                                                                                                                                          Generating a modified protein with reduced antigenicity for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1176 BP; 369 A; 211 C; 263 G; 333 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                     Example 1; Page 170; 176pp; English.
                                               Cheung L;
(RERE-) RES DEV FOUND.
                                                                                                WPI; 2002-750431/81.
                                                                                                                     P-PSDB; ABG71551
                                                                                                                                                                                                                                                   second subject.
                                                 Rosenblum MG,
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Gaps ; 0 Score 24.8; DB 6; Length 1176; Pred. No. 1.4; 2; Indels Pred. No. 1.4; 0; Mismatches 464 CACAATTAAAACAAGACTTCATTTTGGC 491 1 CACATGTAAAACAAGACTTCATTTTGGC 28 88.6%; 26; Conservative Local Similarity Query Match Matches ò 셤

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designer toxin; immunotoxin; proteinaceous compound; cancer; microbial pathogenesis; acquired immunodeficiency syndrome; AIDS; autoimmune disease; hyperproliferative disorder; leukaemia; arthritis; inflammatory disease; cardiovascular disease; diabetes; pathogenic disease; cytostatic; antiarthritic; antiinflammatory; muniabetic; vincide; protozoacide; fungicide; antibacterial; murine; single-chain ZME-018 antibody; recombinant gelonin; rGel; scfvMEL/rGel; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified protein; reduced antigenicity; modified toxin; gelonin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding murine scfvMEL/G. multiflorum rGel fusion protein.
                                                                                                                                                           ABS56029 standard; DNA; 1527 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JAN-2003 (first entry)
                                                                                                                                                                                                                                                                                                        ABS56029;
RESULT 10
ABS56029
ID ABS56029
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AC ABS56
DT 08-JA
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DE DNA e:
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Gelonium multiflorum.

sp.

Synthetic. Chimeric.

Gaps Mouse; ds; cancer-associated protein; gene; cytostatic; cancer; ò 88.6%; Score 24.8; DB 6; Length 1527; 92.9%; Pred. No. 1.5; cive 0; Mismatches 2; Indels 0; Sequence 1527 BP; 458 A; 320 C; 367 G; 382 T; 0 U; 0 Other; Mouse cancer-associated genomic DNA MD13-117. 1071 CACAATTAAAACAAGACTTCATTTTGGC 1098 1 CACATGTAAAACAAGACTTCATTTTGGC ABD32682 standard; DNA; 38142 (first entry) Conservative Query Match Best Local Similarity ! ....hes 26; Conservat 18-NOV-2004 ABD32682; RESULT 11 유

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multiflorum recombinant gelonin (rGel) (scfvMEL/rGel) fusion protein

Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target; gene; ds.

Staphylococcus aureus.

WO200294868-A2. 28-NOV-2002.

Staphylococcus aureus DNA #951

20-NOV-2003 ACF73271;

ACF73271 standard; DNA; 2103 BP

RESULT 12 ACF7327

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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancer associated proteins. Also included are an expression vector comprising the isolated nucleic acid or expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least to contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above compression reading frame of a CA sequence selected from any of the 35 polynucleotide sequences as mentioned in the specification, or its complement), an isolated antibody, (or its antigen binding fragment) that binds a polymeptide, a hybridoma that produces the above monoclonal antibody, a pharmaceutical composition comprising the above antibody and a pharmaceutical composition comprising the above antibody and a pharmaceutical axcipient, a kit for detecting cancer of for detecting the presence or absence of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, an enthod for inhibiting growth of cancer cells in an individual, an electronic library comprising the above polymetide (or their fragments), methods of screening for anticancer activity or for a bioactive agent capable of modulating the accipited and with avareasion of a cap protein (GAP), methods for all cancer cells cancer activity or for a bioactive agent capable of modulating and accipited and accipited and and accipited and and accipited and accipited and accipited and accipited and accipited and accipited and accipited and accipited and accipited and accipited and accipited accipited and accipited accipited and accipited accipited and accipited accipited accipited accipited accipited accipited accipited accipited accipited accipited accipited accipited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.6; DB 13; Length 38142;
Pred. No. 1.2e+02;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disclosure; seqid 236; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malandro MS;
                                                                                                                                                                                                                                                            14-MAR-2003; 2003US-00388838.
15-APR-2003; 2003US-0041775.
13-UNV-2003; 2003US-00461862.
15-SEP-2003; 2003US-00663431.
15-DEC-2003; 2003US-00737318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.6%;
85.2%;
                                                                                                                                                                                          17-FEB-2004; 2004WO-US004730
                                                                                                                                                                                                                                       2003US-00367094
                                                                                                                                                                                                                                                                                                                                                                                                           (SAGR-) SAGRES DISCOVERY INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 85.2
Marches 23; Conservative
leukaemia; lymphoma; CAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-652914/63.
                                                                                          WO2004074320-A2
                                               Mus musculus,
                                                                                                                                                                                                                                       14-FEB-2003;
                                                                                                                                          02-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morris DW,
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Sequence 2103 BP; 786 A; 330 C; 271 G; 716 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the novel S. aureus genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated with expression of a polypeptide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of GA gene in a cell. The composition and methods are useful for detecting, diagnosing, preventing and treating cancers, especially lymphoma and leukaemia. These may also be used in screening for agents that modulate cancer. The present sequence is a mouse CAP genomic sequence. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer. The present sequence is a mouse CAP genomic sequence. Notes as sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 38142 BP; 10396 A; 8310 C; 8130 G; 10863 T; 0 U; 443 Other;
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Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                Gaps
                                ö
                                Indels
Score 20.2; DB 8;
Pred. No. 1.3e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                        Staphylococcus aureus contig SEQ ID #329.
                                                                                         1838 CAGACGTAAAACAAGATTTCATTTT 1862
                                                              25
                                                              1 CACATGIAAAACAAGACTICATITI
                              .
0
                                                                                                                                                                  AAV74640 standard; DNA; 2187 BP
   72.1%;
88.0%;
                                                                                                                                                                                                                             (first, entry)
               Local Similarity 88.0
es 22; Conservative
                                                                                                                                                                                                                                                                                                                                toxic shock syndrome; ds.
                                                                                                                                                                                                                             16-MAR-1999
                                                                                                                                                                                               AAV74640;
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ö

Gaps

g

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Length 2103;

for

Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of

The invention relates to novel genes and encoded proteins from

Claim 6; SEQ ID NO 1901; 49pp; English.

New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.

Scarselli M;

Masignani V, Mora M, 2003-120786/11.

P-PSDB; ABM71711.

CHIR-) CHIRON SPA

27-MAR-2002; 2002WO-IB002637. 27-MAR-2001; 2001GB-00007661.

Staphylococcus aureus.

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Homo sapiens.
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                                                 exon
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  The Sequence in the Paragraphy of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of the sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the computer
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                                             /*tag= a
/note= "these bases represent a line of missing text in
the sequence listing in the specification. They are
included to maintain the nucleotide numbering given in
the specification for this DNA sequence"
                                                                                                                                                                                                                                                                                                                                                        sequence represents one of 5191 Staphylococcus aureus DNA sequences
                                                                                                                                                                                                                                                                                   Staphylococcus aureus -
in the production of anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; immunoglobulin B; high affinity receptor; beta subunit; IgB; Fc epsilon RI beta; exon 7; variant; E237G; atopy; atopic asthma; detection; diagnosis; polymorphism; subgroup; clinical management; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                       Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human high affinity IgE receptor beta chain E237G variant gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.2; DB 2; Length 2187; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                       Fannon MR,
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                                                                                                                                                                                                                                    Dillon PJ,
                                                                                                                                                                                                                                                                                 Polynucleotide(s) and proteins derived from stored on computer readable medium and used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                              Claim 1; Page 1197-1198; 3271pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGACGTAAAACAAGATTTCATTT 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACATGTAAAACAAGACTTCATTTT 25
                        Location/Qualifiers
1321. .1380
                                                                                                                                                                                                                                    Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT86756 standard; DNA; 11298 BP
                                                                                                                                                                97EP-00100117.
                                                                                                                                                                                       96US-0009861P
                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC.
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illarity 88.0%;
Conservative
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                                                                                                                                                                                                                                    Choi GH,
                                                                                                                                                                                                                                                           WPI; 1997-374922/35
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les 22; Conserv
                                                                                                                                                                                                                                                                                                           S.aureus vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           readable medium
                                                                                                                                                               07-JAN-1997;
                                                                                                                                                                                       05-JAN-1996;
                                  misc_feature
                                                                                                                                         30-JUL-1997.
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                                                                                                                                                                                                                                                                                                                                                        This
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AAT86756
ID AAT86756
XX
AC AAT86
XX
DT 12-DE
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XX
DE Human
XX
KW human
XX
KW qc ecc
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This DNA encodes human immunoglobulin E (IgE) high affinity receptor beta subunit (FC epsilon RI beta) exon 7 variath E337G. This variant is associated with atopy and atopic asthma. The variation is in exon 7 and is a nucleotide change from adenine to guanine at nucleotide 7297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= n
/note= "nucleotide change from wild type adenine to
guanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosing atopy, or predisposition to it - by detection of immunoglobulin E high affinity receptor beta subunit exon 7 variant Glu237Gly.
location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page; 25pp; English.
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                                                                                        /number= 1
1381. .1510
/*tag= c
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                                                                                                                                                           1511. .2025
/*tag= d
                                                                                                                                                                                                                                                           161. .4474
/*tag= f
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/*tag= i
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                                                                                                                                                                                                            026. .2160
                                                                                                                                                                                                                                                                                                                                                        532. .5078
                                                'number= 1
                                                                                                                                                                                                                                                                                                         475. .4531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number= 5
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'number= (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-1996;
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(nucleotide 6843 in the Fc epsilon RI beta gene sequence of Kuster, et al. 1992). Detection of the protein is useful for diagnosis of atopy. In particular the E273G polymorphism may also define a subgroup of asthma suffers with a particular clinical course, in which case recognition of the variant/polymorphism would be of value in defining asthma prognosis and management. NB. This sequence was created using the sequence given in Genbank M89796.
                                                                                                  Gaps
                                                                                                                                                                                                                                           Human beta subunit of Fc epsilon RI; ARAM; Fc epsilon RI beta chain; antigen recognition activation motif; human beta subunit; allergy; high-affinity immunoglobulin E receptor; ds.
                                                                Sequence 11298 BP; 3469 A; 2113 C; 2284 G; 3415 T; 0 U; 17 Other;
                                                                                                 ö
                                                                                Match 71.4%; Score 20; DB 2; Length 11298; Local Similarity 82.1%; Pred. No. 1.8e+02; es 23; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                      epsilon RI beta chain"
                                                                                                                                                                                                                           Human beta subunit of Fc epsilon RI coding sequence.
                                                                                                                          /product= "human Fc epsi]
/note= "contains introns'
                                                                                                                 1 CACATGTAAAACAAGACTTCATTTTGGC 28
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              'note= "contains
156. .511
                                                                                                                                                                           AAV54661 standard; DNA; 11298 BP
                                                                                                                                                                                                                                                                                                                                                                                       1381. .1510
/*tag= d
/number= 2
1511. .2025
/*tag= e
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/*tag= k
/number= 5
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/*tag= 1
/number= 6
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2026. .2160
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/*tag= h
/number= 4
4532. .5078
/*tag= i
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5079. .5237
/*tag= j
/number= 5
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'*tag= g
'number= 3
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512. .1380
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/number= 3
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/number= 1
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                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                           AAV54661;
                                                                                Query Match
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Matches
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This represents the coding sequence of a human beta subunit of Fc epsilon RI [high-affinity immunogiboulin B receptor]. The invention provides a peptide fragment (AAW75917) from the human Fc epsilon RI beta subunit protein that contains the amino acid sequence of an ARAM [antigen protein that contains the amino acid sequence of an ARAM [antigen prospirition activation mocifi]. Aspects of the invention are methods and compositions to inhibit the function of human beta subunit, thereby treating or preventing allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IgB receptor beta subunit protein - and corresponding peptide(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.4%; Score 20; DB 2; Le 82.1%; Pred. No. 1.8e+02; ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4423 CACATTGAAAACAAGAACTCATTGTGGC 4450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: June 21, 2005, 14:49:08 Job time: 433 secs
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10213
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/number= 7
7323. .11298
/*tag= o
10114. .10118
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                     /*tag= m
/number= 6
7224. .7319
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Best Local Similarity 82.1
Matches 23, Conservative
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10209.
5739.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jouvin M, Kinet J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW75918
                                                                                                                                                                                                                                                                                                                                                                                           24-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                         16-APR-1992;
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                                                                                                                                                                               polyA_signal
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GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: June 21, 2005, 14:23:52; Search time 3127 Seconds (without alignments) 340:838 Million cell updates/sec  Title: US-10-717-243-59 Perfect score: 28 Sequence: 1 CACATGTAAAACAAGACTTCATTTTGGC 28 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 34239544 seqs, 19032134700 residues Total number of hits satisfying chosen parameters: 68479088	um DB seq length: 0 um DB seq length: 2000000000	se : Pred. No. score gree	No. Score Match Length DB ID Description    1

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1128 bp DNA linear GSS 12-MAY-2003 CH261-74J20 RM1.1 CH261 Gallus ganomic clone CH261-74J20, genomic survey sequence.
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Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phagianinae; Gallus;
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Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
Wallus gallus BAC End Reads
Unpublished (2003)
Contact: Richard K. Wilson
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Washington University School of Medicine
Email: submissions@wateon.wustl.edu
Insert Length: 182000 Std Brror: 0.00
Seq primer: RM1 TACGACTCACTATAGGGACA
Class: BAC ends
Washington University School of Medicine
                   Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.
Seg primer: RM1 TACGACTCATAGGGAGA
Class: BAC ends
High quality sequence start: 24
High quality sequence stop: 676.
Location/Qualifiers
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 1910 (66 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequenching project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neoperygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes; Tetradontoidea, Tetraodontidae, Tetraodon.
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Gallus gallus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1013)
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
Umpublished (2003)
Gontact: Richard K. Wilson
Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                      Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                       Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                              Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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Matches

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kg56c05.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar to WP:Y113G7A.11 CE23282 ;, mRNA sequence.
  AY066661
Schmidtea mediterranea clone H.25.6h unknown mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-DEC-2001) Neurobiology & Anatomy, University of Utah School of Medicine, 50 North Medical Drive, Salt Lake City, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 464)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
Wylie, T., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,
Tagareishyili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
Harvey, N., Schuck, R., Allen, W., Person, B., Swaller, T.,
Harvey, N., Schuck, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone names suffixed with 'T3' were sequenced from their 5' ends. All other clones were obtained by sequencing from their 3' ends. More details and other relevant information can be found at http://planaria.neuro.utah.edu.
                                                                                                                                             Schmidtea mediterranea
Sukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata;
Tricladida; Paludicola; Dugesiidae; Schmidtea.
1 (Dases 1 to 942)
Alvarado, A.S., Newmark, P.A., Robb, S.M.C. and Juste, R.B.
The Schmidtea mediterranea database as a molecular resource for
studying platyhelmithes, stem cells and regeneration
Development 129 (24), 5659-5665 (2002)
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Unpublished (1999)
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to (BC004070) Unknown (protein for
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Alvarado, A.S., Newmark, P.A., Juste, R.B. and Robb, S.M.C.
Direct Submission
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Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Strongyloididae; Strongyloides.
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BE581909
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/note="Vector: ppon 22; Site 1: BsrG I; Site 2: BsrG I;
Created from CloneMiner cDNA Library Construction kit
(catalog #18249-029)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequenced on 2004.05.27. 681 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                         CO646793 B34 bp mRNA linear EST 23-JUL-20 ILLUMIGEN MCQ 39642 Katze MMPB2 Macaca mulatta cDNA clone IBIUW-22782 5' similar to Bases 5 to 734 highly similar to human WDR36 (Hs.175596), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 834)
Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
Large-scale Macaque cDNA Sequencing
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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  Length 1128;
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2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
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                                                   4; Indels
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77.1%; Score 21.6; DB 8;
85.7%; Pred. No. 3.7e+02;
live 0; Mismatches 4;
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/dev_stage="adult"
/lab_host="Electromax_DH10B"
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BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 834 Std Error: 0.00
Plate: CL000217 row: D column: 05
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/mol_type="mRNA"
/strain="Indian"
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POLYA=No.
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/clone="IBIUW:22782"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cmagness@illumigen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="blood"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: C. Magness
                                                   24; Conservative
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Query Match
Best Local Similarity
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Query Match

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CE147952 GSS 25-SEP-2003
tigr-gss-dog-17000371304927 Dog Library Canis familiaris genomic,
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The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH341834 15 CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-64E10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis. 1 (bases 1 to 652)
Kirkness; E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other GSSs: CR230-64810.TV
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
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/strain="Standard Poodle"
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                                                                                                                                                                                                                genomic survey sequence.
                                                                                                                                                                                                                                                             CE147952.1 GI:35264744
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301-838-0200
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                             Canis familiaris
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AUTHORS
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                                                                                                                                                                                                                  /wol type="mRNA"
//wol type="mRNA"
//wol type="mRNA"
//wol type="mRNA"
//wol type="mRNA"
//worfal="Rabditiform larvae obtained from gerbils"
//db xref="texxon.6248"
//lab_host="XX-1.8 Hue MRP' (Stratagene)"
//clone lib="TBN95"
//clone lib="TBN95"
//clone lib="TBN95"
//clone lib="TBN95"
//worfal sarvae which had been isolated from gerbils rhabditiform larvae which had been isolated from gerbils ryperimentally infected dogs. colon was constructed and, using adaptors, was cloned unidirectionally into the vector from the Brooks site to the XhoI site. The library has an unamplified titer of 1 x 10E5 pfu/ml and an amplified, undiluted titer of 9 x 10E11 pfu/ml. The average insert size of the unamplified library is 675 bp (range, 100-1700)."
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Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunguery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 208J5. 208J5 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                             The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutmananih.gov). DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. High quality sequence stop: 262.

Location/Qualifiers
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Actinopterygii; Neopterygii; Teleostel; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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Danio rerio genomic clone DKEY-20045, genomic survey sequence.
BX199941
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                                                                                                                                                                                                             'organism="Strongyloides stercoralis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 74.3%; Score 20.8; DB 2; Best Local Similarity 91.7%; Pred. No. 7.1e+02; Matches 22; Conservative 0; Mismatches 2;
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Location/Qualifiers
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Pred. No. 7.4e+02;
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Humphray, S.J., Huckle, E. and Durham, J.L.
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/note="vector pIndigoBAC-536"
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/db_xref="taxon:7955"
/clone="DKEY-208J5"
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                          Email: est@watson.wustl.edu
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Danio rerio
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Best Local Similarity 91.7%;
Matches 22; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

TITLE JOURNAL REFERENCE AUTHORS

COMMENT

FEATURES

ORIGIN

BX199941/c

RESULT 8

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ORIGIN

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Gaps

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1 CACATGTAAAACAAGACTTCATTT 24

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mol_type="mRNA"
db_xref="taxon:6706"
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Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 85.2
Matches 23; Conservative
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BX859292
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TITLE
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KEYWORDS
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              The Institute for General Rockville, MD 20850, USA 712 Medical Center Dr., Rockville, MD 20850, USA 712 Medical Center Dr., Rockville, MD 20850, USA 713 Medical Center Dr., Rockville, MD 20850, USA 713 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 0208

Email: szhao¢tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 64 row: B column: 10 Seg primer: SP6 Class: BAC ends.
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Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Homarus.
1 (bases 1 to 576)
Towle, D.W. and Smith, C.M.
Expressed sequence tags in a normalized cDNA library prepared from multiple tissues of adult intermolt American lobster, Homarus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell.type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SBNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN951902 576 bp mRNA linear EST 08-JUN-200 MRNA linear EST 08-JUN-200 MR mx0 53e01 SP6 Lobster Multiple Tissues, Normalized Homarus americanus cDNA clone Ha mx0 53e01 5' similar to ref | NP 724983.2 | CG30019-PB - Drosophila melanogaster. Score = 210 bits (534),
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Marine DNA Sequencing and Analysis Center
Mount Desert Island Biological Laboratory
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
Tel: 207-288-2130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%; Score 20.6; DB 8;
85.2%; Pred. No. 8.7e+02;
tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                           1. .546
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-64E10"
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Homarus americanus
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High quality sequence stop: 477.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: dtowle@mdibl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CN951902.1 GI:48433491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="Female"
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Best Local Similarity 85.2
Matches 23; Conservative
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hepatopancreas, brain"

/dev stage="Adult intermolt"
/cloue lib="Lobter Multiple Tissues, Normalized"
/cloue="Vector: prov Sport 6.1; Total RNA samples were
prepared individually from each tissue, checked for
quality, then pooled for construction and normalization
of cDNA library by Invitrogen. Plasmids were isolated
and inserts end-sequenced by the Marine DNA Sequencing and
Analysis Racility at Mount Desert Island Biological
Laboratory. Traces were processed for submission to
dbEST by trace2dbest software (Parkinson, Anthony and
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/lab_host="DH108"
/clone_lib="AGENAE Rainbow trout normalized testis library
/rehi]"
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Oncorhynchus mykiss cDNA clone tcbi0011d.p.11 5prim, mRNA sequence.
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Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA Unpublished (2003)
On Dec. 16, 2003 this sequence version replaced gi:39956980.
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noce="Vector: pT7T3D-pac; Clone distribution : AGENAE Resource centre. Francois PIUMI, Francois Piumiojouy.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LEGG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
/clone="Ha mx0 53e01"
/tissue_type="Gill, epipodite, branchiostegite, heart,
ovary, testis, antennal gland, abdominal muscle,
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Oncorhynchus mykiss
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/db_xref="taxon:8022"
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Location/Qualifiers
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Query Match

ORIGIN

Matches

VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

FEATURES

REFERENCE

AUTHORS

DEFINITION

RESULT 13 CR033848 LOCUS ACCESSION

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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 759)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
(Unpublished (2001)
Other GSSS: BOOAA76TF
                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Ha_mx0_27a03"
/tishde type="Gill, epipodite, branchiostegite, heart,
ovary, teetis, antennal gland, abdominal muscle,
hepatopancreas, brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.6%; Score 20.6; DB 7; Length 725;
85.2%; Pred. No. 9.1e+02;
ive 0; Mismatches 4; Indels
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Fax: 301-888-0208
Email: cdrown@igr.org
DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Drive, Rockville, MD 20850, USA.
Old Bar Harbor Road, Salsbury Cove, ME 04672 USA
                                                                                                                                                                                                                                                                                                              Organism="Homarus americanus"
|mol_type="mRNA"
|db_xref="taxon:6706"
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/mol_type="genomic DNA"
/strain="TO1000DH3"
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/clone="BOOAA76"
/clone_lib="BO_1.6_2_KB_tot"
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                                                                                                                                                          Frace: SP6
Seg primer: SP6
High quality sequence stop: 501.
Location/Qualifiers
                                                                                                   Email: dtowle@mdibl.org
Plate: 27 row: a column: 03
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BZ462328.1 GI:26746914
                                    Tel: 207-288-9880 x474
Fax: 207-288-2130
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Class: sheared ends.
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Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae; Murinae; Mus. 1 (bases 1 to 659)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A. Bincet, Submission
Direct Submission
Submitted (FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 08-JUN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ha mx0_27a03_SP6_Lobster Multiple Tissues, Normalized Homarus americanus cDNA clone Ha mx0_27a03_5' similar to ref[XP_309809.1| ENSANGP00000018221 - Anopheles gambiae. Score = 251 bits (641), Expect = 1e-65, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR033848 linear GSS 05-JUL-200 Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP232j23, genomic survey sequence.
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Sukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Homarus.
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                                                                                                   ch 73.6%; Score 20.6; DB 5; Length 598; Similarity 85.2%; Pred. No. 8.8e+02; 23; Conservative 0; Mismatches 4; Indels
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Marine DNA Sequencing and Analysis Center
Mount Desert Island Biological Laboratory
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GSS; genome survey sequence; MICER.
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/organism="Mus musculus"
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/clone_lib="MHPP"
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Mus musculus
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Cowle,D.W. and Smith,C.M.
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Query Match

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Best Local

Matches

ð 임 RESULT 14 CN949957/c DEFINITION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

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Gaps

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/note="Vector: pHOS1; Site 1: BatXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

0; Gaps Query Match 73.6%; Score 20.6; DB 8; Length 759; Best Local Similarity 85.2%; Pred. No. 9.18+02; Matches 23; Conservative 0; Mismatches 4; Indels (

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AR64791 Sequence
AR64750 Sequence
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AR16498 Sequence
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AC09814 Rattus no
AC118400 Rattus no
AC118409 Human Chr
AC08369 Homo sapi
BX284691 Zebrafish
AC149582 Medicago
AC130903 Rattus no
AC130903 Rattus no
AC130903 Rattus no
AL685801 Penicilli
AL73192 Mouse DNA
AL73182 Mouse DNA
AL73182 Zebrafish
BX55912 Zebrafish
BX571880 Zebrafish
BX571890 Zebrafish
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Unclassified.
1 (bases 1 to 28)
Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
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Better, M.D., Carroll, S.F. and Studnicka, G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 5744580-A 59 28-APR-1998,
Location/Qualifiers
1.28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 28; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.36; Matches 28; Conservative 0; Mismatches 0; Indels
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Sequence 59 from patent US 5744580.
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Sequence 59 from patent US 5756699.
AR010103.1 GI:3968908
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AR164987
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AC130587
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AR055309 Sequence
AR141238 Sequence
AR141475 Sequence
I11949 Sequence 61
I40520 Sequence 59
AR368004 Sequence
AR430985 Sequence
AR403721 Sequence
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AR141429 Sequence
AR164985 Sequence
III901 Sequence 11
III947 Sequence 51
I40474 Sequence 51
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AR010057 Sequence
AR055263 Sequence
AR057747 Sequence
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AR010103 Sequence
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749.998 Million cell updates/sec
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                                                                                  June 21, 2005, 13:50:46; Search time 1809 Seconds
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
                                                                                                                                                                                                              4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                           nucleic search, using sw model
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seq length: 200000000
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Score

Result ŝ PAT 08-AUG-2001

FEATURES

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RESULT 3 AR055309

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1 (bases 1 to 28)
Bernhard, S.L., Better, M.D., Carroll, S.F., Lane, J.A. and Lei, S.-P.
Materials comprising and methods of preparation and use for ribosome-inactivating proteins
Patent: US 5416202-A 61 16 MAY-1995;
Location/Qualifiers
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(Inclasses 1 to 28)

Better,M.D., Carroll,S.F. and Studnicka,G.M.

Immunotoxins comprising ribosome-inactivating proteins
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Better, M.D. and Carroll, S.F.
Proteins encoding gelonin sequences
Patent: US 6146650-A 59 14-NOV-2000;
Location/Qualifiers
                                       28 bp 1
Sequence 59 from patent US 6146850.
AR141475
AR141475.1 GI:15100991
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Sequence 59 from patent US 5621083.
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    /mol_type="unassigned DNA"

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II1949.1 GI:909392
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1 (bases 1 to 28)
Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 6146631-A 59 14.NOV-2000;
Locarion/Qualifiers
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Llarity 100.0%; Pred. No. 0.36;
Conservative 0; Mismatches 0; Indels
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Polynucleotides encoding gelonin sequences
Patent: US 5837491-A 59 17-NOV-1998;
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   Patent: US 5756699-A 59 26-MAY-1998;
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/organism="unknown"
/mol_type="unassigned DNA"

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ARO55309.1 GI:5980886
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 5756699-A 11 26-MAY-1998;
Location/Qualifiers
                                                                                                                                                                     1 (bases 1 to 813)
Better, M.D., Carroll, S.F. and Studnicka, G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 574550-A 11.28-APR-1998;
Location/Qualifiers
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Better,M.D., Carroll,S.F. and Studnicka,G.M. Polynucleotides encoding gelonin sequences
Patent: US 5837491-A 11 17-NOV-1998;
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                                         Sequence 11 from patent US 5744580.
AR003721

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Better, M.D. and Carroll, S.F.
Fusion proteins and polymucleotides encoding gelonin sequences
Patent: US 6376217-A 59 23-APR-2002;
Location/Qualifiers
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 6649742-A 59 18-NOV-2003;
Location/Qualifiers
                                                                                                      100.0%; Score 28; DB 6; Length 28; 100.0%; Pred. No. 0.36; .ive 0; Mismatches 0; Indels
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Patent: US 5621083-A 59 15-APR-1997;
Location/Qualifiers

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Sequence 59 from patent US 6376217.
AR368004.1 GI:34601515
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AR430985
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Better,M.D.
Methods for recombinant microbial production of fusion proteins and BPI-derived peptides
Patent: US 5851802-A 246 22-DEC-1998;
Location/Qualifiers
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Better,M.D., Carroll,S.F. and Studnicka,G.M.
Immunotoxins comprising ribosome-inactivating proteins
Patent: US 6146631-A 11 14-NOV-2000;
Location/Qualifiers
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1 Similarity 92.9%; Pred. No. 5.7;
26; Conservative 0; Mismatches
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Sequence 11 from patent US 6146631.
AR141192 GI:15100709
            1. .813
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ACCESSION
VERSION
KEYWORDS
SOURCE
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ACCESSION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
FEATURES
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AUTHORS
TITLE
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AR067747
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AR141192
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        linear
        DNA
                                                                                                                                                           1 (bases 1 to 813)
Better,M.D. and Carroll,S.F.
Proteins encoding gelonin sequences
Patent: US 6146850-A 11 14.NOV-2000;
Location/Qualifiers
Sequence 11 from patent US 6146850. AR141429
                                                                                                                                                                                                                                                            1. .813
/organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 CACAATTAAAACAAGACTTCATTTTGGC 330
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Job time : 1813 secs
                                                                AR141429.1 GI:15100945
                                                                                                                                             Unclassified.
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Matches 26; Conserva
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TOPOLOGY: linear
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57, Appl
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15, App
494, App
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                                                                                               June 20, 2005, 10:36:43; Search time 29.5 Seconds (without alignments) 50.610 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 15,
Sequence 494,
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-425-336-57

US-08-448-113B-57

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US-08-646-360-57

US-08-610-838-57

US-09-1136-388-57

US-09-610-838-57

US-09-610-838-57

US-09-610-838-57

US-09-610-838-57

US-09-1136-388-15

US-09-053-003-6

US-09-053-003-6

US-09-053-003-6

US-09-053-003-6

US-09-613-313-494

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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: /cgn2 6/ptodata/1, 2: /cgn2 6/ptodata/1, 3: /cgn2 6/ptodata/1, 4: /cgn2 6/ptodata/1, 5: /cgn2 6/ptodata/1, 6: /cgn2 6/ptodata/1, 6: /cgn2 6/ptodata/1, 6: /cgn2 6/ptodata/1, 6: /cgn2 6/ptodata/1, 6:
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Match
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Sequence 48, Appl Sequence 49, Appl Sequence 8, Appli Sequence 9, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 26, Appli Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl		s of e-Inactivating Proteins
19 4 US-09-441-502B-48 13 4 US-08-467-023-44 13 4 US-10-055-485-49 18 3 US-08-390-353A-8 19 3 US-09-390-553A-8 19 2 US-09-66-227-5 12 2 US-09-66-227-5 12 4 US-09-410-889-3 19 4 US-09-411-502B-20 10 1 US-08-16-195A-25 10 2 US-08-436-772-25 10 3 US-09-16-195A-25 10 3 US-09-16-159-339A-215 10 3 US-09-860-276-17 11 4 US-09-860-395-17 12 4 US-09-860-395-17	ALIGNMENTS	lication US/07988430  TION: ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, Susan L. ernhard, O'lephon, F. Marcon, Marcon, O'lephon, F. Elchores, 101 Elchard, O'roole, Gerstein, Murray & Bicknell Elcknell INDARESS: INDARESS INDARESS INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARES INDARE
28 30 30.0 30 29 29.0 31 29 29.0 33 2 29.0 34 28 28.0 35 28 28.0 36 27 27.0 40 27 27.0 44 27 27.0 45 27.0		RESULT 1  US-07-986-430-59 Sequence 59, Application US/0798430 Patent No. 5416202 GENERAL INFORMATION: APPLICANT: Bertner, Marc D. APPLICANT: Carroll, Stephen F. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. APPLICANT: Lane, Julie A. ADDRESSEE: Marshall, O'Toole, Gerian Country: Chicago STREET: Street CITY: Chicago STREET: Street CITY: Chicago STREET: Lilinois COUNTRY: USA COUNTRY: USA APPLICATION NUMBER: US O7/901,707 FILING DATE: 19921209 CICASSICATION NUMBER: US O7/87,567 FILING DATE: 19-JUN-1992 PRIOR APPLICATION NUMBER: US O7/787,567 FILING DATE: 19-JUN-1992 PRIOR APPLICATION NUMBER: 35302 RESTRATION NUMBER: 35303

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Sequence 57, Application US/08488113B

Patent No. 5744580

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS: 169
CORRESPONDENCE ADDRESS: 169
CITY: Chicago
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STREET: Lilinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 100; DB 1; Length 20; 100.0%; Pred. No. 1.8e-10; ive 0, Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TRAP C COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING RELEASE #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 12-MAY-1995
RICH APPLICATION NUMBER: US 08/064,691
FILING DATE: US 09-DEC-1992
RRICH APPLICATION NUMBER: US 07/988,430
FILING DATE: US-UN-1993
RRICH APPLICATION NUMBER: US 07/981,707
FILING DATE: US-UN-1992
RRICH APPLICATION NUMBER: US 07/981,707
FILING DATE: US-UN-1992
RRICH APPLICATION NUMBER: US 07/901,707
FILING DATE: US-UN-1992
RRICH APPLICATION NUMBER: US 07/787,567
FILING DATE: US-NOV-1991
ATTOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-NOV-1991
ATTOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-NOV-1991
ATTOR APPLICATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 31,707-8889
TELECOMMONICATION INDERREY US 07/707-6156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PSGQAGAAASESLFISNHAY 20
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MOLECULE TYPE: peptide
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GY: linear
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Matches 20; Conserv
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
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                                                                    Query Match 100.0%; Score 100; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.8e-10; Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: USAA

ZIP: 6606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Rlopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUSTWARE: APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRICH APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRICH APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTONREY/AGENT INPORMATION:
NAME: MANAYER HOWERS
                                                                                                                                                                                                                                                                                                                                         ; Sequence 57, Application US/08425336; Patent No. 5621083
                                                                                                                                                                                                             PSGQAGAASESLFISNHAY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 3139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSGOAGAASESLFISNHAY 20
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TELERAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-425-336-57
; MOLECULE TYPE: peptide US-07-988-430-59
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STATE: Illinois
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Gaps

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Sequence 57, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Garcil, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 20;
1.8e-10;
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                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CEASITICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984/651
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/981,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: US 07/901,707
FILING NUMBER: US 07/787,567
FILING NUMBER: US 07/787,567
FILING NUMBER: US 07/787,567
FILING NUMBER: US 07/787,567
FILING NUMBER: US 07/787,567
FILING NUMBER: US 07/787,567
FILING NUMBER: US 07/787,567
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FILING NUMBER: US 07/787,567
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FILING NUMBER: US 07/787,567
FILING NUMBER: US 07/787,567
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500 West Madison Street, 34th floor
                      500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 100; I
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-646-360-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60661
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57, Application US/08646360
Patent No. 5837491
CENERAL INFORMATION:
CENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 100; DB 1; Length 20; 100.0%; Pred. No. 1.8e-10;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
RIGHTON APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
RIGHTON APPLICATION NUMBER: US/08/64,691
FILING DATE: 12-MAY-1993
RECOR APPLICATION NUMBER: US/07/98,430
FILING DATE: 09-DEC-1992
RIGHTON APPLICATION NUMBER: US/07/901,707
FILING DATE: 09-DEC-1992
RIGHTON APPLICATION NUMBER: US/07/901,707
FILING DATE: 09-DUN-1992
RIGHTON APPLICATION NUMBER: US/07/901,707
FILING DATE: 09-UN-1992
RIGHTON APPLICATION NUMBER: US/07/87,567
FILING DATE: 09-UN-1991
APPLICATION NUMBER: US/07/87,567
FILING APPLICATION NUMBER: US/07/87,567
FILING APPLICATION NUMBER: US/07/87,567
FILING APPLICATION NUMBER: US/07/87,567
FILING APPLICATION NUMBER: US/07/87,567
FILING NUMBER: US/07/87,567
FILING SAFE NUMBER: US/07/87,567
FILING SAFE NUMBER: US/07/88,099
TELEFRANCE/DOCKET NUMBER: 11022US/07/200-70.P3.C2A
TELEFRANCE/DOCKET NUMBER: 11022US/07/200-70.P3.C2A
TELEFRANCE/DOCKET NUMBER: US/07/8899
TELEFRANCE/DOCKET NUMBER: US/07/8899
TELEFRANCE/DOCKET NUMBER: US/07/8899
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Matches 20; Conservative 0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-646-360-57
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Gaps

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GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STARET: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 100.0%; Score 100; DB 3; Length 20; I. Similarity 100.0%; Pred. No. 1.8e-10; 20; Conservative 0; Mismatches 0; Indel8
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MEDIUM TYPE: Floppy disk
COMPUTER: I Tab PC Compatible
COMPUTER: DISP COMPUTER: COMPUTER: DISP COMPUTER: DISP PC COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILLING DATE: 13-MAY-1994
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAR JACHER
BEGISTRATION NUMBER: 32,918
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAR JACHER
BEGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 57, Application US/09610838 Patent No. 6376217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserva
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDREWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

CLASSIFICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691

FILING DATE: 1-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430

FILING DATE: US-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707

FILING DATE: US-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707

FILING DATE: US-1993

PRIOR APPLICATION NUMBER: US 07/901,707

FILING DATE: US-1993

PRIOR APPLICATION NUMBER: US 07/901,707

FILING DATE: US-1993

ATORNEY/AGENT INFORMATION:
NAME: MCANICADION NUMBER: US-1918

TELEPHONE: 312/707-9155

TELEPHONE: 312/707-9155

TELEPHONE: US-1248

INPORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARASTICS:
INPORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARASTICS:
INPORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARASTICS:
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARASTICS:
INFORMATION ACTION AC
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: PatentIn Release #1.0, Version, #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 100; DB 3; Best Local Similarity 100.0%; Pred. No. 1.8e-10; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-136-389-57; Sequence 57, Application US/09136389; Patent No. 6146850
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60661
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Gaps ; 0

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CT-US92-09487-59
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APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: MCANDIEWS, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 100; DB 3; Length 20; 100.0%; Pred. No. 1.8e-10; Live 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DATE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: 027/US94/05348
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 07/901,707
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PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MONICHOLAS, Janet M.
REGISTRATION NUMBER: 200-70.P4
TELEPONDENT INFORMATION:
TELEPONDENT INFORMATION:
TELEPONDENT INFORMATION:
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TELEPONDENT INFORMATION:
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APPLICATION NUMBER: 08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PSGQAGAAASESLFISNHAY 20
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MOLECULE TYPE: peptide
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PRIOR APPLICATION DATA:
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Matches 20; Conserv
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APPLICANT: Bernhard, Susan L.
APPLICANT: Berter, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell,
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FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATE: 19.
PREPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA: 07/901,707
PRILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA: 07/701,707
PRILING DATE: 19-UNN-1991
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: 32,918
REFERENCE/GOOKET INFORMATION: NAME: MCNICHOLAS, 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
RETERENCE/OWNUITION INFORMATION: TELLEPHONE: 312/707-889
TELLEPHONE: 312/707-889
TELLER: 650 388-1248
INFORMATION FOR SEQ ID NO: 57: SEQUENCE CHARACTERISTICS: LEMTH: 20 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
FTLING DATE: 19921104
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 100; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-10; Matches 20; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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STATE: Illinois
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-818-094-6
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; PERIERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                Sequence 6, Application US/09818094
Patent No. 6682898
GENERAL INFORMATION:
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STRANDEDNESS: <Unknown>
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                                      1 PSGQAGAAASESL 13
                                                                             2 PPGEAGXKAFSSL 14
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7; Conservative
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Matches 7; Conserv
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Matches
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| Sequence 6, Application US/09053003
| Patent No. 6207391
| GENERAL INFORMATION:
| APPLICANT: Wu. Pengquang
| TITLE OF INVENTION: High-Throughput Screening Assays for TITLE OF INVENTION: Modulators of STAT4 and STAT6 Activity NUMBER OF SEQUENCES: 64
| CORRESPONDENCE ADDRESS: A CORRESPONDENCE ADDRESS: 7 ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
| STATE: California
                                                                                                                                                                                                                                                                                                    ; DB 5; Length 20;
1.8e-10;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
SOFTWALE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/053,003
FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
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/note= "Xaa = phosphotyrosine'
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Pred. No. 35;
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100.0%; Pred. No. 1
tive 0; Mismatche
               REGISTRATION NUMBER: 35302
REFRERNCE/DOCKET NUMBER: 3113:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               1 PSGQAGAAASESLFISNHAY 20
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NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 01874
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPROREY: (415) 576-0200
INFORMATION FOR SEQ ID NO: 6:
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53.8%;
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  Noland, Greta E.
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Best Local Similarity 100.
Matches 20; Conservative
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MOLECULE TYPE: peptide
PCT-US92-09487-59
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; OTHER INFORMATION:
US-09-053-003-6
                                                                                                                                                                                                        TYPE: AMINO ACID
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Best Local Similarity
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APPLICANT: Wu, Pengguang
APPLICANT: Wu, Pengguang
MCKinney, Judi
TITLE OF INVENTION: High-Throughput Screening Assays for
Modulators of STAT4 and STAT6 Activity
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,094
FILING DATE: 26-Mar-2001
CLASSIFICATION DATA:
APPLICATION DATA:
RILING DATE: 31-MAR-1998
ATTORNEY/AGENT INFORMATION:
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                                                                                                          NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 018781-000800US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.0%; Score 33; DB 4; 53.8%; Pred. No. 35; tive 1; Mismatches
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US-09-636-215-494
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APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21012.1427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 494
LENGTH: 20
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION FILE REFERENCE: 65823/JPW/PT CURRENT APPLICATION WUBBER: US/10/092,138A CURRENT FILING DATE: 2002-03-06 NUMBER OF SEO ID NOS: 2.1
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                                                                                                                                                                                                                                                                                                                 Score 33; DB 4; Length 15;
Pred. No. 35;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial ; OTHER INFORMATION: Sequence: source: synthesized US-10-092-138A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%; Score 31.5; I 60.0%; Pred. No. 91; ative 1; Mismatches
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Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 494, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Made in a lab US-09-439-313-494
                                                                                                                                                                                                                                                                                                             33.0%;
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                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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Reed, Steven G.
Kalos, Michael
                                                                                                                                                                                                                                                                                                                 Query Match 33.0
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
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LENGTH: 15
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## APPLICANT: Harlocker, Susan L.
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## APPLICANT: Harlocker, Susan L.
## APPLICANT: Henderson_OR Robert A.
## APPLICANT: Relea, Marc M.
## APPLICANT: Relea, Marc M.
## APPLICANT: Bay, Carig H.
## APPLICANT: Carier, Darrick
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Sequence 15, Appl

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11. | cgn2_6/ptodata/2/pubpaa/US07_puBCOMB.pep:*

12. | cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

12. | cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

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17. | cgn2_6/ptodata/2/pubpaa/US16_PUBCOMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 57, Appl	Sequence 57, Appl	Sequence 40, Appl	Sequence 141, App	Sequence 443, App	Sequence 17, Appl	Sequence 6, Appli	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl
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	127-890-57  nce 57, Application US/10127890 cation No. US2003166196A1 EARL INCRMATION: APPLICANT: Better, Marc D. Carroll, Stephen F. Studnika, Gary M. TITLE OF INVENTION: Immunotoxins C NUMBER OF SEQUENCES: 173 CORRESPONDENCE ADDRESS: ADDRESSES: McAndrews, Held & STREET: 500 West Madison Stre CITY: Chicago STREET: 111inois COMPUTER: ELDAPH FC-DOS/MS-D STATE: 111inois COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-D SOFTWARE: PAD-LOS OF STEM: US/10/127 FILING DATE: 23-Apr-2002 CLASSIFICATION NUMBER: US/01/27 FILING DATE: 13-MAY-1996 APPLICATION NUMBER: PCT/US94/ FILING DATE: 12-MAY-1993 FILING DATE: 12-MAY-1993 FILING DATE: 12-MAY-1993
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INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-717-243-57
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Matches 6; Conservative
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Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 100; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 20; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COFFWARE: PAtentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US/08/839,765

FILING DATE: 15-APR-1997

APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/64,691

FILING DATE: 12-APR-1993

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 08/98430
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ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                    FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 1000 NOT 
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FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 07/901,707
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 57: US-10-127-890-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ 1D NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 169
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COMPUTER READABLE FORM:
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US-10-022-066-40

i Sequence 40, Application US/10022066

j Publication No. US20030166057A1

j GENERAL INFORMATION:

APPLICANT: HILDEBRAND, WILLIAM H.

APPLICANT: PRILLIMAN, KILEY RAE

TITLE OF INVENTION: WESTHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND

TITLE OF INVENTION: USES THEREOF

TILLE OF INVENTION: USES THEREOF

TILLE OF INVENTION: USES THEREOF

FILE REPRENCE: 6680.034

CURRENT FILING DATE: 2002-09-09

FRIOR PRILCATION NUMBER: 60/256,410

PRIOR FILING DATE: 2000-12-18

PRIOR FILING DATE: 1999-12-17

PRIOR FILING DATE: 1999-12-17

PRIOR FILING DATE: 1999-12-17

PRIOR FILING DATE: 2001-10-10

NUMBER OF SEQ ID NOS: 638

SOFTWARE: PATENTIN UVEN: 2.1

SEQ ID NO 40

MANDER OF SEQ ID NOS: 638

SEQ ID NO 40

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A APPLICANT: HILDEBRAND, WILLIAM H.; APPLICANT: PRILLIMAN, KILEY RAE; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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US-10-022-066-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
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Pred. No. 1.6e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
JOTHER INFORMATION: Description of Artificial Sequence: Synthetic US-10-022-066-443
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                                                                                                                                                                                                                                                                                                                                    Score 38; DB 14; Length 7;
Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                        CURRENT APPLICATION NUMBER: US/10/022,066
CURRENT FILING DATE: 2002-09-09
PRIOR PELING DATE: 2002-12-18
FRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2000-12-18
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 1999-12-17
PRIOR PILING DATE: 1999-12-17
PRIOR PILING DATE: 2001-10-10
PRIOR PILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 638
SOFTWARE: PATENTING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 638
SEQ ID NO 141
USES THEREOF
                                                                                                                                                                                                                                                                                                                                    38.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 85.7
Matches 6, Conservative
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Best Local Similarity
Matches 6; Conserv
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1 FVSNHAY 7
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 TITLE OF INVENTION:
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US-10-022-066-443
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RESULT

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Sequence 17, Application US/08681219
Publication No. US20020058607A1
GENERAL INFORMATION:
APPLICANT: Takaaki Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
TITLE OF INVENTION: 102/DHR) DOWAIN AND USES THEREOF
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Unnham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JUSTELO-7--0
Sequence 6, Application US/09818094
Publication No. US20020039749A1
GENERAL INFORMATION:
APPLICANT: Wu, Pengguang
MCKIANEY, Judi
TITLE OF INVENTION: High-Throughput Screening Assays for
MODIATORS OF STATA and STATE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/681,219
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 8; I
Pred. No. 2.7e+02;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8
Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
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STRANDEDNESS: sin
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Gaps
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; Sequence 15, Application US/10820403
; Publication No. US20040229287A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
; TITLE OF INVENTION: BIOCHEMICAL PROTEIN INTERACTION
; TITLE OF INVENTION: BIOCHEMICAL PROTEIN INTERACTION
; FILE REFERENCE: 65823/JPW/PT
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/10/092,138
; RICH RILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
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                                            APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED OF TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION FILE REFERENCE: 65923/JPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 15
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Pred. No. 2.7e+02;
1; Mismatches 1.
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33.0%; Score 33; DB 16;
Best Local Similarity 77.8%; Pred. No. 2.7e+02;
Matches 7; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial COTHER INFORMATION: Sequence: Source: synthesized US-10-092-138-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence:Source:Synthesized
US-10-820-403-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Weil
APPLICANT: Ring, David
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Rock, Kenneth L.
APPLICANT: Rock, Amneth L.
APPLICANT: ROCK, APPLICANT ANTIBODIES TO TREAT CANCER FIEE REFERENCE: 07917-205001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 15, Application US/10318397; Publication No. US20040115204A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
US20030170723A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 77.8
Matches 7; Conservative
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; Sequence 15, Application US/09230111C
; Publication No. US20030203414A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Taka-Aki
; APPLICANT: Yanagisawa, Junn
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
; TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
; TITLE OF INVENTION: BOMAIN AND USES THEREOF
; TITLE OF INVENTION: USPS2-A-POT-US
; CURRENT APPLICATION NUMBER: US/09/230,111C
; CURRENT FILING DATE: 1999-05-17
; SOFTWARE: PATENTING VET. 2.1
; SEQ ID NO: 15
; LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                 FILING DATE: 26-Mar-2001
CIASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/053,003
FILING DATE: 31-MRR-199
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REFIRENCE/DOCKET NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 018791-000800US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 9;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "OTHER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial COTHER INFORMATION: Sequence:source:synthesized US-09-230-111C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
APPLICATION NUMBER: US/09/818,094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 8
OTHER INFORMATION: /product= 'OTHER INFORMATION: ADOUGH INCOME SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
US-10-092-138-15
.; Sequence 15, Application US/10092138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: 8
                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.0%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 PSGQAGAAASESL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPGEAGXKAFSSL 14
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Gaps
                                                               APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPRENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SEQ ID NO 494
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.497074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.5%; Score 31.5; DB 9; Length 20; Best Local Similarity 60.0%; Pred. No. 6.3e+02; Matches 9; Conservative 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 20;
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Pred. No. 6.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/780,669; CURRENT APPLICATION NUMBER: US/09/780,669; CURRENT FILING DATE: 2001-02-09; NUMBER OF SEQ ID NOS: 943; SOFTWARE: PastSEQ for Windows Version 3.0; SEQ ID NO 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 494, Application US/09780669 Patent No. US20020051977A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FEATURE:
; OTHER INFORMATION: Made in a lab
US-09-780-669-494
                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Made in a lab
US-09-759-143-494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William
Hural, John
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ,
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.5%;
      Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GQAGAAASE-SLFIS 16
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Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stolk, John A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-09-780-669-494
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Pred. No. 3.9e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                   Score 32; DB 16; Length 15;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                             3, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     JOS-1317-74/15

JOS-1317-74/15

Publication No. US20040126378A1

GENERAL INFORMATION:

APPLICANT: FANGEr, Gary R.

APPLICANT: FANGEr, Gary R.

APPLICANT: FANGEr, Neil

APPLICANT: King, David

APPLICANT: Reck, Kenneth L.

TITLE OF INVENTION: ANTIBODIES TO TREAT CANCER

FILE REFERENCE: 07917-184001

CURRENT APPLICATION NUMBER: US 60/339,736

PRIOR APPLICATION NUMBER: US 60/339,736

PRIOR PILING DATE: 2002-01-12-11

PRIOR APPLICATION NUMBER: US 60/399,103

PRIOR FILING DATE: 2002-06-14

PRIOR PELING DATE: 2002-06-14

PRIOR PLING DATE: 2002-07-26

PRIOR PLING DATE: 2002-07-26

PRIOR PLING DATE: 2002-07-26

PRIOR FILING DATE: 2002-07-26

PRIOR PLING DATE: 2002-07-26

PRIOR PLING DATE: 2002-08-01

NUMBER OF SEQ ID NOS: 26

NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                             3; Mismatches
; CURRENT APPLICATION NUMBER: US/10/318,397; CURRENT FILING DATE: 2002-11-12; NUMBER OF SEQ ID NOS: 26; SOFTWARE: Patentin version 3.1; SEQ ID NO 15; LENGTH: 15; TYPE: PRT: ORGANISM: Cricetulus migratorius US-10-318-397-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-759-143-494

; Sequence 494, Application US/09759143
; Patent No. US20020022248A1
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Cricetulus migratorius
US-10-317-747-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Similarity 50.0%;
6; Conservative
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Retter, Marc W.
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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LENGTH: 15
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  Gaps
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                                                                                                                              RESULT 15
US-09-822-827-494
; Sequence 494, Application US/09822827
; Patent No. US2002081680A1
; GENERAL INFORMATION:
    APPLICAMY: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT PILLING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFUMARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 494
  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 31.5%; Score 31.5; DB 9; Length 20; Best Local Similarity 60.0%; Pred. No. 6.3e+02; Matches 9; Conservative 1; Mismatches 4; Indels
4; Indels
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Made in a lab
US-09-822-827-494
                                    3 GQAGAAASE-SLFIS 16
                                                           6 GDTGGASSEDSLMIS 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GOAGAAASE-SLFIS 16
9; Conservative
Matches
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Search completed: June 20, 2005, 11:15:09 Job time : 105 secs

6 GDTGGASSEDSLMIS 20

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

June 20, 2005, 10:27:32; Search time 23 Seconds (without alignments) 83.667 Million cell updates/sec Run on:

US-10-717-243-57 100 1 PSGQAGAAASESLFISNHAY 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

3886 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		,			SUMMARIES	
Result		* Query				,
No.	Score	Match	Length	8	ជា	Description
	28	28.0	12	7	A28856	fructose-bisphosph
7	26	26.0	13	~	A23695	myosin heavy chain
٣	26	26.0	18	~	173024	T_cell receptor be
4	25	25.0	15	~	B56661	
2	25	25.0	19	~	C56661	specific
9	24	24.0	60	~	PT0527	eceptor b
7	24	24.0	17	7	S57519	T cell receptor be
ω	24	24.0	17	~	\$57556	T cell receptor be
6	23	23.0	80	~	I48934	oprotêin A
10	23	23.0	13	~	B61233	conceptus protein
11	23	۳,	13	~	150173	alpha-2 collagen -
12	23	23.0	17	~	S18534	hypothetical prote
13	23	23.0	20	~	S27351	lysophospholipase
14	22	ö	10	~	S23371	T-cell receptor al
15	22	22.0	13	~	PQ0491	self-incompatibili
16	22	22.0	13	~	866558	serine proteinase
17	22	22.0	15	~	A56891	gamma 1 gliadin -
18	22	22.0	15	~	B56891	gamma 2 gliadin -
19	22	22.0	15	~	A61391	lpha-1
20	22		16	~	PH1477	_
21	22	22.0	16	~	PH1480	T-cell receptor be
22	22		17	~	PH0757	T-cell receptor be
23	22	ς.	18	~	S52125	- i
24	22		18	N	B48839	
25	22	ä	19	7	S43652	serpin WSZCI - whe
56	22	ä	19	۲	PQ0492	self-incompatibili
27	22	22.0	20	N	S33867	quinaldic acid 4-0
28	22	22.0	20	7	A49142	hyaluronidase (EC

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Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cispecies: Oryctolagus cuniculus (domestic rabbit)
Cistate: 19-May-1989 #sequence_revision 19-May-1989 #text_change 31-Oct-1997
Cistatesion: A28856
Ritannappel, E.; MacGregor, J.S.; Davoust, S.; Horecker, B.L.
Arch. Biochem. Biophys. 214, 293-298, 1982
A;Title: Limited proteolysis of liver and muscle aldolases: effects of subtilisin, cather A;Reference number: A28856
A;Reference number: A28856
A;Reference number: A28856
A;Reference number: A28856
A;Reference number: A28856
C;Roperfamily: fructose-bisphosphate aldolase
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; pent

ö Gaps ; Query Match 28.0%; Score 28; DB 2; Length 12; Best Local Similarity 33.3%; Pred. No. 2.3e+02; Matches 4; Conservative 6; Mismatches 2; Indels

9 ASESLFISNHAY 20 :::||| ::: | 1 STQSLFTASYTY 12 В ઠ

## RESULT 2

. . . . . . . . . . . . . .

Augusta heavy chain, smooth muscle - chicken (fragment)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Species: Gallus gallus (chicken)
C,Accession: A23695
R,Garabedian, T.E.; Yount, R.G.
J. Biol. Chem. 265, 22547-22553, 1990
A,Title: Direct photoaffinity labeling of gizzard myosin with [3H]uridine diphosphate pla A,Reference number: A23695; MuID:91093106; PMID:1979981
A,Reference number: A23695
A,Status: preliminary
A,Rolecule type: protein
A,Residues: 1.13 <GAR>
A,Cross-references: UNIPROT:002015; UNIPROT:09PS67
C,Superfamily: myosin heavy chain; myosin motor domain homology
C,Superfamily: myosin heavy chain; myosin motor domain homology
C,Superfamily: myosin heavy chain; myosin motor domain homology
F;2-9/Region: nucleotide-binding motif A (P-loop)

Similarity 36.0%; Score 26; DB 2; Length 13; Similarity 36.4%; Pred. No. 5.3e+02; Conservative 5; Mismatches 2; Indels Query Match Best Local Similarity Matches 4; Conserv

-a 0 0 0 0 0 0 0 -a 0

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S-locus specific

2 D56661

13

21.0

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Gaps

; 0

2 SGQAGAAASES 12 1 TGESGAGKTEN 11 ò qq A;Residues: 1-19 <GAU>

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A;Cross-references: UNIPROT:098923
A;Experimental source: stigma extracts, var. acephala
A;Note: sequence extracted from NCBI backbone (NCBIP:72301)
C;Comment: This glycoprotein, expressed only in stigmas, plays an important role in the I
C;Keywords: glycoprotein; polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57519
Submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified by A;Reference number: S5749
A;Accession: S57519
A;Status: preliminary
A;Molecule type: man,AA
A;Residues: 1-17 <-BURA
A;Residues: 1-17 <-BURA
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-051 receptor beta chain V-D-J region (100-41) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Accession: PT0527
R.Feney, A.J.
B.Feney, A.J.
A.Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions. A.Reference number: PT0509; MUD:91277601; PMID:1711558
A.Accession: PT0527
A.Accession: PT0527
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-e FFES
A.Resperimental source: adult thymus, strain BALB/c
C.Keywords: T-cell receptor
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                                                                                                                                                                                    25.0%; Score 25; DB 2; Length 19; 50.0%; Pred. No. 1.2e+03; ive 4; Mismatches 1; Indels
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Pred. No. 1.5e+03;
4; Mismatches 2;
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Pred. No. 2.8e+05;
0; Mismatches 2;
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71.4%;
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ilarity 45.5%;
Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
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Matches 5; Conservative
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Matches 5, Conserv
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R,Gaude, T.; Denoroy, L.; Dumas, C.
Electrophoresis 12, 646-653, 1991
A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal seq A;Reference number: A56661; MUID:92090397; PMID:1752245
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Experimental source: stigma extracts, var. acephala, self-compatible line P57

Experimental source: stigma extracts backbone (NCBIP:72302)

Note: sequence extracted from NCBI backbone (NCBIP:72302)

Comment: This glycoprotein, expressed only in stigmas, plays an important role in the superfamily: S-locus-specific glycoprotein, S-locus-specific glycoprotein homology
                                                                                                                                                              C; Accession: I73024
Wang, X.; Golkar, L.; Uyemura, K.; Ohmen, J.D.; Villahermosa, L.G.; Fajardo, T.T.
J. Immunol. 151, 7105-7116, 1993
A;Title: T cells bearing V beta 6 T cell receptors in the cell-mediated immune response
A;Reference number: 156207; MUID:94081361; PMID:8258714
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C5661
S-locus specific glycoprotein (allele S9) - wild cabbage (fragment)
S-locus specific glycoprotein (allele S9) - wild cabbage (fragment)
C;Species: Brassica cleracea (wild cabbage)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C;Accession: C5661
R;Gaude, T.; Dumas, C.
Blctrophoresis 12, 646-653, 1991
A;Title: Use of a fast protein electrophoretic purification procedure for N-terminal A;Reference number: A56661; MUID:92090397; PMID:1752245
A;Accession: C56661
A;Status: preliminary
A;Molecule type: protein
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                                                                    T cell receptor beta chain variable region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-locus specific glycoprotein P57 beta - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
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66.7%; Pred. No. 9e+02;
iive 2; Mismatches 1; Indels
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A,Note: sequence extracted from NCBI be C,Comment: This glycoprotein, expressed C,Superfamily: S-locus-specific glycopr C,Keywords: glycoprotein; polymorphism

A,Status: preliminary A,Molecule type: protein A,Residues: 1-15 <GAU>

6; Conservative

Best Local Similarity Matches 6; Conserv

Query Match

8 AASESLFIS 16 SSSESLTIS 15

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DB 2; I

Score 26; DB 2 Pred. No. 7.5e+ 1; Mismatches

26.0%;

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

SSLAGGAYNEOFF 15 SCOAGAAASESLF 14

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7

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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-18 <RES>

A; Accession: I73024

C;Genetics:

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aipna-2 collagen - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50173
R;Avvedimento, B.V.; Vogeli, G.; Yamada, Y.; Maizel, J.V.
Cell 21, 689-569; 1980
A;Title: Correlation between splicing sites within an intron and their sequence complemer A;Reference number: I50172; MUID:81064671; PMID:6159982
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C;Species: Homo sapiens (man)
C;Accession: S27351
R;Garsetti, D.; Holtsberg, F.; Steiner, M.R.; Egan, R.W.; Clark, M.A.
Biochem J. 288, 831-837, 1992
A;Title: Butyric acid-induced differentiation of HL-60 cells increases the expression of A;Reference number: S27350; MUID:93111958; PMID:1471998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Accession: S18534
R, Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.
Mol. Gen. Genet. 230, 120-128, 1991
A, Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in
                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-13 <AVV>
A;Cross-references: UNIPROT: P02467; GB:M10540; NID: 9211324; PIDN: AAA48638.1; PID: 9555428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 7 (eryG 3' region) - Saccharopolyspora erythraea (fragment)
C;Species: Saccharopolyspora erythraea
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
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A;Note: the authors translated the codon CTG for residue 12 as Gly
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Pred, No. 1.6e+03;
1; Mismatches 1; Indels
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A;Reference number: $18530; MUID:92079886; PMID:1840640
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nes 4; Conservative
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A; Residues: 1-17 <HAY>
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A;Introns: 12/3
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Best Local S:
Matches 4
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R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: I48934; MUID:94319082; PMID:8043949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q60615; EMBL:U05691; NID:g497010; PIDN:AAB60462.1; PID:g6428
C;Accession: S57556; S57557
R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaet, V.P.
submitted to the EMBL Bata Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified layceeslene. S57494
A;Reference number: S57494
A;Reference number: S5744
A;Residues: 1-17 <BUR>
A;Residues: 1-17 <BUR>
A;Residues: BmBL:Z49926; NID:g887498; PIDN:CAA90172.1; PID:g887499
A;Recession: S57557
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A; Title: Characterization of feline conceptus proteins during pregnancy. A; Reference number: A61233; MUID:91198359; PMID:2015342
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C;Species: Felis silvestris catus (domestic cat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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A;Experimental source: clone TF1
C;Keywords: T-cell receptor
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Pred. No. 1.6e+03;
1; Mismatches 5; Indels
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Pred. No. 2.8e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apolipoprotein A-II - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision C;Accession: I48934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.0%;
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Best Local Similarity 57.1%;
Matches 4; Conservative :
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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GETGSAA 7
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A; Residues: 1-17 <BUW>
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A;Residues: 1-8 <RES>
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T-cell receptor alpha chain J region - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: 823371
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmarn R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmarn A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu A;Reference number: 823364; MUID:92037820; PMID:1657615
A;Accession: S23371
A;Status: preliminary; translation not shown
A;Residues: 1-10 cPLU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     self-incompatibility locus glycoprotein delta - wild cabbage (fragment)
(Species: Brassica oleracea (wild cabbage)
(C)date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
(C)Accession: PQ0491
(R)Gaude, T.; Firky, A.; Heizmann, P.; Mariac, C.; Rougier, M.; Fobis, I.; Dumas, C.
(A) Title: Expression of a self-incompatibility gene in a self-compatible line of Brassica A; Reference number: JQ1733; MUID:93177215; PMID:8439745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9SXH5; UNIPROT:Q9SXH7; UNIPROT:021846; UNIPROT:023837; UNIPPOT:Q9SXH4; UNIPROT:023833; UNIPROT:Q8SSH4; UNIPROT:023834; UNIPROT:Q8XH6; UNIPROT:023834; UNIPROT:Q8XH6; UNIPROT:023834; UNIPROT:Q8W A;Experimental source: stigma, var. acephala P5781
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein C;Keywords: glycoprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.0%; Score 22; DB 2; Length 10; 80.0%; Pred. No. 1.8e+03; Attive 1; Mismatches 0; Indels
Best Local Similarity 66.7%; Pred. No. 2.6e+03; Matches 6; Conservative 1; Mismatches 2; Indels
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C;Keywords: T-cell receptor
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                2 ASISLYNSN 10
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A, Molecule type: protein
A, Residues: 1-13 <GAU>
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2 SGEAG 6
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SEQUENCE FROM N.A.
STRAIN=sample 2/01/4.8;
STRAIN=sample 2/01/4.8;
Willerslev E., Hansen A.J., Binladen J., Brand T.B., Gilbert M.T.P.,
Shairo B., Bunce M., Wiuf C., Gilichinsky D.A., Cooper A.;
"Diverse plant and animal genetic records from holocene and
pleistocene sediments.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unclassified, environmental samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                            HLX1 protein (Fragment). Name=HLX1;
                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uncultured organism.
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Best Local Similarity
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01-OCT-2003
01-OCT-2003
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mytilus edu
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plasmodium
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bos taurus
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                                                      June 20, 2005, 10:15:52; Search time 110.5 Seconds (without alignments) 92.684 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9p867
Q9e924
Q9uc18
Q9uc10
Q7jj51
Q7jj51
Q7j952
Q9e923
Q7jmy8
Q7jmy8
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Q9s8m9
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Q37016
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07gef4
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                          1612378 segs, 512079187 residues
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095854
095824
090C88
090C10
061BY3
07JJ51
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07JM78
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Maximum Match 100%
Listing first 45 summaries
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Q15989
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length
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Perfect score:
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          nicotiana a
citrus tris
gallus gall
pseudomonas
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homo sapien
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trimeresuru
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                                                                                                                        homo sapien
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BEDLINE-S1941813; PubMed=8095486;
Nibhimura D.Y., Purchio A.F., Murray J.C.;
"Linkage localization of TGFB2 and the human homeobox gene HLX1 to
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
         Q7gef2
Q7Te17
Q7Te17
Q5Gif2
Q53345
Q6Gif2
Q6Gif2
P92680
Q945f2
Q945f2
Q94664
Q94660
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Pred. No. 2.5e+03;
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Last annotation update)
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        Q7GEF2
Q7TE17
Q6QIF2
Q60615
Q60615
P83161
P92680
Q945F2
C1QA RAT
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Q96DJ6
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Genomics 15:357-364(1993).
EMBL; S56767; AAD13883.1; -.
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SEQUENCE 20 AA; 2012 MW;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAY-1999 (TrEMBLrel. 10,
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5 PSGPSGA 11
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                           GO; GO:0009573; C:ribulose bisphosphate carboxylase complex (. . .; IEA. GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA. GO; GO:001694; F:ribulose-bisphosphate carboxylase activity; IEA. InterPro; IPR000685; RuBisCO_large.

Pfam; PF02788; RuBisCO_large_N; 1.

NON TER 16 16
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Yamaguchi K., Subramanian A.R.;
Yamaguchi K., Subramanian A.R.;
Submitted (APR-2000) to Swiss-Prot.
-!- SIMILARITY: BELONGS TO THE 121E FAMILY OF RIBOSOMAL PROTEINS.
GO; GO:0003735; F: Structural constituent of ribosome; IEA.
InterPro; IPR001147; Ribosomal L21E; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Spinacia oleracea (Spinach).
Spinacia oleracea (Spinach).
Spinacia oleracea (Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophylales; Amaranthaceae; Spinacia.
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Sukaryota; Metazoa, Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
NCBI_TaxID=6550;
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Qin X., Waite J.H.;
"Exotic collagen gradients in the byssus of the mussel Mytilus
edulis.";
                                                                                                                                                                                                                                                                                                                                 DB 2; Length 16;
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                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
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01-UN3-2000 (TrEMBLrel. 14, Last annotation update)
Proximal collagen (Fragment)
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Last annotation update)
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Pred. No. 2.4e+03;
2; Mismatches 2
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EMBL; AY262604; AAP85185.1; -.
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4 PPEEAGAAVAAES 16
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Best Local Similarity
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MIDLINE=22737999; PubMed=12.0. Organizer R.P., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M.E., Schaller M., Harris A., Strowmatt C., Dauphin-Kohlberg S., Schaller M., Abbott A., Minne P., Maupin R., Strowmatt C., Lenrard B., Minne P., Maupin R., Strowmatt C., Latreille P., Miller N., Minne P., Maupin R., Strowmatt J. M. Abbott A., Winner B.R., Wallian J., Spieth J., Markin B.R., Wallian D.E., Cook L.L., M. Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis B.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE=94272301; PubMed=8003938;
Lopez F., Vansuyt G., Derancourt J., Fourcroy P., Casse-Delbart F.;
"Identification by 2D-page analysis of salt-stress induced proteins in
                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raphanus sativus (Radish).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Surosids II; Brassicales; Brassicaces; Raphanus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0
                                                                                                Score 27; DB 2; Length 19;
Pred. No. 3.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%; Score 26; DB 2; Length 15; 41.7%; Pred. No. 3.9e+03; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      radish (Raphanus Sativus).";
Cell. Mol. Biol. 40:85-90(1994).
SEQUENCE 15 AA; 1683 MW; D38B598E5EF892B4 CRC64;
J. Exp. Biol. 198:633-644(1995).
SEQUENCE 19 AA; 1605 MW; BDC1622E63973220 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein AUTS2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                    1; Mismatches
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                                                                                                Query Match 27.0%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity 41./v.
Best Local Similarity 41./v.
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Chloroplast.
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                           RESULT 8
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Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E., Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K., Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S., Baertsch R.A., Brent M.R., Keibler E., Plicek P., Bork P., Suyama M., Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R., Rddy S.R., Mchherson J.D., Olson M.V., Bichler E.B., Green E.D., Watterston R.H., Wilson R.K.;
"The DNA sequence of human chromosome 7.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=93194183; PubMed=8095486; Nishimura D.Y., Purchio A.F., Murray J.C.; Linkage localization of TGFB2 and the human homeobox gene HLX1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 5.3e+03;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC093679; AAS07486.1; -.
Hypothetical protein.
                                                                                                                                                                                                                        Cotton M., Holmes A., Spalding L.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         Waterston R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AA; 2028 MW; 6BB655F09B4036E4 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 1g.";
Genomics 15:357-364(1993).
EMBL; S56768; AAD13884.1; -.
EMBL; S56769; AAD13885.1; -.
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Q15989; Q15990;
01-NOV-1996 (TYEMBLEE]. 01,
01-NOV-1996 (TYEMBLEE]. 01,
05-JUL-2004 (TYEMBLEE]. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.0%;
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Matches 7; Conservative
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Best Local Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Q15989
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                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93028388; PubMed=1329085;
Timerman A.P., Mayrleitner M.M., Lukas T.J., Chadwick C.C., Saito A.,
Watterson D.M., Schindler H., Fleischer S.;
"Inositol polyphosphate receptor and clathrin assembly protein AP-2
are related proteins that form potassium-selective ion channels in
planar lipid bilayers.";
Proc. Natl. Acad. Sci. U.S.A. 89:8976-8980(1992).
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                                                                 ul-мax-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Inositol polyphosphate receptor, IPXREC (Fragment).
Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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MEDLINE=96397499; PubMed=8804393; DOI=10.1007/8004389670022;
Goulding S.E., Olmstead R.G., Morden C.W., Wolfe K.H.;
"Ebb and flow of the chloroplast inverted repeat.";
Mol. Gen. Genet. 252:195-206(1996).

EMBL; Z71244; CAA94954.1; -.
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 26; DB 2; Length 20;
Pred. No. 5.3e+03;
0; Mismatches 1; Indels
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GO; GO:0030125; C:clathrin vesicle coat; IEA.
GO; GO:0006886; P:intracellular protein transport; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR011012; Longin_like.
NON TER 20
SEQUENCE 20 AA; 2310 MW; 546EDDD34940494B CRC64;
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2388 MW; ZFC9AA300459DEID CRC64;
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InterPro; IPR00222; Ribosomal S19.
Pfam; PF00203; Ribosomal_S19; 1.
20 AA
                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
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Similarity 83.3%;
5; Conservative
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PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
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MEDLINE=93099171; PubMed=1463770; DOI=10.1016/0925-4439(92)90068-X; Baba S., Takahashi T., Kasama T., Shirasawa H.; Baba S., Takahashi T., Kasama T., Shirasawa H.; Indentification of two novel amyloid A protein subsets coexisting in an individual patient of AA-amyloidosis."; Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Biochim. Securecallust IEA. GO; GO:0005576; C:extracelluse response; IEA. InterPro; IRN0000965; Sectum_amyloid_A. Bran. PF60277; SAA: 1. SECUENCE 16 AA; 1585 MW; 1CAB41E77C839CCI CRC64;
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                                                                                                                                                                                                                                                                                                  SEQUENCE.
MEDLINE-95169134; PubMed=7864881;
Minafra I.P., Andriolo M., Basirico L., Aquino A., Minafra S.,
Boutillon M.M., and der Rest M.;
"Onco-fetal/laminin-binding collagen from colon carcinoma: detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                               of new sequences.";
Biochem. Biophys. Res. Commun. 207:852-859(1995).
GO; GO:0005581; C:collagen; NAS.
GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
GO; GO:000515; F:protein binding; NAS.
NON_TER 1 1
NON_TER 16 16
SEQUENCE 16 AA; 1385 MW; F7F93D20B39D3B1B CRC64;
                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ONCOFETAL-laminin binding COLLAGENALPHA 1(1) chain, of-LB collagen alpha 1(1) (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 6.1e+03;
0; Mismatches 2; Indels
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Best Local Similarity 71.4
Matches 5, Conservative
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                                                                                                             PRELIMINARY;
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7 SSSESLTIS 15
   8 AASESLFIS 16
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"Direct photosoffinity labeling of gizzard myosin with vanadate-trapped adenosine diphosphate.";
Biochemistry 30:10126-10132(1991).
BIR, A23695, A23695.
NON TER 12 12
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Brassica oleracea (Cauliflower).
Brassica oleracea (Cauliflower)
Buxaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 4.5e+03;
4; Mismatches 2; Indels
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26.0%; Score 26; DB 2; Length 20; 42.9%; Pred. No. 5.3e+03; ive 3; Mismatches 1; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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MEDLINE=92031443; PubMed=1931944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stigmas of Brassica Oleracea.";
Electrophoresis 12:646-653(1991).
PIR; B56661; B56661.
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12 AA; 1178 MW;
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Best Local Similarity 40.0
Matches 4; Conservative
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                               3; Conservative
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                                                                                                                                                                                                                                                      Myosin (Fragment).
Gallus gallus (Chicken).
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                                                            14 FISNHAY 20
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Search completed: June 20, 2005, 10:46:19 Job time : 111.5 secs

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MEDLINE=99016714; PubMed=9800332;
Du F., Ray J.;
"A tetranucleotide polymorphism in the canine type II collagen gene (COLZA1).";
Anim. Genet. 29:400-400(1998).
EMBL; AF036484; AAC24763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 6.9e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.0%; Score 25; DB 2; Length 18; Best Local Similarity 71.4%; Pred. No. 6.9e+03; Matches 5; Conservative 0; Mismatches 2; Indels
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18 18
18 AA; 1590 MW; 4D3CD1638CB03A1C CRC64;
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                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last annotation update)
                                                                                                                                        18 AA
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                                                                                                                                                                                                                                   Pro-alpha 1(II) collagen (Fragment).
Homo sapiens (Human).
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Best Local Similarity 62.5
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                      2 GPGGAWAAEAI 12
3 GOAGAAASESL 13
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 20, 2005, 10:14:47; Search time 62.5 Seconds (without alignments) 123.763 Million cell updates/sec Run on:

US-10-717-243-57

100 1 PSGQAGAAASESLFISNHAY 20 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

716780 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* 1: genesecm1090r. Database :

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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uol	Rabbit Mu	HLA bindi	HLA bindi	B15 class	B15 class	Human leu	Human leu	Human leu	Human leu	Human leu	Human leu	Human len	Human len	Human leu	A. oryzae	Signal-tr	Library p	D-alanine	Anti-gang	Anti-mono	CDR1 regi	Human pro	Human pro	Human pro	Prostate
Description	Aar37301	Adn63558	Adn64270	Abp55800	Abp55717	Abg96843	Abg96597	Abg96695	Abg97023	Ad198512	Ad198370	Ad198676	Ad198857	Ad198439	Abg70560	Aaw50174	Ade65831	Ad146355	Abr82269	Adp84124	Ads31786	Aam01149	Aau69794	Aag99034	Abu71685
ΩΙ	AAR37301	ADN63558	ADN64270	ABP55800	ABP55717	ABG96843	ABG96597	ABG96695	ABG97023	ADL98512	ADL98370	ADL98676	ADL98857	ADL98439	ABG70560	AAW50174	ADE65831	ADL46355	ABR82269	ADP84124	ADS31786	AAM01149	AAU69794	AAG99034	ABU71685
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Query Match	100.0	46.0	46.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	37.0	33.0	33.0	33.0	32.0	32.0	32.0	31.5	31.5	31.5	31.5
Score	100	46	46	38	38	38	38	38	38	38	38	38	38	38	37	33	33	33	32	32	32	31.5	31.5	31.5	31.5
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ABB95254 ABB13944 ABB13944 ABB13944 AAGB7980 AAAGB7982 AAAGB321 AAGB7981 AAGB7981 AAGB7981 AAGB7981 AAGB7981 AAGB7981 AAGB7981 AAGB7981 AAGB7981 AAGB7983 AAAG1140 AAGB7983 AAAG11983 AAAG17983			Abp58843 RNA bindi Ade25841 Anti-alph Aau75276 Leucine-r Aaw49140 Human leu		Adā03267 Angiotens Abr58637 Angiotens Abr58791 Alzheimer Adn31816 Human Alz
00000000000000000000000000000000000000	ABB95254 ABR54366 ADB13944 ADG26360	AAG87980 AAG87982 AAG87981 AAR88321	ABP58843 ADE25841 AAU75276 AAW49140	AAW42816 AAX33475 AAG93377 AAG87983	ADA03267 ABR56637 ABR58791 ADN31816
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	26 27 28 29	33 33 33	3 3 3 4 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	38 39 41 41 41	4 4 4 4 G & 4 3

## ALIGNMENTS

AAR37301 standard, protein; 20 AA. 25-MAR-2003 13-SEP-1993 AAR37301; RESULT 1 AAR37301

(first entry)

Rabbit Muscle aldolase peptide segment.

Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; human engineered antibody; variable region; light chain; cell targetting; chimeric antibody; RMA;

Oryctolagus cuniculus.

Location/Qualifiers 1. .20 /note= "contains several potential cathepsin cleavage 92WO-US009487. sites" Key Cleavage-site 04-NOV-1992; WO9309130-A1 13-MAY-1993. 

04-NOV-1991;

91US-00787567. 19-JUN-1992;

(XOMA ) XOMA CORP.

SP; Lei Carroll SF, Lane JA, Berhard SL, Better MD,

WPI; 1993-167617/20

cytotoxic Analogues of type I ribosome inactivating protein - useful as cytotoxion agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.

Example 10; Page 115; 163pp; English.

The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules

infections or cancer, such as prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyloma acuminatum. The composition is also be used for diagnosing such diseases.

This sequence represents a peptide of the invention

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Gaps ;;

Score 46; DB 8; Length 9; Pred. No. 1.8e+06; 1; Mismatches 0; Indels

46.08; 88.98;

Query Match Best Local Similarity

Sequence 9 AA;

8888888

8; Conservative

Matches

12 SLFISNHAY 20

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are antibodies or their fragments, esp. human engineered H65 antibody fragments. Fusion constructs were assembled that included a natural sequence gelonin gene fused to an H65 truncated heavy chain gene or an H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of the rabbit muscile aldotase was inserted between the gelonin gene and the Ab gene. The resulting immunoconjugates can be used as cytotoxic therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; hepatotropic; virucide; antlinflammatory; anti-HIV; gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome; prostate specific antigen; prostate specific membrane antigen; hepatitis B virus antigen; hepatitis C virus antigen; hepatitis C virus antigen; malignant melanoma antigen; ADS; renal carcinoma; cancer; prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
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100.0%; Pred. No. 8.2e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADN63558 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                  20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chondyloma acuminatum
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                                                                                                                                                                                                                                                                   Sequence 20 AA;
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The invention relates to a novel composition comprising one or more peptides or nucleic acids encoding an HLA binding peptide. The composition further comprises an HTL epitope. It also comprises a spacer comprosition further comprises an HTL epitope. It also comprises a spacer molecule, a carrier, an MHC targeting sequence or a lipid. The peptides are incorporated as part of a liposome. The peptide is from an antigen selected from prostate specific antigen (PSA), prostate specific membrane selected from prostate specific antigen (PSA), prostate specific membrane antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV) antigen, malignant melanoma antigen (MAGB), gosteln Barr virus, Human immunodeficiency type-2 (HIV-2), antigen, malignant melanoma antigen (MAGB), posteln Barr virus, Human immunodeficiency type-2 (HIV-2), papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53, murine p53 (Mp53), CEA, HER2/neu, and tyrosine kinase related protein (TKP). The composition is useful for preventing or treating viral conformatum. The composition is also be used for diagnosing such diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition of peptides and nucleic acids capable of binding Major Histocompatibility Complex molecules, useful for diagnosing, preventing or treating viral infections or cancer, such as prostate cancer,
                                                                                                                                                                                                           cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV; gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome; prostate specific antigen; prostate specific membrane antigen; hepatitis B virus antigen; hepatitis C virus antigen; hepatitis C virus antigen; malignant melanoma antigen; MAGB; Epstein Barr virus; cancer; prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 870; 186pp; English.
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                                    ADN64270 standard; peptide; 9 AA.
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                                                                                                                            (first entry)
                                                                                                                                                                    HLA binding peptide #870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIM-) EPIMMUNE INC.
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or treating viral in
hepatitis B or AIDS.
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                                                                                                                                                                                                                                                                                                                                                                                        Unidentified.
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                                                                                 ADN64270;
RESULT 3
                  ADN64270
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The invention relates to a novel composition comprising one or more peptides or nucleic acids encoding an HLA binding peptide. The composition further comprises an HTL epitope. It also comprises a spacer molecule, a carrier, an WHC targeting sequence or a lipid. The peptides are incorporated as part of a liposome. The peptide is from an antigen are incorporated specific antigen (PBA), prostate specific membrane antigen (PBM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV) antigen, malignant melanoma antigen (MAGB), Epstein Barr virus, human immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2), Papillona virus, Lassa virus, Mycobacterium tuberculosis (MT), p53, murine p53 (Mp53), CEA, HERZ/neu, and tyrosine kinase related protein (TKP). The composition is useful for preventing or treating viral

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ligands likely to bind a particular HLA class I or class II protein. The database allows the user to screen an unknown peptide sequence for potential matches with SHLA ligand discrete sequences or SHLA ligand motifs of sequences. Due to the completeness and concentration of SHLA obtained to date, better sequencing data of numerous endogenously loaded HLA ligands to face to she with a ligand database, and by comparison of such ligands to each other and to the genomic sequence, better motifs are also found in the SHLA ligand database, and by comparison of such ligands to each other and to the genomic sequence, better motifs are also found in the SHLA ligand database. ABPS5692 to ABPS5912 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA ligand; human leukocyte antigen; predictive algorithm; database; MHC ligand; major histocompatibility complex; viral; bacterial; tumour.
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                                                                                                                                            46.0%; Score 46; DB 8; Length 9; 88.9%; Pred. No. 1.8e+06; Live 1; Mismatches 0; Indels
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   This sequence represents a peptide of the invention.
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10-OCT-2001; 2001US-00974366.
18-DEC-2001; 2001US-00022066.
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                                                                        Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen ligand database assembled by producing HLA having loaded ligands, isolating and sequencing loaded ligands to obtain HLA ligand data and populating database in computer system with ligand data.
amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA ligand, human leukocyte antigen; predictive algorithm; database,
MHC ligand, major histocompatibility complex; viral; bacterial; tumour.
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                                                                                                                       Gaps
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                                                                                                                   0; Indels
                                                                            Score 38; DB 5; Length 7;
Pred. No. 1.8e+06;
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                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                               ABP55717 standard; peptide; 7 AA
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10-OCT-2001; 2001US-00974366.
18-DEC-2001; 2001US-00022066.
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85.7%;
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                                                                                                                   6; Conservative
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(PRIL/) PRILLIMAN K R.
(HICK/) HICKMAN H D.
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                                                                                                                                                          14 FISNHAY 20
                                                                                            Local Similarity
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                                       Sequence 7 AA;
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ligand maps from the peptide pools extracted from series of distinct yet related class I HIA-B15 allotypes; compare the different ligand maps to identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (WHC) can be produced in mammalian or insect/becreial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HIA (human leukocyte antigen) peptide ligand

Sequence 7 AA;

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The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a cPCR product (PI), inserting P1 into mammalian expression vector; electroporating the plasmid into a host cell; inoculating the cell pharm produces sHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune complex (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune consistence                                                                                                                                                  ö
amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                       Gaps
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                                                                                                  Score 38; DB 5; Length 7; Pred. No. 1.8e+06; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen (HLA) B15 ligand #168.
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                                                                                                                                                                                                                                                                                                                                                                                     ABG96843 standard; peptide; 7 AA.
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18-DEC-2000; 2000US-0256410P.
10-OCT-2001; 2001US-00974366.
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                                                                          Query Match
Best Local Similarity 85...
6; Conservative
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                                               Sequence 7 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing soluble human leukocyte antigen (HLA) in cell pharm useful for studies of peptide loading for characterizing human immune responses involves using HLA allelic cDNA or genomic DNA as starting material.
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                                       Gaps
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                                     0; Indels
   Length 7;
Score 38; DB 5; 
Pred. No. 1.8e+06; 
1; Mismatches 0
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                                                                                                                                                                                                    ABG96597 standard; peptide; 7 AA.
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18-DEC-2000; 2000US-0256410P.
10-OCT-2001; 2001US-00974366.
   38.0%;
85.7%;
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   Query Match 38.0
Best Local Similarity 85.7
Matches 6; Conservative
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1 FVSNHAY 7
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                                                                                                                                                                  RESULT 7
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diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in vaccine development) and too the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the MHC molecule and characterised. The secreted MHC molecules allow the secreted MHC molecules allow the assessment of structural and functional impact of HHA class I was assessment of structural and functional impact of HHA class I colymorphism. The molecules are also useful to generate ligands and hence ligand maps from the peptide pools extracted from series of distinct yet related class I HHA-BIS allotypes; compare the different ligand maps to identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I in molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) peptide ligand.
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                                                                                                                                                                                                                                                                                                                                                                                 38.0%; Score 38; DB 5; Length 7; 85.7%; Pred. No. 1.8e+06; live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human leukocyte antigen (HLA) B15 ligand #118.
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18-DEC-2000; 2000US-0256410P.
10-OCT-2001; 2001US-00974366.
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1 FVSNHAY 7
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with the host cell such that cell pharm produces sHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in vaccine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the mile molecules and characterised. The secreted MHC molecules allow the assessment of structural and functional impact of HLA class I collymorphism. The molecules are also useful to generate ligands and hence ligand maps from the peptide pools extracted from series of distinct yet in the content of the compare the different ligand maps to related.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing soluble human leukocyte antigen (HLA) in cell pharm useful for
                                                                                                                                                                                                                                                                                                                                 identify potentially shared elements, and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained This sequence represents a HLA (human leukocyte antigen) peptide ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble human leukocyte antigen; HLA; sHLA; cell pharm;
multimeric HLA complex; cytotoxic T lymphocytes; CTL; immune response;
viral infection; cancer; autoimmune disease; vaccine development; MHC;
major histocompatibility complex; diagnostic development;
HLA class I polymorphism; HLA-B15 allotype; ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 5; Length 7;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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18-DEC-2000; 2000US-0256410P.
10-OCT-2001; 2001US-00974366.
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Best Local Similarity
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Producing soluble human leukocyte antigen molecules, for testing the functionality of peptide ligands, comprises utilizing a locus-specific primer having a stop codon incorporated into a 3' primer, or that

Hildebrand WH, Prilliman KR;

WPI; 2003-863700/80.

The invention describes a method of producing soluble human leukocyte

Disclosure; Page; 148pp; English.

primer having a stop codon truncates the allelic cDNA

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The invention describes a method of producing soluble human leukocyte antigen (HIA) molecules (sHIA) in cell pharm involving amplifying HIA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (PI), inserting Pl into mammalian expression vector; clock product (PI), inserting Pl into mammalian expression vector; electroporating the plasmid into a host cell; inoculating the cell pharm with the host cell such that cell pharm produces sHIA. A multimeric HIA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HIA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLS) and induce immune responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for cytotoxic and infections and cancer, and for molecules produced are useful for studies of peptide loading (i.e., in concerted MHC molecules, naturally loaded peptides can be eluted from the secreted MHC molecules and tuctional impact of HIA class I with the casessment of structural and functional impact of HIA class I collymorphism. The molecules are also useful to generate ligands and hence ligand maps from the peptide pools extracted from series of distinct yet casessment of an entity land to the development colligand maps to identify not entity locating the different ligand maps to identify not characterially shared alments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) peptide ligand
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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Disclosure; Page 183; 300pp; English.
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; 2000US-0256410P.
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PRILLIMAN K R.
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Best Local Similarity
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(PRIL/)
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antigen (HLAM) molecules comprising utilising a locus-specific primer having a stop codon incorporated into a 3' primer, or a locus-specific primer primer that truncates the allelic cDNA resulting in a truncated PCR product having the coding regions encoding cytoplasmic and transmembrane domains of the allelic cDNA removed so that the truncated PCR product has a coding region encoding a soluble HLAA molecule. Also described is a multimeric HLAA complex comprising a substrate, and at least two soluble HLAA molecules attached to the substrate and an apparatus or a bioreactor unit for producing major histocompatibility complex molecules. The methods are useful for producing soluble human leukocyte antigen (HLA) concented. The molecules are useful for producing soluble human leukocyte antigen (HLA) concented ligands bound to the soluble HLAA molecules. The HLAA complex is useful for testing the Clunctionality of peptide ligands bound to the soluble HLAA molecules. The HLAA complex is useful for testing the molecules are also useful in vaccine development. This is the amino acid sequence of a ligand derived from a human leukocyte antigen (HLAA).

B15 family member. Note: This sequence is shown in table 4 on pages 69-70
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18-DEC-2000; 2000US-0256410P.
24-MAY-2001; 2001US-0293261P.
09-OCT-2001; 2001US-00974366.
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(PRIL/)
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The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules comprising utilising a locus-specific primer. Thay ing a stop codon incorporated into a 3' primer, or a locus-specific primer that truncates the allelic CDNA resulting in a truncated PCR product having the coding regions encoding cytoplasmic and transmembrane domains of the allelic CDNA removed so that the truncated PCR product has a coding region encoding a soluble HLA molecule. Also described is a multimeric HLA complex comprising a substrate, and at least two soluble HLA molecules attached to the substrate and an apparatus or a bioreactor unit for producing major histocompatibility complex molecules. The methods are useful for producing soluble human leukocyte antigen (HLA) molecules. The multimeric HLA complex is useful for testing the functionality of peptide ligands bound to the soluble HLA molecules are also useful in vaccine development. This is the amino acid sequence of a human leukocyte antigen (HLA)-B15 peptide found in allotypes B*1508 and B*1501.
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                                                                    Producing soluble human leukocyte antigen molecules, for testing the functionality of peptide ligands, comprises utilizing a locus-specific primer having a stop codon incorporated into a 3' primer, or that truncates the allelic cDNA.
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                                                                                                                                                           Disclosure; Fig 26; 148pp; English.
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 Hildebrand WH, Prilliman KR;
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85.7%;
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18-DEC-2000; 2000US-0256410P.
24-MAY-2001; 2001US-0293261P.
09-OCT-2001; 2001US-0327907P.
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                                   WPI; 2003-863700/80.
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Gaps

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The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules comprising utilising a locus-specific primer having a stop codon incorporated into a 3 primer, or a locus-specific primer that truncates the allelic CDNA resulting in a truncated PCR product having the coding regions encoding cytoplasmic and transmembrane domains of the allelic CDNA removed so that the truncated PCR product has a coding region encoding a soluble HLA molecule. Also described is a multimeric HLA complex comprising a substrate, and at least two soluble HLA molecules attached to the substrate and an apparatus or a bioreactor unit for producing major histocompatibility complex molecules. The methods are useful for producing soluble human leukocyte antigen (HLA) molecules. The multimeric HLA complex is useful for testing the molecules are also useful in vaccine development. This is the amino acid sequence of a human leukocyte antigen (HLA)-B15 allocype B+1501 peptide. Note: This sequence is shown in table A on pages 88-90 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soluble human leukocyte antigen; HLA; locus-specific primer; truncation; multimeric HLA complex; bioreactor; major histocompatibility complex molecule; MHC; vaccine; HLA-B15;
                                                                                            Producing soluble human leukocyte antigen molecules, for testing the functionality of peptide ligands, comprises utilizing a locus-specific primer having a stop codon incorporated into a 3' primer, or that truncates the allelic cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen-B15 allotype B*1508 peptide #11.
                                                                                                                                                                                                                                                                      Disclosure; Page; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADL98857 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2000; 2000US-0256409P.
18-DEC-2000; 2000US-0256410P.
24-MAY-2001; 2001US-029561P.
09-OCT-2001; 2001US-037907P.
10-OCT-2001; 2001US-0974366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2001; 2001US-00022066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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(PRIL/) PRILLIMAN K R.
                            WPI; 2003-863700/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 FISNHAY 20
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HILDEBRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FVSNHAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003166057-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
DIXA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA BERRETA B
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The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules comprising utilising a locus-specific primer having a stop codon incorporated into a ' primer, or a locus-specific primer that truncates the allelic CDNA resulting in a truncated PCR product having the coding regions encoding cytoplasmic and transmembrane domains of the allelic CDNA removed so that the truncated PCR product has a coding region encoding a soluble HLA molecule. Also described is a multimeric HLA complex comprising a substrate, and at least two soluble HLA molecules attached to the substrate and an apparatus or a bioreactor unit for producing major histocompatibility complex molecules. The methods are useful for producing soluble human leukocyte antigen (HLA) molecules are useful for producing soluble human leukocyte antigen (HLA) complex is useful for testing the conclusionality of peptide ligands bound to the solubble HLA molecules are also useful in vaccine development. This is the amino acid sequence of a human leukocyte antigen (HLA)-BLS allotype B*1508 peptide. Note: This sequence is shown in table C on page 93-94 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        soluble human leukocyte antigen; HLA; locus-specific primer; truncation; multimeric HLA complex; bioreactor; major histocompatibility complex molecule; MHC; vaccine; HLA-B15; ligand.
                                                  Producing soluble human leukocyte antigen molecules, for testing the functionality of peptide ligands, comprises utilizing a locus-specific primer having a stop codon incorporated into a 3' primer, or that truncates the allelic CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.0%; Score 38; DB 7; Length 7; 85.7%; Pred. No. 1.8e+06; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human leukocyte antigen-B15 ligand #20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADL98439 standard; peptide; 7 AA.
                                                                                                                                                Disclosure; Page; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001; 2001US-00022066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-DEC-1999; 99US-00465321.
18-DEC-2000; 2000US-02564109P.
18-DEC-2000; 2000US-0256410P.
24-MAY-2001; 2001US-0293261P.
09-OCT-2001; 2001US-0327907P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hildebrand WH, Prilliman KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-OCT-2001; 2001US-00974366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HILD/) HILDEBRAND W H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PRIL/) PRILLIMAN K R.
                   WPI; 2003-863700/80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 FISNHAY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 FVSNHAY 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL98439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             figures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules comprising utilising a locus-specific primer chaving a stop codon incorporated into a 3' primer, or a locus-specific primer that truncates the allelic CDNA resulting in a truncated PCR product having the coding regions encoding cytoplasmic and transmembrane domains of the allelic CDNA removed so that the truncated PCR product has a coding region encoding a soluble HLA molecule. Also described is a multimeric HLA complex comprising a substrate, and at least two soluble HLA molecules attached to the substrate and an apparatus or a bioreactor unit for producing major histocompatibility complex molecules. The multimeric HLA complex is useful for testing the molecules. The multimeric HLA complex is useful for testing the control of peptide ligands bound to the soluble HLA molecules. The HLA complex is useful for testing the HLA molecules are also useful in vaccine development. This is the amino acid sequence of a ligand derived from a human leukocyte antigen (HLA).

Els family member. Note: This sequence is shown in table 4 on pages 69-70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to the isolation of glutaminase (EC 3.5.1.2) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104, and the polynucleotide sequences encoding them. The invention also describes
                                      Producing soluble human leukocyte antigen molecules, for testing the functionality of peptide ligands, comprises utilizing a locus-specific primer having a stop codon incorporated into a 3' primer, or that truncates the allelic CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.0%; Score 38; DB 7; Length 7; 85.7%; Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 8; 43pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG70560 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A. oryzae glutaminase, peptide #1.
                                                                                                                                    Disclosure; Page; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AICH-) AICHI KEN PREFECTURE. (ICHI-) ICHIBIKI KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-2001; 2001JP-00019108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-2001; 2001JP-00019108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus oryzae; KBN616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (revised)
WPI; 2003-863700/80.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7 AA;
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25-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG70560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
ABG70560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Gaps ;

a vector containing a polynucleotide sequence encoding glutaminase, a host cell containing such a vector, and a method for the preparation of glutaminase. The glutaminase is useful for enhancing the taste of soy and miso. The present sequence represents a peptide from A. oryzae KBN616 glutaminase. (Updated on 29-AUG-2003 to standardise OS field) 88888888

Sequence 20 AA;

Gaps 0; Query Match 37.0%; Score 37; DB 5; Length 20; Best Local Similarity 61.5%; Pred. No. 51; Matches 8; Conservative 0; Mismatches 5; Indels

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6 GAAASESLFISNH 18

2 GAVASESAICSRH 14

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Search completed: June 20, 2005, 10:42:34 Job time : 65.5 secs

Oden MDA SOOd E. W.

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                      Copyright
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using sw model OM protein - protein search, June 20, 2005, 10:00:54; Search time 24 Seconds Run on:

(without alignments)
80.181 Million cell updates/sec

US-10-717-243-57 Title: Perfect score:

100 1 PSGQAGAAASESLFISNHAY Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	fructose-bisphosph	fructose-bisphosph	fructose-bisphosph	fructose-bisphosph	aldolase C - chick	fructose-bisphosph	fructose-bisphosph	fructose-bisphosph	hypothetical prote	zebrin II - mouse	fructose-bisphosph	aldolase A - chick	fructose-bisphosph	fructose-bisphosph	fructose 1,6-bisph	hypothetical prote	fructose-bisphosph	probable exported	major merozoite su	fructose-bisphosph	conserved domain p	hypothetical prote	<ul> <li>cytosine-specific</li> </ul>	fructose-bisphosph	hypothetical prote	fructose-bisphosph	fructose-bisphosph	fructose-bisphosph	dynein light chain
SUMMARIES	ID	ADRBA	ADHUA	ADMSA	ADRTA	151291	JC4189	.JC4188	ADHUC	T24514	153145	ADRTC	151292	S45346	ADFF	C42263	T15951	ADRTB	AF0981	A45532	S48810	D95178	C98045	AE1950	ADHUB	T46277	ADSPAC	T12416	ADCHB	T02846
	DB	-	-	-	-	~	N	~	٦	~	7	Н	7	~	-	~	~		~	~	7	~	~	~	٦	~	Н	~	н	~
	Length	363	364	364	364	42	364	363	364	365	363	363	137	364	361	361	3,66	364	179	1772	364			293	364	644	357	357	364	627
d	Query Match	100.0	0.66	97.0	97.0	95.0	77.0	69.5	68.0	61.0	60.5	59.5	58.0	57.0	55.5				48.0			46	4	46.0	4	4	4	4	45.0	44.0
	Score	100	66	97	97	95	77	69.5	68	61	•	59.5	58	in	55.5	55.5	52	20	48	48	47	46	46	46	46	46	45	45	45	44
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## ALIGNMENTS

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fructose-bisphosphate aldolase (BC 4.1.2.13) A - rabbit NyAlternate names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A C;Specias: Oryctolagus cuniculus (domestic rabbit) C;Date: 24-Apr-1984 #sequence revision 27-Nov-1985 #text change 09-Jul-2004 C;Accession: A92444; A90059; A90050; A90060; I46474; I46475; A01103 R;Tolan, D.R.; Amsden, A.B.; Purney, S.D.; Urdea, M.S.; Penhoet, B.E. A;Title: The complete nucleotide sequence for rabbit muscle aldolase A messenger RNA.

A;Accession: A92444
A;Accession: A92444
A;Molecule type: mRNA
A;Residues: 1-363 -470LA;Crossicues: 1-363 -470LA;Crossicues: T-363 -470LA;Crossicues: T-364 -1206
A;Note: initiator Met not shown
B;Lai, C:Y; Nakai, N: Chang, D.
A;Title: Amino acid sequence of rabbit muscle aldolase and the structure of the active of A;Reference number: A94244; MUID:74094688; PMID:4812352

A; Contents: annotation
A; Note: the sequence reported in this paper has been revised in references A90305 and A90
R; Nakai, N.; Chang, D.; Lai, C.Y.
A; Chang, D.; Lai, C.Y.
A; Chang, D; Lai, C.Y.
A; Chang, D; Lai, C.Y.
A; Title: Studies on the structure of rabbit muscle aldolase. Ordering of the tryptic pept A; Reference number: A90059; MUID: 75145171; PMID:1122141

Accession: A90059

A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Residues: 1-33, 'Q', 55-164 < NAK>
R,Besidues: 1-33, 'Q', 55-164 < NAK>
Biochem. J. 183, 429-444, 1979
A,Title: Extended amino acid sequences around the active-site lysine residue of class-I for the factore number: A90305; MUID:80109133; PMID:534504
A,Rolecule type: protein
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A; Map position: 16q22.2-16q22.2
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A;Reaidues: 1-33;357-354 <SAK>
Lee, K.N.; Maxwell, M.D.; Pat
Biochim. Biophys. Acta 1136, 12
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R; Izzo, P; Costanzo, P; Lupo, A; Rippa, E; Paciella, G; Salvatore, F.
Eur. J. Biochem. 174, 569-578, 1988
A; Title: Human aldolase A gene. Structural organization and tissue-specific expression B
A; Reference mumber: S01014; MUID:88271327; PMID:339172
A; Accession: S01004
A; Molecule type: DNA
A; Residues: 1-72, G', 74-195, 'A', 197-229, 'N', 231-279, 'S', 281-364 <1Z2>
A; Cross-references: GB:X12447; NID:g28613; PIDN:GA30979.1; PID:g28614
B; Freemont, P.S.; Dunbar, B.; Fothergill-Gilmore, L.A.
Biochem. J, 249, 779-788, 1988
A; Title: The complete amino acid sequence of human skeletal-muscle fructose-bisphosphate
A; Reference number: S00290; MUID:88183272; PMID:3355497
A; Residues: 2-358, 'I', 360-364 <FRE>
B; Maire, P; Gautron, S; Hakim, V; Gregori, C; Mennecier, F; Kahn, A.
J, Mol. Biol. 197, 425-438, 1987
A; Title: Characterization of three optional promoters in the 5' region of the human aldc
A; Reference number: S02338; MUID:88155643; PMID:3441006
A; Reference number: S02338; MUID:88155643; PMID:3441006
A; Reference number: S02338
                                                                                                                                   A.Accession: 146475
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated type: mRNA
A.Residues: 349-352, 7R', 354-363 < PUZ>
A.Cross-references: EMBL:V00877; NID:g1446; PIDN:CAA24246.1; PID:g833792
C.Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, a C.Superfamily: fructose-bisphosphate aldolase
C.Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; pe F;2-363/Product: fructose-bisphosphate aldolase A #status predicted <MAT>
F;146,229,363/Active site: Lys, Lys, Tyr #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P04075

R;Izzo, P.; Costanzo, N.; Lupo, A.; Rippa, E.; Borghese, A.M.; Paolella, G.; Salvatore, Bur. J. Biochem. 164, 9-13, 1987

A;Title: A new human species of aldolase A mRNA from fibroblasts.

A;Reference number: A27186; MUID:87161904; PMID:3030757
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A;Cross-references: EMBL:X06352; NID:g28594; PIDN:CAA29654.1; PID:g28595
R;Freemont, P.S.; Dunbar, B.; Fothergill, L.A.
                                                                                                         A; Cross-references: EMBL: V00876; NID: g1444; PIDN: CAA24245.1; PID: g929753
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A;Residues: 1-364 <1ZZ>
A;Residues: 1-364 <1ZZ>
A;Cross-references: GB:X05236; NID:g28596; PIDN:CAA28861.1; PID:g28597
A;Experimental source: fibroblast
R;IZZO, P.; Costanzo, P.; Lupo, A.; Rippa, E.; Paolella, G.; Salvatore, Eur. J. Biochem. 174, 569-578, 1988
A;Title: Human aldolase A gene. Structural organization and tissue-spec
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A;Status: translated from GB/EMBL/DDBJ
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A; Residues: 37-55 < PUT>
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A; Molecule type: DNA
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Arch. Biochem. Biophys. 228, 342-352, 1984
A;Title: Human skeletal-muscle aldolase: N-terminal sequence analysis of CNBr- and o-iodd
A;Reference number: A05177; MUID:84126818; PMID:6696436
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Kr&ywords: aldohyde-lysase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; per
F;2-364/Product: fructose-bisphosphate aldolase A #status experimental <MAT>
F;147,230,364/Active site: Ly9, Ly9, Tyr #status experimental
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Biochem. Biophys. Res. Commun. 131, 413.420, 1985
A;Title: Vucleotide sequence of a cDNA clone for human aldolase: a messenger RNA in the
A;Reference number: 139429; WUID:85306986; PMID:3840020
A;Accession: 139429
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A;Title: Identification of transglutaminase substrates in HT29 colon cancer cells: use A;Reference number: $23919; MUID:92353128; PMID:1353685
A;Accession: $23919
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A;Residues: 139-364 <TOL>
A;Cross-references: GB:M21190; NID:g178403; PIDN:AAA51697.1; PID:g178404
C;Comment: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found,
C;Genetics:
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A;Residues: 2-16 <LBE>
R;Gamblin, S.J.; Davies, G.J.; Grimes, J.M.; Jackson, R.M.; Littlechild, J.A.; Watson,
J. Mol. Biol. 219, 573-576, 1991
A;Title: Activity and Specificity of Human Aldolases.
A;Reference number: A43787; MJD:91278081; PMID:2056525
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
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C; Species: Musculus (house mouse)
C; Species: Musculus (house mouse)
R; Mestek, A.; Stauffer, U.; Tolan, D.R.; Ciejek-Baez, E.
R; Musclaic Acids Res. 15, 10595, 1987
A; Title: Sequence of a mouse brain aldolase A CDNA.
A; Reference number: S06323; MUID:88096598; PMID:3697100
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A; Residues: 1-364 <RES>
A; Cross-references: GB:M11560; NID:g178350; PIDN:AAA51690.1; PID:g178351
A; Colon. D.R.; Niclas, J.; Bruce, B.D.; Lebo, R.V.
Am. J. Hum. Genet. 41, 907-924, 1987
A; J.F. Hum. Genet. 41, 907-924, 1987
A; Title: Evolutionary implications of the human aldolase-A, -B, -C, and A; Reference number: 139435; MUID:88046782; PMID:3674018
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fructose-bisphosphate aldolase (EC 4.1.2.13), non-muscle-type - Pacific lamprey
NyAlternate names: non-muscle-type aldolase
Cispecies: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)
Cipate: 27-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
Cipacession: JC4189
Rizhang, R.; Yatuski, H.; Kusakabe, T.; Iwabe, N.; Miyata, T.; Imai, T.; Yoshida, M.; Hon
J. Biochem. 117, 545-551, 1995
A;Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of lam
A;Reference number: JC4188; MUID:95355304; PMID:7629020
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                                                                                                                                                                                                                                    C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle; per
F;2-364/Froduct: fructose-bisphosphate aldolase A #starus predicted <MAT>
F;147,230,364/Active site: Lys, Lys, Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Meighan-Mantha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995
A;Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and alc
A;Reference number: 151291; MUID:95286677; PMID:7768978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:Q92007; GB:S78288; NID:g999389; PIDN:AAB34479.1; PID:g999390; Superfamily: fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aldolase C - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: IS1291
                                                             A,Molecule type: DNA
A,Residues: 1-108 <RE2>
A;Cross-references: EMBL:X04261; NID:g55639; PIDN:CAA27815.1; PID:g1619605
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                          97.0%; Score 97; DB 1; Length 364; llarity 95.0%; Pred. No. 5.8e-08; Conservative 1; Mismatches 0; Indels
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                                       Status: preliminary; translated from GB/EMBL/DDBJ
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Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 95.0%;
Matches 19; Conservative
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tes 19; Conserv
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A; Residues: 1-364 <ZHA>
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   A, Accession: 156408
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C; Superfamily: 1
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A; Residues: 1-364 <JOH>
A; Residues: 1-364 <JOH>
A; Residues: 1-364 <JOH>
A; Residues: 1-364 <JOH>
A; Crose-references: UNIPROT: P05065; UNIPROT: Q63038; GB:M14420; NID:g202836; PIDN: AAA4071
B; Mukai, T., Joh, K.; Arai, Y.; Yatsuki, H.; Hori, K.
J. Biol. Chem. 261, 3347-3354, 1986
A; Title: Tissue-specific expression of rat aldolase A mRNAs: three molecular species dif A; Reference number: A25383; MUID: 86140113; PMID: 3753977
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A; Cross-references: GB:M28282; NID:9202849; PIDN:AAA40720.1; PID:9202850
A; Cross-references: GB:M28282; NID:9202849; PIDN:AAA40720.1; PID:9202850
B; JOh, K.; Arai, Y.; Mukai, T.; Hori, K.
J. Mol. Biol. 190, 401-410, 1986
A; Title: Expression of three mRNA species from a single rat aldolase A gene, differing A; Reference number: 156408; MUID:87060996; PMID:3783705
                                                                                          A;Cross-references: UNIPROT:P05064; GB:Y00516; NID:g49914; PIDN:CAA68571.1; PID:g49915
A;Experimental source: brain
R;Paodella, G.; Buono, P.; Mancini, F.P.; Izzo, P.; Salvatore, F.
Eur. J. Biochem. 156, 229-235, 1986
A;Title: Structure and expression of mouse aldolase genes. Brain-specific aldolase C am
A;Reference number: A91165; MUID:86192445; PMID:3009179
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C;Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; muscle;
F;2-364/Product: fructose-bisphosphate aldolase A #status predicted <MAT>
F;147,230,364/Active site: Lys, Lys, Tyr #status predicted
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N/Alternate_names: aldolase A; fructose-1,6-bisphosphate triosephosphate-lyase A
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A24532; A55383; I53307; I66408
R;Joh, K.; Mukai, T.; Yatsuki, H.; Hori, K.
Gene 39, 17-24, 1985
A;Title: Rat aldolase A messenger RNA: the nucleotide sequence and multiple A;Reference number: A24532; MUID:86083188; PMID:2416636
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Ristauffer, J.K.; Colbert, M.C.; Ciejek-Baez, E.
J. Biol. Chem. 265, 11773-11782, 1990
AjTitle: Nonconservative utilization of aldolase A alternative promoters.
A,Reference number: A37062; MUID:90307699; PMID:2365699
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A,Residues: 1-144, F',146-164, M',166-364 <MUK>
A,Cross-references: GB:M12919; NID:g202834; PIDN:AAA40714.1; PID:g202835
R,Tsutsumi, R.; Tsutsumi, K.
Eur. J. Biochem. 142, 161-164, 1984
                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 99-280,'C',282-355 <PAO>
A;Cross-references: GB:X03797; NID:g49916; PIDN:CAA27423.1; PID:g929677
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Best Local Similarity
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A; Accession: S06323
A; Molecule type: mRNA
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fructose-bisphosphate aldolase (EC 4.1.2.13) C - rat
N;Alternate names: aldolase C; fructose-1,6-bisphosphate triosephosphate-lyase C; fructose C; Species: Rattus norvegicus (Norway rat)
C;Baceis: Asttus norvegicus (Norway rat)
C;Bate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S00326; A38817; JN0127; I53313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-365 <WIL>
A;Cross-references: UNIPROT:P54216; EMBL:Z81115; PIDN:CAB03291.1; GSPDB:GN00021; CESP:T06
A;Experimental source: clone T05D4
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C;Date: 02-Aug-1996 #text_change 22-Jun-1999
C;Accession: I53145
R;Ahn, A.H.; Dztennis, S.; Hawkes, R.; Herrup, K.
Development 120, 2081-2090, 1994
A;Title: The cloning of zebrin Ir reveals its identity with aldolase C.
A;Reference number: I53145; MUID:95009537; PMID:7925012
                                                                                                                                                                                                                                                                                                                                                      hypothetical protein T05D4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24514
C;McMurray, A.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19902
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A,Residues: 1-56 - KBS.
A;Cross-references: GB:S72537; NID:g619372; PIDN:AAB32064.1; PID:g619373
C;Superfamily: fructose-bisphosphate aldolase
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                            Length 364;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                        Score 68; DB 1;
Pred. No. 0.003;
5; Mismatches
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68.8%; Pred. No. 0.041;
iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 3
A;Introns: 32/1; 190/3
C;Superfamily: fructose-bisphosphate aldolase
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                                                                                                                                                                                 346 SGEDGGAAAQSLYIANHAY 364
                                                                                                                                               2 SGQAGAAASESLFISNHAY 20
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                               68.0%;
63.2%;
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Best Local Similarity 68.8
Matches 11; Conservative
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                                                                                       Conservative
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                            Query Match
Best Local Similarity
Matches 12; Conserv
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zebrin II - mouse
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                                                                                                                         fructose-bisphosphate aldolase (EC 4.1.2.13), muscle-type - Pacific lamprey
N.Alternate names: muscle-type aldolase
C;Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)
C;Species: Lampetra tridentata, Entosphenus tridentatus (Pacific lamprey)
C;Date: 2.7-Sep-1955 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JC4188
R;Zhang, R:; Yatsuki, H:; Kusakabe, T:; Iwabe, N:; Miyata, T:; Imai, T:; Yoshida, M:; HC
J: Biochem: 117, 545-553, 1995
A;Title: Structures of cDNAs encoding the muscle-type and non-muscle-type isozymes of la
A;Reference number: JC4188; MUID:95355304; PMID:7629020
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A;Cross-references: GB:X07292; NID:g28600; PIDN:CAA30270.1; PID:g312137
R;Buono, P.; Mancini, F.P.; Izzo, P.; Salvatore, F.
Bur. J. Blochem. 192, 805-811, 1990
A;Title: Characterization of the transcription-initiation site and of the promoter regic
A;Reference number: S13192; MUID:91006178; PMID:2209624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-363 <ZHA>
A;Residues: 1-363 <ZHA>
A;Coss-references: DBJ:DB8620; NID:g1619827; PIDN:BAA07608.1; PID:g974732
C;Comment. This is a glycolytic enzyme that catalyzes the reversible cleavage of fructos C;Superfamily: fructose-bisphosphate aldolase
C;Superfamily: fructose-bisphosphate aldolase
C;Reywords: aldehyde-lyase; carbon-carbon lyase; muscle
F;230/Active site: Lys #status predicted
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A; Residues: 1-364 < ROT>
A; Residues: 1-364 < ROT>
A; Residues: 1-364 < ROT>
A; Residues: 1-364 < ROT>
A; Crose service cores: UNIPROT: P09972; GB: X05196; NID: g28598; PIDN: CAA28825.1; PID: g28599
B; Bbuono, P.; Paolella, G.; Mancini, F.P.; Izzo, P.; Salvatore, F.
Nucleic Acids Res. 16, 4733, 1988
A; Title: The complete nucleotide sequence of the gene coding for the human aldolase C.
A; Reference number: S00863; MUID: 88247784; PMID: 3267224
A; Reference number: S00863
A; Status: Leanslation not shown
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A;Introns: 38/1; 108/3; 127/1; 180/3; 267/1; 333/3
C;Superfamily: fructose-bisphosphate aldolase
C;Keywords: aldehyde-lyase; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; E;2-364/Product: fructose-bisphosphate aldolase C #status predicted <MAT>
F;2-364/Product: fructose-bisphosphate aldolase C #status predicted
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A; Residues: 1-310,'V',312-364 <BUO2>
A; Cross-references: GB:X07292; GB:M84921; NID:g28600; PIDN:CAA30270.1; PID:g312137
C; Genetics:
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A;Cross-references: GDB:119670; OMIM:103870
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345 PTG-TGAAAGESLFVANHAY 363
PAGSSGSAASESLFIANHNY 364
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345
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Gaps

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Gaps

Molecule type: protein Residues: 2-21 <KU2>

Molecule type: mRNA Residues: 1-363 <KUK>

A; Accession: S00326 A; Molecule type: mR A; Residues: 1-363 <

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Atsuchi, Y.; Yamana, K.; Yatsuki, H.; Hori, K.; Ueda, S.; Shiokawa, K. Acta 1218, 153-157, 1994
Rochim. Blophys. Acta 1218, 153-157, 1994
Fittle: Cloning of a brain-type aldolase cDM and changes in its mRNA level during ooger; Reference number: 151247; MUID:94289472; PMID:8018714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A;Residues: 2-110, K',112-200, R',202-250, A',252-361 < MAL>
A;Residues: 2-110, K',112-200, C.
B;Brenner-Holzach, O.; Zumsteg, C.
Arch. Biochem. Blophys. 214, 89-101, 1982
A;Title: Fructose 1,6-bisphosphate aldolase of Drosophila melanogaster: comparative seque
A;Reference number: A28855; MUID:82205133; PMID:6805442
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C;Kaywords: aldehyde-lyase, carbon-carbon lyase; gluconeogenesis; glycolysis; pentose phr
F?2-361/Product: fructose-bisphosphate aldolase #status experimental <MAT>
F;147,230,361/Active site: Lys, Lys, Tyr #status predicted
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; Cross-references: UNIPROT: Q91384; GB:S73606; NID: g688323; PIDN: AAB31152.1; PID: g688324
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A;Note: sequence extracted from NCBI backbone (NCBIN:76664, NCBIP:87828)
R;Malek, A.A.; Hy, M.; Honegger, A.; Rose, K.; Brenner-Holzach, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fructose-bisphosphate aldolase (EC 4.1.2.13) - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 30-Sep-1991 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004 C;Accession: B42027; S06439; Ā28855; S22186 R;Kim, J; Yim, J.J; Wang, S.; Dorsett, D. Mol. Cell. Biol. 12, 773-783, 1992
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A;Title: Fructose-1,6-bisphosphate aldolase from Drosophila melanogaster: primary
A;Reference number: 806439; MUID:89024658; PMID:3140728
A;Accession: 806439
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   Alternate names: aldolase C
Species: Xenopus laevis (African clawed frog)
|Date: 16-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
|Accession: 845346; IS1247
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;Residues: 170-179,'QS',182-200,'R',202-224,'Q',226-250,'A',252-272 <BRE>;Note: peptides were ordered by homology with the rabbit sequence
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C;Keywords: aldehyde-lyase; carbon-carbon lyase
F;2-364/Product: fructose-bisphosphate aldolase C #status predicted
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Pred. No. 0.18;
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A; Note: translation of initiator Met is not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.0%; Score 57; DB ilarity 47.4%; Pred. No. 0.18 Conservative 5; Mismatches
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les 9; Conserv
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Best Local
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A;Residues: 1-336,'LAA',340-363 <MUK>
A;Residues: 1-336,'LAA',340-363 <MUK>
A;Croser-references: GB1M63656, NID:92202841; PIDN:AAA40717.1; PID:9202842
R;Cxdla, H; Vibert, M; Lamas, B.; Maire, P.; Schweighoffer, F.; Kahn, A.
Bur. J. Biochem. 163, 513-518, 1987
Bur. J. Biochem. 163, 513-518, 1987
A;Title: Molecular cloning and expression of rat aldolase C messenger RNA during develop
A;Reference number: IS3313; MUID:87161851; PMID:3830170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 38/1; 108/3; 127/1; 180/3; 208/3; 267/1; 333/3
C; Superfamily: fructose-bisphosphate aldolase
C; Keywords: aldehyde-lysse; brain; carbon-carbon lyase; gluconeogenesis; glycolysis; per
F;2-363/Product: fructose-bisphosphate aldolase C #status experimental <MAT>
F;147,230,363/Active site: Lys, Lys, Tyr #status predicted
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A;Molecule type: mRNA
A;Residues: 1-137 <MEI>
A;Residues: 1-137 <MEI>
A;Cross-references: UNIPROT:P53449; GB:S78291; NID:g999391; PIDN:AAB34480.1; PID:g999392
C;Superfamily: fructose-bisphosphate aldolase
R;Kukita, A.; Mukai, T.; Miyata, T.; Hori, K.
Eur. J. Biochem. 171, 471-478, 1988
A;Title: The structure of brain-specific rat aldolase C mRNA and the evolution of aldola A;Reference number: S00326; MUID:88151941; PMID:2831050
                                                                                                                                                                                                                                                                                                                                                                                                      RiMukai, T.; Yatsuki, H.; Masuko, S.; Arai, Y.; Joh, K.; Hori, K.
Biochem. Biophys. Res. Commun. 174, 1035-1042, 1991
A; Title: The structure of the brain-specific rat aldolase C gene and its regional expres A; Reference number: JN0127; MUID:91128359; PMID:1993044
A; Accession: JN0127
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A;Accession: A38817
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: 151292
T;Meighan-Mantha, R.L.; Tolan, D.R.
J. Cell. Biochem. 57, 423-431, 1995
A;Title: Noncoordinate changes in the steady-state mRNA expressed from aldolase A and A;Reference number: 151291; MUID:95286677; PMID:7768978
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S45346
fructose-bisphosphate aldolase (EC 4.1.2.13) C, brain-type - African clawed frog
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A;Cross-references: EMBL:X05277; NID:g55632; PIDN:CAA28889.1; PID:g55633
C;Genetics:
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Pred. No. 0.071;
4; Mismatches 2;
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Molecule type: mRNA
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52.6%; Pred. No. 0.043;
iive 4; Mismatches
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346 SGDGGAAA-QSLYVANHAY 363

SGQAGAAASESLFISNHAY 20

12; Conservative

Matches

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Local Similarity

Accession: I53313

59.5%;

SGDDSGAAGQSLYVANHAY 137

SGQAGAAASESLFISNHAY 20

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10; Conservative

Local Similarity

Query Match Matches

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Wed Jun 22 05:53:34 2005
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344 AGSAG-AGSGSLFVANHAY 361

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Fructose 1,6-bisphosphate aldolase - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 04-Mar.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: C42263
R;Shaw-Lee, R.; Lissemore, J.L.; Sullivan, D.T.; Tolan, D.R.
J. Biol. Chem. 267, 3395-3367, 1992
A;Title: Alternative splicing of fructose 1,6-bisphosphate aldolase transcripts in Drosc
A;Reference number: A42263; MUID:92156139; PMID:174044
A;Reference number: A42263; MUID:92156139; PMID:174044
A;Resatus: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Resatus : 261 < SABA
A;Cross-reference extracted from NCBI backbone (NCBIN:82659, NCBIP:93286)
C;Genteics:
A;Gene: FlyBase:Ald
A;Cross-references: FlyBase:FBgn0000064
C;Superfamily: fructose-bisphosphate aldolase
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Search completed: June 20, 2005, 10:14:37 Job time : 25 secs

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Q9bwd9 homo sapien
Q6fh76 homo sapien
Q6fh76 homo sapien
Q6fh76 homo sapien
D05065 rattus norv
Q6nyO0 mus musculu
Q92007 gallus gall
Q8wnt7 macaca fasc
Q76bg8 ambystoma m
Q9crg1 mus muscu
Q9crg1 mus muscu
Q6g164 xenopus tro
Q6g164 xenopus tro
Q6g164 xenopus tro
Q6g175 xenopus lae
Q12975 xenopus lae
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Q766f4 lepisosteus
P53446 lampetra ja
Q76bi2 protopterus
Q81h72 brachydanio
Q8047 brachydanio
Q76bbl callorhinch
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Putney S.D., Herlihy W.C., Schimmel P.R.; "A new troponin T and cDNA clones for 13 different muscle proteins,

found by shotgun sequencing."; Nature 302:718-721(1983).

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                                                                                                                                                                                                                       Hartman F.C., Brown J.P.;
"Affinity labeling of a previously undetected essential lysyl residue
in class I fructose bisphosphate aldolase.";
J. Biol. Chem. 251:3057-3062(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure of a fructose-1,6-bis(phosphate) aldolase liganded to its natural substrate in a cleavage-defective mutant at 2.3 A."; Biochemistry 38:12655-12664(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.46 ANGSTROMS), AND MUTAGENESIS OF GLU-187;
                                                                                        MEDLINE=74163196; PubMed=4857186;
Hartman F.C., Welch M.H.;
Tidentification of the histidyl residue of rabbit muscle aldolase alkylated by N-bromoacetylethanolamine phosphate.";
Biochem. Biophys. Res. Commun. 57:85-92(1974).
                                                                                                                                                                                                                                                                                                                  MEDLINE=80046697; PubMed=499203;
Patthy L., Varadi A., Thesz J., Kovacs K.;
"Identification of the C-1-phosphate-binding arginine residue of
"abbit-muscle aldolase. Teolation of 1,2-cyclohexanedione-labeled
peptide by chemisorption chromatography.";
Eur. J. Biochem. 99:309-313(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 2-344 IN COMPLEX WITH SUBSTRATE, AND MUTAGENESIS OF GLU-34; ARG-42; LYS-146 AND ARG-303 PubMed=10504235; DOI=10.1021/bi9828371;
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97143309; PubMed=8989320;
Blom N., Sygusch J.;
"Product binding and role of the C-terminal region in class I D-
fructose 1,6-bisphosphate aldolase.";
Nat. Struct. Biol. 4:36-39(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi K.H., Mazurkie A.S., Morris A.J., Utheza D., Tolan D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATABASE: NAME-Worthington enzyme manual; WWW="http://www.worthington-biochem.com/ALD/".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLU-189 AND LYS-229.
PubMed=11779856; DOI=10.1074/jbc.M107600200;
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MEDLINE=76190154; PubMed=5453;
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                                                                               ACTIVE SITE.
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L'é-phiosphate group of the substrate, alkylation inactivates the enzyme.
C-6-phosphate group of the substrate.
Deamidated asparagine (in beta chain).
E-A: Reduces activity 14-fold.
R-A: Reduces activity 14-fold.
R-A: Reduces activity 14-fold.
E-A: Reduces activity 20-fold.
E-A: Reduces activity over 100-fold.
E-A: Reduces activity over 100-fold.
E-A: Reduces activity over 100-fold.
E-A: Reduces activity 400-fold.
E-A: Reduces activity 20-fold.
E-A: Reduces activity 50-fold.
E-A: Reduces activity 60-fold.
                                                                                                                                                                                                                                               essential for the subsequent hydrolysis of the dihydroxyacetone Schiff base. Necessary for preference for fructose 1,6-bisphosphate over fructose 1
                                                                                                                                                                                                                                       Alkylation inactivates the enzyme;
                                                                                                                                                                                               Alkylation inactivates the enzyme
                                                                                                                                                                          Essential for substrate cleavage.
Essential for substrate cleavage.
                                                                                                                                          3D-structure, Direct protein sequencing, Glycolysis, Lyase, Multigene family, Schiff base.
INIT_MET 0 0 Essential for substrate cleava SITE 72 72
                                                                                                                                                                                                         Proton acceptor.
Schiff-base intermediate with
dihydroxyacetone-P.
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PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
EMBL; V00876; CAA24245.1; -...
EMBL; V00877; CAA24246.1; -...
PIR; A9244; ADRBA.
PDB; LADO; X-ray; A/B/C/D=1-363.
PDB; LEWE; X-ray; A/B/C/D=1-363.
PDB; LEWE; X-ray; A/B/C/D=1-363.
PDB; LEWE; X-ray; A/B/C/D=1-363.
PDB; LEXE; X-ray; A/B/C/D=1-363.
PDB; LASE; X-ray; A/B/C/D=1-363.
PDB; LASE; X-ray; A/B/C/D=1-363.
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INTERPO; IPROUGNIT; A/B/C/D=1-363.
INTERPO; IPROUGNIT; A/B/C/D=1-363.
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Glycolysis; Lyase.
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buerlow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerlow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Altschul S.F., Zeeberg B. Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garden R.D., Wullahy S.J.,
Rahey J., Helton E., Ketteman M., Madan A., Young A.C., Sheckonko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Sheckonko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Noriski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
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Jones S.J., Marra M.A.,
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Submitted (CTT-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
                                                                                                                                    Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Vertebrata; Buteleostomi, Bukaryota; Butharia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                         100.0%; Score 100; DB 1; Length 363; 100.0%; Pred. No. 1e-07; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ALDOA protein (Similar to aldolase A, fructose-bisphosphate)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
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ProDom; PD001128; Aldolase_1; 1.
PROSITE; PS00158; ALDOLASE_CLASS_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                               260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                    344 PSGQAGAAASESLFISNHAY 363
                                                                                                                                                                                       1 PSGQAGAAASESLFISNHAY 20
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                                                                                                                                                                                                                                                                                                                                                                                                Q9BWD9; Q96BL5;
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2004 (TrEMBLrel. 26,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
                                                                                                                                  20; Conservative
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                                                                                                        Local Similarity
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Matches
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TISSUB-Cervix, Eye, Lung, Testis, and Uterus;

X MEDLINE-2238827; Pubmed-12477932; DOI-LO.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Earmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Glunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1986 (Rel. 03, Created)
01-APR-1988 (Rel. 07, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
[Lung cancer antigen NY-LU-1).
                                                                                                                                                      Gaps
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"Nucleotide sequence of a cDNA clone for human aldolase: a messenger
RNA in the liver.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-88271327; PubMed=3391172;
Izzo P., Costanzo P., Lupo A., Rippa E., Faolella G., Salvatore F.;
"Human aldolase A gene. Structural organization and tissue-specific
expression by multiple promoters and alternate mRNA processing.";
Eur. J. Biochem. 174:569-578(1988).
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Mukai T., Arai Y., Yatsuki H., Joh K., Hori K.;
"An additional promoter functions in the human aldolase A gene, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Izzo P., Costanzo P., Lupo A., Rippa E., Borghese A.M., Paolella Salvatore {\bf F}.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A new human species of aldolase A mRNA from fibroblasts.";
                                                                     99.0%; Score 99; DB 2; Length 260; 95.0%; Pred. No. 1.1e-07; ive 1; Mismatches 0; Indels
27898 MW; 861B9CDE0F1F2784 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 AA.
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MEDLINE=85306986; PubMed=3840020;
                                                                                                                                                                                                                                                                             241 PSGQAGAAASESLFVSNHAY 260
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MEDLINE-87161904; PubMed=3030757;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=ALDOA; Synonyms=ALDA;
                                                                                                                  Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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260 AA;
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phosphate + D-glyceraldehyde 3-phosphate.
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    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marza M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                               Freemont P.S., Dunbar B., Fothergill L.A.; "Human skelterla-muscle aldolase: N-terminal sequence analysis of CNBrand o-iodosobenzoic acid-lavage fragments."; Arch. Biochem. Biophys. 228:342-352(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-107 FROM N.A.
MEDLINE-88155643; PubMed-3441006;
Maire P., Gautron S., Hakim V., Gregori C., Mennecier F., Kahn A.;
"Characterization of three optional promoters in the 5' region of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE=90242948; Pubmed=2335208; DOI=10.1016/0014-5793(90)80211-Z;
Gamblin S.J., Cooper B., Millar J.R., Davies G.J., Littlechild J.A.,
                                                                                                                                                                                                                                    MEDLINE-88183272; PubMed=3355497;
Freemont P.S., Dunbar B., Fothergill-Gilmore L.A.;
"The complete amino acid sequence of human skeletal-muscle fructose-
bisphosphare aldolase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=99156067; bubMed=10048322;
Dalby A. Dauter Z., Littlechild J.A.;
"Crystal structure of human muscle aldolase complexed with fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT HEMOLYTIC ANEMIA GLY-128.

WEDLINES-30135340. PubMed=2229018.

Takasaki Y., Takahashi I., Mukai T., Hori K.;

"Human aldolase A of a hemolytic anemia patient with Asp-128-->Gly
substitution: characteristics of an enzyme generated in B. coli
transfected with the expression plasmid pHAAD128G.";
J. Biochem. 108:153-157(1990).
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MEDLINE=88068641; PubMed=2825199;
Kishi H., Mukai T., Hizono A., Fujii H., Miwa S., Hori K.;
Kishi Huan aldolase A deficiency associated with a hemolytic anemia:
thermolabile aldolase due to a single base mutation.";
Proc. Natl. Acad. Sci. U.S.A. 84:8623-8627(1987).
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MEDIJUBE-88046782; PubMed=3674018;
Tolan D.R., Niclas T. Wiche B.D., Lebo R.V.;
"Evolutionary implications of the human aldolase-A, -B, -C, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gamblin S.J., Davies G.J., Grimes J.M., Jackson R.M., Littlechild J.A., Wateson H.C., "Activity and specificity of human aldolases."; Activity Biol. 219:573-576 (1991).
                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1,6-bisphosphate: mechanistic implications.";
Protein Sci. 8:291-297(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE-91278081; Pubmed=2056525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pseudogene chromosome locations.";
Am. J. Hum. Genet. 41:907-924(1987).
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-62 AND 147-357.
MEDLINE=84126818; PubMed=6696436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human aldolase A gene.";
J. Mol. Biol. 197:425-438(1987).
[9]
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                                                                                                                                                 mouse cDNA sequences."
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  CCERTIFY SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVI
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Pfam; PF00274; Glycolytic; 1.
Problem; PD001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE CLASS I; 1.
3D-structure; Direct protein sequencing; Disease mutation; Glycolysis; Lyase; Multigene family; Schiff base.
                                                             [MIM.103850].
MISCELLANEOUS: In vertebrates, three forms of this ubiquitous MISCELLANEOUS: In vertebrates, three forms of this ubiquitous glycolytic enzyme are found, aldolase A in muscle, aldolase B in liver and aldolase C in brain.
SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C-1-phosphate group of the substrate.
C-1-phosphate group of the substrate.
D -> G (in hemolytic anemia;
thermolabile).
/FIId=VAR_000550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 103850; -.
GO; 600004332; F.fructose-bisphosphate aldolase activity; TAS.
GO; GO:00006000; P.fructose metabolism; TAS.
GO; GO:0006096; P.glycolysis; TAS.
GO; GO:0006941; P:striated muscle contraction; TAS.
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PATHWAY: Glycolysis; sixth step.
SUBUNIT: Homotetramer.
DISEASE: Defects in ALDOA are a cause of hemolytic anemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proton acceptor (By similarity). Schiff-base intermediate with dihydroxyacetone-P.
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BC010560; AAH10660.1;
BC012860; AAH12880.1;
BC01284; AAH13614.1;
BC012888; AAH1388.1;
BC015888; AAH1588.1;
BC016800; AAH16800.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aarhus/Ghent-2DPAGE; 1302; NEPHGE.
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X05236; CAA28861.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M21190; AAA51697.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  M11560; AAAS1690.1; -.
X06352; CAA29654.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDB; 1ALD; X-ray; @=1-363.
PDB; 2ALD; X-ray; A=1-363.
PDB; 4ALD; X-ray; @=1-363.
SWISS-2DPAGE; P04075; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Genew; HGNC:414; ALDOA.
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Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
Korn B., Zuo D., Hu Y., Laber J.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
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05-JUL-2004 (Rel. 44, Last amotation update)
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
(Aldolase 1)
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%; Score 99; DB 2; Length 364; 95.0%; Pred. No. 1.5e-07; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 AA; 39448 MW; 0B7DD9DDA4897BEB CRC64;
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"Sequence of a mouse brain aldolase A cDNA.";
Nucleic Acids Res. 15:10595-10595(1987).
                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00274; Glycolytic; 1.—
ProDom; PD001128; Aldolase_I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 AA
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                                                    344 PSGQAGAAASESLFVSNHAY 363
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01-AUG-1988 (Rel. 08, Last seq
05-JUL-2004 (Rel. 44, Last ann
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STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                                                                                                                                                                                           ALDOA protein (Fragment).
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                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                       Name=ALDOA;
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Astrausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jozdan H., Moore T., Max. S.I., Wang J., Heisle F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Romentein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Basas S.B., McKernan R.J., Mallek J.A., Gunzarne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones Chua A., Schein J.E., Jones C., Shevetha A., Schein J.E., Jones C., Shevetha A., Schein J.E., 
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-i- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stauffer J.K., Colbert M.C., Ciejek-Baez E.;
"Nonconservative utilization of aldolase A alternative promoters.";
J. Biol. Chem. 265:11773-11782(1990).
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MEDLINE=8612945; PubMed=3009179;

Paolalla G., Buono P., Mancini P., Izzo P., Salvatore F.;

Paolalla G., Buono P., Mancini P., Izzo P., Salvatore F.;

"Structure and expression of mouse aldolase genes. Brain-specific aldolase C amino acid sequence is closely related to aldolase A.";

Eur. J. Blochem. 156:229-2251(1986).

-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.

-|- PATHWAY: Glycolysis; sixth step.
-|- SUBUNIT: Homotetramer.
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GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Pfam; PF00274; Glycolytic; 1.
Probom; PD001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE CLASS I; 1.
Glycolysis; Lyase; Multigene family; Schiff base.
INIT_MET
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EMBL; BC043026; AAH43026.1; -.
EMBL; BC050896; AAH50896.1; -.
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SWISS-2DPAGE; P05064; MOUSE.
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**REDIAINE=87060965; PubMed=37837055;

**MEDIAINE=87060965; PubMed=37837055;

**Joh K., Arai Y., Mukai T., Hori K.;

**Joh K., Arai Y., Mukai T., Hori K.;

**Joh K., Arai Y., Mukai T., Hori K.;

**Joh K., Arai Y., Mukai T., Hori K.;

**Joh K., Arai Y., Mukai T., Hori K.;

**Joh K., Arai Y., Mukai T., Hori K.;

**Joh K., Arai Y., Mukai T., Hori Coding regions.";

**John M. Biol. 190:401-410(1986).

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13.AUG-1987 (Rel. 05, Last sequence update)
05.JUL-2004 (Rel. 44, Last annotation update)
Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase)
                                                                                                                                                                                                                                                                                               Gaps
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Mukai T., Joh K., Arai Y., Yatsuki H., Hori K.;
"Tissue-specific expression of rat aldolase A mRNAs. Three molecular species differing only in the 5'-terminal sequences.";
J. Biol. Chem. 261:3347-3354(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                              C-1-phosphate group of the substrate.
C-1-phosphate group of the substrate.
C-2 in Ref. 4)
C-2027089F284BF74 CRC64;
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                                                                                                                                                                                    Score 97; DB 1; Length soc. Pred. No. 3.2e-07; Or Indels
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EMBL; M14420; AAA40715.1; -.
EMBL; X04261; CAA27815.1; -.
EMBL; X04262; CAA27815.1; JOINED.
EMBL; X04263; CAA27815.1; JOINED.
EMBL; X04264; CAA27815.1; JOINED.
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146 146 C-
280 280 S
363 AA; 39224 MW;
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                                                                                                                                                                                                                                                            Local Similarity
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                                  BINDING
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TISSUE-Hematopoletic Stem Cell, and Osteoblast;

X Strausberg KL., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg K.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.F.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.H., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Scheen E.D., Dickson M.C.,

Rayminki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              dihydroxyacetone-P.
Necessary for preference for fructose
1,6-bisphosphate over fructose 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        substrate
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                                                                                                                                                                                                                                                                                                                                                 Proton acceptor (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                        Schiff-base intermediate with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphate.
C-1-phosphate group of the su
C-1-phosphate group of the su
F -> S (in Ref. 2).
M -> V (in Ref. 2).
4; 48A0468B9E3B9DB8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEGUENCE FROM N.A.
STRAIN=CS7BL/6NCr; TISSUE=Hematopoietic Stem Cell;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                               RGD; 2089; Aldoa.
InterPro; IRR000741; Aldolase_I.
Profam; PF00274; Glycolytic; 1.
Profam; PD00118; Aldolase_I; 1.
PROSITE; PS00158; ALDOLASE_CLASS I; 1.
PROSITE; PS00158; ALDOLASE_CLASS I; 1.
ROYALYSIS; Lyase; Multigene family; Schiff base.
INIT MET
ACT_SITE 187 187 Proton acceptor (By a ACT_SITE 229 229 Schiff-base intermediance.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 97; DB 1; L
Pred. No. 3.2e-07;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344 PSGQSGAAASESLFISNHAY 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PSGOAGAAASESLFISNHAY 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39220 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.0%;
PIR; A24532; ADRTA.
HSSP; P00883; 1ADO.
Rat-heart-2DPAGE; P05065; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 27, (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aldolase 1, A isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
146 1
144 1
164 1
363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
Les 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Aldoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING
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Query Match
Best Local Similarity 95.0°
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8296;
                                                                                                                                                                                                                                                                                                         01-MAR-2002
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                                                                                                                                                                                                                    RESULT 9
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                                                                                  Strausberg R.; Submitted (FBB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meighan-Mantha R.L., Tolan D.R.;
"Noncoordinate changes in the steady-state mRNA expressed from aldolase A and aldolase C genes during differentiation of chicken moohlasts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S78288; AAB34479.1; ...
EMBL; L25374; AAA9864.1; -.
EMBL; L25373; AAA48588.1; -.
EMBL; L25373; AAA48588.1; -.
HSSP; P00883; GALD.
GO; GO:000433; F:fructose-bisphosphate aldolase activity; IEA.
Pfam; PF00274; Glycolytic; 1.
                                                                                                                                                                                                                                                                        GO: GO:000433; F:fructose-bisphosphate aldolase activity; IDA. InterPro; IPR000741; Aldolase I. Pfam; PF00274; Glycolytic; 1. Propom; PD001128; Aldolase I; 1. Propom; PD001128; Aldolase I; 1. PROSITE; PS00158; ALDOLASE_CLASS_I; 1. Glycolysis; Lyase. SEQUENCE 364 AA; 39312 MW; 5BD82BBE3E6D738A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.0%; Score 97; DB 2; Length 364; 95.0%; Pred. No. 3.2e-07; ive 1; Mismatches 0; Indels
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tolan D.R.;
to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meighan-Mantha R.L., Tolan D.R.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 AA; 4384 MW; 7E0E34B8C695DC4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Lat sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Aldolase C (Aldolase A) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=95286677; PubMed=7768978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biochem. 57:423-431(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 PSGQSGAAASESLFISNHAY 364
                                            SEQUENCE FROM N.A. STRAIN=C3H/He; TISSUE=Osteoblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PSGQAGAAASESLFISNHAY 20
                                                                                                                                                                                                             EMBL; BC066801; AAH66801.1; -. EMBL; BC066218; AAH66218.1; -. HSSP; P00883; 1ADO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 95.0
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=aldolase C;
Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meighan-Mantha R.L.,
Submitted (FEB-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myoblasts.
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kikugawa K., Katoh K., Kuraku S., Sakurai H., Ishida O., Iwabe N.,
Miyata T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Ambystoma mexicanum (Axolotl).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae;
                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TTEMBLrel. 20, Last sequence update)
01-MAR-2004 (TEMBLrel. 26, Last annotation update)
8ructose-1,6-bisphosphate aldolase A.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, PO4075; ZALD.
GO, GO:0004332, F:fructose-bisphosphate aldolase activity; IEA.
GO: GO:0006096; P:glycolysis; IEA.
Pfam; PF00274; Glycolytic; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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           Score 95; DB 2; Length 42;
Pred. No. 7.1e-08;
                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycolysis; Lyase.
SEQUENCE 704 AA; 74686 MW; 02D9A004C37DFF39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 94.0%; Score 94; DB 2; Local Similarity 90.0%; Pred. No. 2e-06; nes 18; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom, PD001128; Aldolase 1; 1.
PROSITE; PS00158; ALDOLASE_CLASS_1; UNKNOWN_1.
331 AA.
                                                                                                                                                                                                                                                            704 AA
                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 20, Created)
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                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       685 PSGHAGAAASESLFVSNHAY 704
                                                                                                   1 PSGOAGAASESLFISNHAY 20
                                                                                                                                 23 PSGHAGAAASESLFISNHAY 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PSGQAGAAASESLFISNHAY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB066558; BAB84033.1; -. HSSP; P04075; 2ALD.
                                                                                                                                                                                                                                                            PRELIMINARY;
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and subtraction of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=2049314; PUMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>임</u>
           BMC Biol. 2:3-3(2004).
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Testis; MEDLINE=99279273; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933417120 product:FRUCTOSE-BISPHOSPHATE ALDOLASE A (4.1.2.13) (MUSCLE-TYPE ALDOLASE) homolog (Mus musculus adult male
testis cDNA, RIKEN full-length enriched library, clone:4921524E03
product:FRUCTOSE-BISPHOSPHATE ALDOLASE A (EC 4.1.2.13) (MUSCLE-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                   EMBL; ABIJ1374; BAD17888.1; -.
HSSP; P04075; LALD.
GO; GO:00043132; F:fructose-bisphosphate aldolase activity; IEA.
GO; GO:000696; F:gructose-bisphosphate aldolase activity; IEA.
InterPro; IPR000741; Aldolase_I.
Pfam; PF00274; Giycolytic; 1.
ProDom; PD001128; Aldolase_I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
                                                                                                                                                                                                                     89.0%; Score 89; DB 2; Length 331;
85.0%; Pred. No. 5.8e-06;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                              331 AA; 36170 MW; B7374F829DE6C591 CRC64;
                                                                                                                                                                                                                                                                                                                                                           364 AA
                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                     312 PSAQAGAAAGESLFVSNHAY 331
                                                                                                                                                                                                                                                                        1 PSGQAGAAASESLFISNHAY 20
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STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Aldoa; Synonyms=Aldo1;
                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALDOLASE) homolog).
                                                                                                                                                                                                                                     Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
 genes.";
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                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                   RESULT 11
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prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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Adachi J., Aizawa K., Akahira S., Akimura T., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A. Hayeleu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kosukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
-! SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase family.
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05-JUL-2004 (TERMELE: 17, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:493425111 product:fructose-bisphosphate aldolase (EC
4.1.2.13) A homolog (Mus musculus adult male testis cDNA, RIKEN full-
length enriched library, clone:1700027120 product:fructose-
bisphosphate aldolase (EC 4.1.2.13) A homolog).
Name=493342511R1k;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmania; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                                                                                                                                                                     STRAIN=C57BL/61; TISSUB=Testis; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumanda T., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matuminoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rike integrated sequence analysis (RISA) system-384-format genencing pipeline with 384 multicapillary sequencer.";
cap-trapper-selected cDNAs to
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EMBL; AK014956; BAB29638.1; -.

EMBL; AK014956; BAB29638.1; -.

EMBL; AK014956; BAB29638.1; -.

EMBL; AK014956; BAB29638.1; -.

GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.

GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IDA.

FROM: PF00074; Glycolytic; I.

PROSTIS: PRO01128; Aldolase I; I.

PROSTIS: PS001158; ALDOLASE_CLASS_I; I.
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85.0%; Pred. No. 9.4e-06;
ive 1; Mismatches 2; Indels
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SEQUENCE 364 AA;
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PS00158; ALDOLASE_CLASS_I; 1.

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Arakawa T., Azaminci B., Rukuda S., Fukunishi Y., Furuno M., Arakawa T., Bono H., Carninci B., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., Hanagaki T., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., M. Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakio R., Shinagawa A., Saha K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tajima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramateu M., Hayashizaki Y.,
                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Testis;
STRAIN=C57BL/6J; TISSUB=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i - CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 3-phosphate.
                                         STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CSTBL/GJ TISSUE=Testis;
STRAIN=CSTBL/GJ TISSUE=Testis;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Komno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Sumamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Nuramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA GO; GO:0006096; P:glycolysis; IEA. InterPro; IPR00741; Aldolase_I. Ffam; PF00274; Glycolytic; I.
                                                                                                                [2]
SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=21085660; Pubmed=11217851; DOI=10.1038/35055500;
                                                                     Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
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                             SEQUENCE FROM N.A.
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 NCBI_TaxID=10090;
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Alausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antechno L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
A Brownstein M.J., Widdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IPR000741; Aldolase_I.
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84.2%; Pred. No. 2.9e-05;
live 2; Mismatches 1; Indels
                                                                                         Query Match 88.0%; Score 88; DB 2; Length 364; Best Local Similarity 85.0%; Pred. No. 9.4e-06; Matches 17; Conservative 2; Mismatches 1; Indels
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Glycolysis; Lyase.
SEQUENCE 364 AA; 39370 MW; 0360CD12B8509A0D CRC64;
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roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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ProDom; PD001128; Aldolase_I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                        345 PSNESGAAASESLFISNHAY 364
                                                                                                                                                                                                                              1 PSGQAGAAASESLFISNHAY 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aldoa-prov protein.
Name=aldoa-prov;
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Matches 16; Conserv
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SEQUENCE 364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
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Q6GL64
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RESULT 14

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MEDILINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

XI MEDILINE-2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

XI Alausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Alachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Alachul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A piatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A piatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A piatchenko L., Judin T.B., Toehlywiki S., Carninci P., Prange C.,

A promstein M.J., Ugdin T.B., Toehlywiki S., Carninci P., Prange C.,

A promstein M.J., McEwan R.J., McEwan R.D., Mullahy S.J.,

A piatched S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A piatched S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A pilaton D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

A hiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Raheseley R.W., Touchman J.W., Green B.D., Dickson M.C.,

A proper R.W., Malaka D., Schmutz J., Myers R.M., Butterfield Y.S.,

A proper R.M., Malan M., Salaska U., Smailus D.E., Schnerch A., Schein J.E.,

A proper R.M., Malan A., Salaska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone phosphate + D-glyceraldehyde 1-phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98087400; Pubmed=9427528; DOI=10.1016/S0167-4781(97)00086-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Hikasa H., Hori K., Shiokawa K.;
"Structure of muscle-type (type-A) aldolase cDNA and its regulated
expression in occytes, embryos and adult tissue of Xenopus laevis.";
Biochim. Biophys. Acta 1354:189-203(1997).
                                                                                                                       Aldolase (MGC53030 protein).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoldea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22341132; Pubmed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P00883; 1ADC.
GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
GO; GO:0006096; P:glycolysis; IEA.
InterPro; IRR00741; Aldolase I.
Probom, PP001128; Aldolase I; 1.
PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
Glycolysis; Lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                        01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB002267; BAA19524.1; -. EMBL; BC046673; AAH46673.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.
                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yatsuki H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       initiative.
WHEN THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carnhon P.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carnhon P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rapask S.A., McKernan N.J., Mackernan R.J., Marke J.J., Gunsarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.W., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
phosphate + D-glyceraldehyde 3-phosphate.
-!- SIMILARITY: Belongs to the class I fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rāttus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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80.0%; Pred. No. 6.1e-05;
live 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Testis;
PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 AA.
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Local Similarity 80.0%; Pred. No. ...
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ProDom; PD001128; Aldolase 1; 1.
PROSITE; PS00158; ALDOLASE_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                   Created)
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SEQUENCE 364 AA; 39492 MW; B7
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012975
ID 012975
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Matches

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SQ SEQUENCE 364 AA; 39386 MW; 2F2A5142A4BB3986 CRC64;

0; Gaps Query Match 83.0%; Score 83; DB 2; Length 364; Best Local Similarity 84.2%; Pred. No. 6.1e-05; Matches 16; Conservative 1; Mismatches 2; Indels

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Search completed: June 20, 2005, 10:13:44 Job time : 115.5 secs

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OM protein - protein search, using sw model

June 20, 2005, 09:48:14; Search time 119 Seconds (without alignments) 65.002 Million cell updates/sec Run on:

US-10-717-243-57

100 1 PSGQAGAAASESLFISNHAY 20 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003bs:* geneseqp2003bs:* A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:* 4. 7. 8. 8.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Aar37301 Rabbit Mu		Aay07116 Lung canc	-	_	Adj68731 Human hea	Ade77178 Human pro	Adi02918 Human fru	Adq76754 Human fru	Abm81754 Tumour-as	Adb79827 Rat aldol	Aab44017 Human can	Abp65148 Hypoxia-r		Adl12661 Human ste	Adn23270 Bacterial	Abb66969 Drosophil	Adn23082 Bacterial	Abo60233 Human gen	Abr83671 Human bK1	_	Ado85827 Different	Adr12606 Gene vacc	Abb63399 Drosophil	Adn63558 HLA bindi
ID	AAR37301	ABP42706	AAY07116	AAY06992	ADF76857	ADJ68731	ADE77178	ADI02918	ADQ76754	ABM81754	ADB79827	AAB44017	ABP65148	ADJ68292	ADL12661	ADN23270	ABB66969	ADN23082	AB060233	ABR83671	ADM05015	AD085827	ADR12606	ABB63399	ADN63558
DB	2	S	7	7	7	7	Φ	Φ	Φ	Φ	7	m	Ŋ	7	œ	60	4	ω	σ,	7	7	60	60	4	ω
% Query Match Length	20	153			364	364	364	364	364	364		31	364	364	364	365	361	366	215	836	836	836	1772	1223	σ
* Query Match	100.0	99.0	99.0	99.0	99.0	99.0	99.0	99.0	99.0	0.66	97.0	95.0	68.0	68.0	68.0	61.0	55.5	52.0	50.5	50.5	50.5	50.5	48.0	47.0	46.0
Score	100	66	66	66	66	66	66	66	66	66	97	95	68	68	99	61	55.5	52	50.5	50.5	50.5	50.5	48	47	46
Result No.	-	7	٣	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Adn64270 HLA bindi Abp96323 Human AGE		Adk46838 Streptoco	Adr95229 Novel S.	Aam93735 Human pol	Adl31668 Human pro	Aao19583 Human pho	Abb99461 Protein 5	Aao19582 Human pho	Adr10068 Human pro	Human	Adp29611 Human sec	Abr47389 Breast ca	Abu64480 Human fru	Abm81063 Tumour-as	Adj69390 Human hea	Abp43842 DKFZp564M	Adg67676 Novel hum	Abo58476 Human gen
8 ADN64270 6 ABP96323	6 ABU01993	8 ADK46838	8 ADR95229	4 AAM93735	8 ADL31668	6 AAO19583	6 ABB99461	6 AAO19582	8 ADR10068	5 ABP69378	8 ADP29611	6 ABR47389	7 ABU64480	8 ABM81063	7 ADJ69390	5 ABP43842	8 ADQ67676	8 ABO58476
132	170	170	171	283	283	292	292	295	295	324	324	364	364	364	644	811	896	902
46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0	46.0
4 4 6 6	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46	46
26. 27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	. 43	44	45

## ALIGNMENTS

AAR37301 standard; protein; 20 AA. RESULT 1 **AAR3730**3

AAR37301;

(revised)
(first entry) 25-MAR-2003 13-SEP-1993

Rabbit Muscle aldolase peptide segment.

Type I ribosome-inactivating protein, ricin, momordin, immunoconjugate, autoimmune disease, cell killing, toxin, human engineered antibody; variable region, light chain, cell targetting, chimeric antibody; RMA; 

Oryctolagus cuniculus.

Location/Qualifiers 1. .20 /note= "contains several potential cathepsin cleavage sites" Key Cleavage-site

WO9309130-A1

13-MAY-1993.

92WO-US009487. 04-NOV-1992; 91US-00787567. 04-NOV-1991; 19-JUN-1992;

(XOMA ) XOMA CORP.

SP; Lei Berhard SL, Better MD, Carroll SF, Lane JA,

WPI; 1993-167617/20.

Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.

Example 10; Page 115; 163pp; English.

The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
are antibodies or their fragments, esp. human engineered H65 antibody fragments. Fusion constructs were assembled that included a natural sequence gelonin gene fused to an H65 truncated heavy chain gene or an H65 light chain (kappa) gene. A DNA linker encoding a peptide segment of the rabbit muscle aldolase was inserted between the gelonin gene and the Ab gene. The resulting immunoconjugates can be used as cytotoxic therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to 2175 novel human ovarian antigens (ABP41054-
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
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                                                                                                                                                                                                      100.0%; Score 100; DB 2; Length 20; 100.0%; Pred. No. 8.2e-10; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian antigen HOPKN14, SEQ ID NO:3838.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP42706 standard; protein; 153 AA
                                                                                                                                                                                                                                                                                                                1 PSGOAGAAASESLFISNHAY 20
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                                                                                                                                                                                                                                                20; Conservative
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                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                  Sequence 20 AA;
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disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorthoea), endocrine disorders, infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorthoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vapinitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders. Close in a creamia, cardiovascular disorders, and urinary system disorders. Ovarian antigen polypeptides and oplymentatory disorders. Ovarian antigen polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may entitle expression or activity. The polynucleotides may entitle expression or activity. The polynucleotides may entitle and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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Pfreundschuh M, Tureci O, Sahin U;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%; Score 99; DB 5; I
95.0%; Pred. No. 1.3e-08;
iive 1; Mismatches 0;
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97US-0061765P.
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nes 19; Conservative
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Obata Y,
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 153 AA;
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lung cancer
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression broduct complexed with an HAA molecule, and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast encer.

Sequence 363 AA;

Gaps ö Length 363; 0; Indels 99.0%; Score 99; DB 2; 1 95.0%; Pred. No. 3.6e-08; 1; Mismatches Local Similarity 95.0 nes 19; Conservative Query Match Matches

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1 PSGOAGAASESLFISNHAY 20

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344 PSGQAGAAASESLFVSNHAY 363

RESULT 4

AAY06992 standard; protein; 364 AA.

AAY06992;

(first entry) 02-JUL-1999 Glycolytic enzyme aldolase A.

Cancer associated antigen; diagnosis; research; treatment; human; breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer; prostate cancer

Ното варіепв.

WO9904265-A2

28-JAN-1999

98WO-US014679 15-JUL-1998;

97US-00896164. 97US-0061599P. 97US-0061765P. 97US-00948705. 97GB-00021697. 17-JUL-1997 10-OCT-1997

98US-00102322 10-OCT-1997; 10-OCT-1997; 11-OCT-1997; 22-JUN-1998; (LUDW-) LUDWIG INST CANCER RES

Chen Y, Gout I; Pfreundschuh M, Tureci O, Gure A, Stockert E, Scanlan MJ, Obata Y, hare M, old LJ,

WPI; 1999-132448/11. N-PSDB; AAX40193.

 isolated the New isolated cancer associated nucleic acids and polypeptides using sera from cancer patients, used to develop products for diagnosis, monitoring or treatment of cancers.

Example 8; Page 769-770; 787pp; English.

The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises; (a) contacting a

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biological sample isolated from a subject with an agent that specifically biological sample isolated from a subject with an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disporder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antigens. The invention provides mucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
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                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferation; cell migration; cell differentiation;
mitogenic factor; survival factor; cytotoxic factor;
differentiation factor; neuropeptide; hormone; cell receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor-ligand interaction; cytostatic; chondrocyte; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; PRO; membrane bound protein; membrane bound receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schoenfeld JR;
                                                                                                                                                                                                                                                                                Score 99; DB 2; Length 364; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark H,
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                                                                                                                                                                                                                                          Sequence 364 AA;
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and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tummour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the
   cell receptors or membrane bound proteins. These membrane bound proteins
                                                                                                                                                                                                                                                                                                                                              invention.
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Sequence 364 AA;

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Gaps
                            ;
  Length 364;
99.0%; Score 99; DB 7; 1
95.0%; Pred. No. 3.7e-08;
                        1; Mismatches
                                                                      345 PSGQAGAAASESLFVSNHAY 364
                                                     1 PSGQAGAAASESLFISNHAY 20
            Local Similarity 95.0
ses 19; Conservative
  Query Match
                           Matches
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ADJ68731 standard; protein; 364 AA

ADJ68731;

(first entry) 06-MAY-2004 Human heat mitochondrial protein as a therapeutic target SeqID537.

Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidoses and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis; osteopathic, ophthalmological; cytostatic. ADJOSATIL 6
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Homo sapiens

WO2003087768-A2.

23-OCT-2003.

04-APR-2003; 2003WO-US010870.

12-APR-2002; 2002US-0372843P. 17-JUN-2002; 2002US-0389987P. 20-SEP-2002; 2002US-0412418P.

(MITO-) MITOKOR. (BUCK-) BUCK INST AGE RES.

Gibson BW, Taylor SW, Fahy ED, Zhang B, SS, Ghosh

Glenn GM

Warnock DE;

WPI; 2003-845369/78.

Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.

Claim 1; SEQ ID NO 537; 180pp; English.

This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidemmia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the CDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the CDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically
useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and expensive in this polypeptide sequence is a human heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
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                                                                                                                                                                                                                                                                                             99.0%; Score 99; DB 7; Length 364; 95.0%; Pred. No. 3.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein expressed in a liver disorder #87.
                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                              mitochondrial protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADE77178 standard; protein; 364 AA
                                                                                                                                                                                                                                                                                                                                                                                                     345 PSGQAGAAASESLFVSNHAY 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUL-2001; 2001US-00919039.
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KASE/) KASER M R.
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                                                                                                                                                                                                                                                        Sequence 364 AA;
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                                                                                                                                                                                                                                                                                                                                     Matches
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(first entry)

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Use of an inhibitor of a member of a biological pathway for inhibiting, suppressing, treating, or preventing human immunodeficiency virus (HIV)
                                                                                                                      Human fructose bisphosphate aldolase A, target for anti-HIV agent.
                                                                                                                                                      Human; fructose bisphosphate aldolase A; enzyme;
human immunodeficiency virus; HIV; anti-HIV; virucide
                   ADQ76754 standard; protein; 364 AA.
                                                                                                                                                                                                                                                                                                             30-DEC-2003; 2003WO-US041790.
                                                                                                                                                                                                                                                                                                                                                 30-DEC-2002; 2002US-0436936P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-534379/51.
                                                                                                                                                                                                                                                                                                                                                                                (PPDP-) PPD DEV LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADQ76753
                                                                                                                                                                                                                                           WO2004061088-A2.
                                                                                                                                                                                                           Ното варіепв.
                                                                                      07-OCT-2004
                                                                                                                                                                                                                                                                             22-JUL-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infection
                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn SJ;
   4DQ76754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for preparing a gene database. The method comprises a search unit searching homology of a candidate sequence determined by a primer probe designing unit, for determining homologous presence or absence of a determined candidate sequence. The method of the invention is useful for the preparation of a microarray, such as a cDNA microarray. The present amino acid sequence represents a human fructose-
                       ဌ
binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene database production method for microarray preparation, comprises searching homology of a candidate sequence determined by a primer probe designing unit, for a matching candidate sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%; Score 99; DB 8; Length 364; 95.0%; Pred. No. 3.7e-08; .ive 1; Mismatches 0; Indels
                                                                                                                                                     Score 99; DB 8; Length 364; Pred. No. 3.7e-08; i. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene database preparation; cDNA microarray; human; fructose-bisphosphate aldolase; GP2; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
(KOKU-) KOKURITSU SEISHIN SHINKEI CENT SOCHO.
                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human fructose-bisphosphate aldolase
                                                                                                                                                                                                                                                                                                                                             ADI02918 standard; protein; 364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 9; 33pp; Japanese.
                                                                                                                                                                                                                                             PSGQAGAAASESLFISNHAY 20
                                                                                                                                                     99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2002; 2002JP-00123176,
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                                                                                                                                                                                        19; Conservative
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                                                                                                                     Sequence 364 AA;
                                                                                     liver disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2004005319-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                      Query Match
                                                                                                                                                                                      Matches
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The present sequence is that of human fructose bisphosphate aldolase A (ALDDA), which has been identified as a cellular target for HIV inhibition. The invention relates to methods for identifying human cellular genes that encode products that are necessary for productive HIV infection for use as targets in the design of therapeutic agents for identifying biological pathways comprising the products of these pathways, and methods for identifying additional human cellular genes that encode products comprising other members of such pathways for use as targets in the design of therapeutic agents for suppressing HIV infection. It also the design of therapeutic agents for suppressing HIV infection. It also captured for identifying protective compounds that inhibit HIV infection and to the use of such compounds in the treatment or prevention of HIV. The compounds include chemical compounds such as small molecule inhibitors or substrate compounds such as products of chemical combinatorial libraries, or biological compounds including peptides, antisense molecules and antibodies. In one embodiment of the invention, the target gene encodes a target product that is a member of the compounds. The constructed from mRNA isolated from HI-60 and HE-60 an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived genetic suppressor elements (GSEs) exhibiting HIV suppressive activity. The human cellular genes from which these GSEs were derived were identified, and included the ALDOA gene from a PBMC library.
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Claim 1; SEQ ID NO 22; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PSGQAGAAASESLFISNHAY 20
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Gaps

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RESULT 10

PSGQAGAAASESLFVSNHAY 364

345

1 PSGQAGAAASESLFISNHAY 20

19; Conservative

Matches

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Analgesic; pain; streptozocin-induced diabetes; rat.

Rattus norvegicus

EP1279744-A2

29-JAN-2003

27-JUL-2001; 2001GB-00018354. 07-FEB-2002; 2002GB-0002910. 26-JUL-2002; 2002EP-00255249.

ADB79827 standard; protein; 364 AA.

(first entry)

04-DEC-2003

ADB79827;

Rat aldolase A, SEQ ID 67

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RESULT 11
                  ADB79827
                                                The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide to general sequences at least 80% identical to the TAT nucleic acids and polypeptide to polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosis of cancer in mammals. TAT polypeptides and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, carvical cancer, lung cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide.
                                                                                                             Tumour-associated antigenic target (TAT) polypeptide PRO69617, SEQ:4521.
                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acids,
                                                                                                                                         Tumour-associated antigenic target; TAT; human; overexpression; cattumour; diagnosis, call proliferative disorder; breast cancer; colorectal cancer; lung cancer; ovarian cancer; liver cancer; central nervous system cancer; bladder cancer; pancreatic cancer; extracal cancer; melanoma; bladder cancer; pancreatic cancer; chromosome identification; chromosome mapping; gene mapping; gene therapy; extostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tumor-associated antigenic target polypeptides and nucleic aci
useful in preparing a medicament for treating or detecting a
proliferative disorder, e.g. breast, lung, colorectal, ovarian or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%; Score 99; DB 8; Length 364; 95.0%; Pred. No. 3.7e-08; ive 1; Mismatches 0; Indels
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               ABM81754 standard; protein; 364 AA
                                                                                                                                                                                                                                                                                                                                                                         29-SEP-2003; 2003WO-US028547.
                                                                                                                                                                                                                                                                                                                                                                                                         02-OCT-2002; 2002US-0414971P.
                                                                             18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu TD, Zhang Z, Zhou Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate cancer or tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-347921/32.
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hes 19; Conser
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                                               ABM81754;
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ABM81754
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                                                                                                                                                                                                                                                                                                                                                                          are useful in
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                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to nucleotide sequences which are useful the screening of compounds for the treatment of pain, or for the diagnosis of pain. The nucleotide sequences are up-regulated in the spinal cord in response to streptozocin-induced diabetes. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                  Use of isolated gene sequences and encoded polypeptides that are upregulated in the spinal cord in response to streptozocin-induced diabetes for screening compounds for the treatment of pain, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cancer associated protein sequence SEQ ID NO:1462.
                                                    Lee K, Pinnock RD;
                                                                                                                                                                                                                                                                                                                     Claim 1, Page 135-136; 334pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB44017 standard; protein; 31 AA
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(WARN ) WARNER LAMBERT CO
                                                    Dixon AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                       WPI; 2003-395407/38.
                                                                                                                             N-PSDB; ADB79828.
                                                                                                                                                                                                                                                                     diagnosing pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 364 AA;
                                                    Brooksbank RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001
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Gaps

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1 PSGQAGAAASESLFISNHAY 20

Conservative

Best Loca Matches

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10-DEC-2001; 2001WO-GB005458.

WO200246465-A2 Homo sapiens.

13-JUN-2002

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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiathmatic; antihemmatic; antibateria; antibateria; antibateria; antipathmatic; antihemmatory; antipathmatic; antihempatic; antibacterial; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; conorropic; antipsoriatic and antianglogenic. The notropic; antipsoriatic and antianglogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells; to treat disorders of haematopoietic cells, autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, mucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78419 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer; ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing; inflammaton; erythropoiesis; hair loss; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 2142; 2352pp; English.
neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP65148 standard; protein; 364 AA
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                                                                                                                                                           08-MAR-2000; 2000WO-US005882
                                                                                                                                                                                                99US-0124270P
                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                      WPI; 2000-587533/55.
N-PSDB; AAC78226.
                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                             WO200055350-A1
                                                                                                                                                                                              12-MAR-1999;
                                         Homo sapiens.
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pathology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  second specialised cell type, under two experimental conditions, and dentifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABV7813-ABV78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated conditions, and for regulating tumourigenesis, angiogenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
mycolonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                               Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two cell types under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comparies comparing the transcriptome/proteome specialised cell type implicated in a disease or condition with that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                 Ward NR, Krige D, Kingsman SM, Harris RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 35; Page 345; 538pp; English
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                                                                                                                                                                                                                                                          (OXFO-) OXFORD BIOMEDICA UK LTD
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                                                                                                                                                                        08-DEC-2000; 2000GB-00030076.
08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
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                                                                                                                                                                                                                                                                                                 Mundy CR,
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulated gene
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                                                                                                                                                                                                                                                                                                                      Rayner WN;
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                                                                                                                                                                                                                                                                                                 White J,
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12-OCT-2001; 2001US-00976594. 12-OCT-2000; 2000US-0240409P.

Furness LM, Buchbinder JL;

(INCY-) INCYTE CORP

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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRE) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glenn GM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fahy ED, Zhang B,
                                                                                                                                                                                                                                                                                                        04-APR-2003; 2003WO-US010870.
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17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
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(BUCK-) BUCK INST AGE RES.
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                                                                                                                           WO2003087768-A2.
                                             Homo sapiens.
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Warnock DE;
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Query Match
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                                                                         68.0%; Score 68; DB 7; Length 364; 63.2%; Pred. No. 0.0075; ative 5; Mismatches 2; Indels
                                                                                                                              2 SGQAGAAASESLFISNHAY 20
                                                                                                      12; Conservative
                                                                                        Local Similarity
                                                                                                      Matches
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Hepatotropic, Gene therapy, Wilson disease, liver disorder, steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.

Homo sapiens US6673549-B1

06-JAN-2004

Human steroid-induced C3A liver cell protein #58.

06-MAY-2004 (first entry)

ADL12661;

ADL12661 standard; protein; 364 AA

346 SGEDGGAAAQSLYIANHAY 364

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The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high to detect throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with Wilson disease and comparison of a strandard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human protein which is differentially expressed in steroid-induced cDNA liver cells. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent electronic format directly from USPTO
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                                                                                                                                                                                                                                                                                                       Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNAs that are differentially expressed in response to steroid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 390; 141pp; English.
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Matches 12; Conservative
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Sequence 3140, Ap Sequence 44042, A Sequence 44220, A Sequence 45571, Sequence 9, Appli Sequence 44097, A Sequence 44097, A Sequence 44097, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978, A Sequence 55978

Sequence 1196, Ap Sequence 32110, A Sequence 46406, A

Sequence 351374, 70495,

Sequence

50, Appl 50, Appl 114024,

Sequence Sequence S

Sequence

Sequence 65982, A Sequence 269100, Sequence 33867, A Sequence 3700, Ap Sequence 161041, Sequence 2, Appli

Sequence

sequence

Sequence

Perfect score:

Sequence:

OM protein

on:

Run

Scoring table:

Searched:

Database

```
## Sequence 57, Application US/10127890

## Sequence 57, Application US/10127890

## Publication No. US2003016619641

## GENERAL INFORMATION:

## Carroll, Stephen F.

## Carroll, Stephen F.

## Studnika, Gary M.

## TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

## NUMBER OF EQUENCES: 173

## CORRESPONDENCE ADDRESS:

## ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDR
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WEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-APPL-2002
CLASSIFICATION STATE: APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
                                        US-10-369-493-5735

US-10-767-701-46629

US-10-425-115-269098

US-10-425-115-269100

US-10-029-386-33867

US-10-029-386-33867

US-10-029-386-33867

US-10-425-114-44042

US-10-425-114-44042

US-10-425-114-44042

US-10-425-114-44097

US-10-425-114-44097

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US-10-425-114-55918

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US-10-425-115-351374
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US-10-127-890-57
                                                                                                                                                                  Sequence 57, Appl Sequence 37, Appl Sequence 343, App Sequence 537, App Sequence 532, App Sequence 67, Appl Sequence 196160, Sequence 1462, App Sequence 259, Appl Sequence 98, Appl Sequence 98, Appl
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                                                                                                                                                                                         (without alignments)
70.780 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.ppp:*
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| Cgn2_6/ptodata/2/pubpaa/USO10_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.ppp:*
                                                                                                                                                                  June 20, 2005, 10:13:56 ; Search time 108.5 Seconds
                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 US-10-127-890-57
7 US-10-717-243-57
1 US-10-26-049-388
6 US-09-919-039-343
6 US-10-408-765A-537
6 US-10-370-715B-532
4 US-10-205-219-67
6 US-10-425-115-196160
US-09-925-301-1462
5 US-10-170-385-259
6 US-10-408-765A-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1714042 segs, 383979560 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                     - protein search, using sw model
                                                                                                                                                                                                                                                            US-10-717-243-57
100
1 PSGQAGAAASESLFISNHAY 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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1000.0
990.0
990.0
990.0
997.0
995.0
680.0
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Score

Result Š. 1000 1000 999 997 995 995 995

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Mismatches
                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TYPE: amino acid
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-264-049-3838
; Sequence 3838, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 PSGQAGAASESLFVSNHAY 153
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                                                                                                    TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
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Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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; ORGANISM: Homo sapiens
US-10-264-049-3838
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserval
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Sequence 57, Application US/2005054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proceins
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COMPUTER READABLE FORM:

MEDIUM TYPE: FOPPOMPATIBLE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 100; DB 14; 100.0%; Pred. No. 5.5e-09;
                FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-7UN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 22,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEFRANCE/DOCKET NUMBER: 200-70.P4
TELEFRANCE/JOCKET NUMBER: 200-70.P4
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APPLICATION NUMBER: US/08/039,765
FILING DATE: 15-AR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/908,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 57: US-10-127-890-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
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Best Local Similarity
Matches 20; Conserv
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Sequence 343, Application US/09919039
Fublication No. US20030108871A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVERTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: 08/09/919,039
CURRENT APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 343
LENGTH: 344
TYPE: PRT
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PAI3391
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
NUMBER: OF SEQ ID NOS: 4360
SOFTWARE: PALENTIN Ver. 3.1
SEQ ID NO 3818
LENGTH: 153
                                                                                                                                                                                                                                                                                                                                                       Length 20;
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REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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us-10-717-243-57.open.rapb

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TYPE: PRT
ORGANISM: Zea mays
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US-10-370-715B-532
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APPLICANT: BODARY, SARAH C.
APPLICANT: GLARK, HILLARY
APPLICANT: ARISDELL, HUNTE
APPLICANT: ARCHAN, JANET
APPLICANT: SCHOENFELD, JILL R.
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WILLIAMS, D.
TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Marnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: TARGETS TOWNERS.
FILE REFERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                   Query Match 99.0%; Score 99; DB 10; Length 364; Best Local Similarity 95.0%; Pred. No. 1.9e-07; Matches 19; Conservative 1; Mismatches 0; Indels
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                     FEATURE:
NAME/KEY: misc feature
CATHER INFORMATION: Incyte ID No. US20030108871A1 2706606CD1
US-09-919-039-343
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CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
                                                                                                                                                                                                                                                                                                                                                                 US-10-408-765A-537, Application US/10408765A; Sequence 537, Application US/10408765A; Publication Oc. US20040101874A1; Publication No. US20040101874A1; APPLICANT: Ghosh, Soumitra S.; APPLICANT: Fahy, Egin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 532, Application US/10370715B Publication No. US20040258678A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                             345 PSGQAGAAASESLFVSNHAY 364
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Best Local Similarity 95.0
Matches 19; Conservative
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US-10-408-765A-537
ORGANISM: Homo sapiens
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ORGANISM: Homo sapien
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US-10-370-715B-532
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LENGTH: 364
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Sequence 196160, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart Chart
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APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Dieo, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TILE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT APPLICATION NUMBER: GB 0118354.0
FILE REPERENCE: 2001-07-27
NUMBER OF SEQ ID NOS: 197
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 67
LENGTH: 364
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          Length 364;
                                                                                                        0; Indels
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US-10-425-115-196160
     99.0%; Score 99; DB 16; 95.0%; Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(112)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 67, Application US/10205219
Publication No. US20030138803A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                               345 PSGQAGAAASESLFVSNHAY 364
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ORGANISM: Rattus norvegicus
FEATURE:
Query Match
Best Local Similarity 95.01
Matches 19; Conservative
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Gaps

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Sequence 98, Application US/10408765A

| Sequence 98, Application US/10408765A
| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Sounitra S.
| APPLICANT: Zhang, Bing
| APPLICANT: Zhang, Bing
| APPLICANT: Taylor, Steven W.
| APPLICANT: Taylor, Steven W.
| APPLICANT: Glenn, Gary M.
| APPLICANT: Glenn, DENTRIPED IN THE MITOCHONDRIAL PROTEOME ITILE OF INVENTION: IDENTRIPED IN THE MITOCHONDRIAL PROTEOME ITILE OF INVENTION: DENTRIPED IN THE MITOCHONDRIAL PROTEOME ITILE OF INVENTION: UNMBER: US/10/408,765A
| CURRENT APPLICATION NUMBER: US/10/408,765A
| CURRENT FILING DATE: 2003-04-04
| NUMBER OF SEQ ID NOS: 3077-3-04-04
| SOFTWARE FRAISE FOR WINDOWS VERSION 4.0
| SEQ ID NO 98
| LENGTH: 364
| TYPE: PRT
                                                                Score 68; DB 15; Length 364;
Pred. No. 0.019;
5; Mismatches 2; Indels
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-5923
                                                                                                                                                                                                               2 SGOAGAASESLFISNHAY 20
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                                                                       68.0%;
63.2%;
                                       Query Match
Best Local Similarity 63.2%
...a 12; Conservative
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Matches 12; Conservative
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US-10-369-493-5923
   US-10-170-385-259
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j. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1462
                                                                       Gaps
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| Sequence 1462, Application US/09925301
| Patent No. US20020052308A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PA106
| CURRENT APPLICATION NUMBER: US/09/925,301
| CURRENT FILING DATE: 2001-08-10
| PRIOR FILING DATE: 2000-03-08
| PRIOR FILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 1694
| SOFTWARE: PatentIN Ver. 2.0
| SEQ ID NO 1462
96.0%; Score 96; DB 16; Length 112; 95.0%; Pred. No. 1.6e-07; ive 0; Mismatches 1; Indels
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PUDLICANT: Ward, Neil Raymond
APPLICANT: Wandy, Christopher Robert
APPLICANT: Kan, On
APPLICANT: White, Onathan
APPLICANT: White, Jonathan
APPLICANT: White, Jonathan
APPLICANT: White, Jonathan
APPLICANT: BAYNEY, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Kingsman, Susan Mary
APPLICANT: Kingsman, Susan Mary
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Publication No. US20030203372A1
                                                                                                                                                                                          93 PSGQXGAAASESLFISNHAY 112
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Matches 19; Conservative
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ORGANISM: Homo Sapiens
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   Query Match
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Sequence 5223, Application US/10369493
; Sequence 5223, Application US/10369493
; Sequence 5223, Application No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Gldman, Barry S.
; APPLICANT: Gldman, Barry S.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Barry S.
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: 109-02-28
; FILE REFERENCE: 2003-02-28
; FILE REPRIENCE: 2003-02-28
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; ROWBER OF SEQ ID NOS: 47374
; SEQ ID NO 5923
**LENGTH: 365
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinda
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 46229
LENGTH: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.0%; Score 51; DB 16; Length 358; 52.6%; Pred. No. 10; tive . 3; Mismatches 6; Indels
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US-10-767-701-46629
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                                              Sequence 46629, Application US/10767701
Publication No. US20040172684A1
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Best Local Similarity 52.6°
Matches 10; Conservative
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ORGANISM: Sorghum bicolor
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                                                                                                                                                            Sequence 255, Application US/10108605
| Publication No. US20020160934A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Broadus, Julie
| APPLICANT: Broadus, Julie
| APPLICANT: Broadus, Julie
| APPLICANT: Broadus, Julie
| APPLICANT: Broadus, Julie
| APPLICANT: Amenan, Jane
| TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
| TITLE OF INVENTION: NUCLEIC ACID SEGUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
| TITLE OF INVENTION: NUMBER: US/10/108,605
| CURRENT APPLICATION NUMBER: US/02-03-27
| CURRENT APPLICATION NUMBER: US 60/761,142
| PRIOR FILING DATE: 2001-01-16
| PRIOR FILING DATE: 2000-01-14
| NUMBER OF SEQ ID NOS: 361
| SOOTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5735, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INPORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: UNMBER: US/10/369,493
; FILE REFERENCE: 38-10 (52052)B
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR APPLICATION UNMBER: US 60/360,039
; PRIOR APPLICATION NUMBER: US 60/360,039
; RIGHT APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5735
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Pred. No. 7.4;
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344 AGSAG-AGSGSLFVANHAY 361
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-5735
                            350 ADAAASQSLFVANHSY 365
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5 AGAAASESLFISNHAY 20
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Best Local Similarity 56.2.
Best Local 9; Conservative
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                     RESULT 13
US-10-108-605-255
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LENGTH: 361
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Gaps

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APPLICANT: Bernbard, Susan L.
APPLICANT: Berter, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Pine A.
APPLICANT: Lei, Shau-Pine A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
CORRESPONDERS 101
CORRESPONDERS: 101
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MEDIUM TYPE: Floppy disk
COMPUTER: Elem PC compatible
COMPUTER: Elem PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION ADATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATPRING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-988-430-58
; Sequence 58, Application US/07988430
; Patent No. 5416202
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
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TYPE: AMINO ACID
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Chicago
STATE: Illinois
COUNTRY: USA
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6, Appli
14, Appl
6, Appli
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                                                                                                                                                                                                                                     (without alignments)
50.610 Million cell updates/sec
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Sequence 12,
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Sequence 56,
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                                                                                                                                                                                                 June 20, 2005, 10:36:43; Search time 29.5 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COWB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COWB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-219-849-11
US-09-809-517A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513545 segs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                       114
1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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Match Length
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58:

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Sequence
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    US-09-331-362-8

US-09-823-266-5

US-09-823-017B-28

US-08-706-945D-145

US-08-933-995A-31

US-08-687-226-70

US-08-556-978B-10

US-08-556-978B-10

US-08-556-978B-10

US-08-556-978B-40

US-08-556-978B-40

US-08-955-177-15

US-08-955-177-15

US-08-955-177-15
                                                                         US-09-239-043D-2319
US-07-616-910-25
PCT-US91-08497-25
                                                                                          US-07-906-871-3
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## ALIGNMENTS

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RESULT 4
US-08-477-484B-56
; Sequence 56, Application US/08477484B
; Eath to 5756699
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CHHHASRVARMASDEFPSMC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                          ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 20; Conserve
                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-488-113B-56
  US-08-488-113B-56
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                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                              Length 20;
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                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: 111.016
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FLING DATE: 18-APR-1995 .
FLING DATE: 18-APR-1995 .
RILOR DATE: 19-APR-1995 .
FILING DATE: 19-APR-1993 APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAYER: Thomas C.
REGISTRATION NUMBER: P-36,999
REGISTRATION NUMBER: P-36,999
REGISTRATION NUMBER: P-36,999
                                                              Query Match 100.0%; Score 114; DB 1; Best Local Similarity 100.0%; Pred. No. 1.9e-12; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              ; Sequence 56, Application US/08425336; Patent No. 5621083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 31.
THELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: peptide US-08-425-336-56
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chicago : Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
      ; MOLECULE III
US-07-988-430-58
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Sequence 56, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating CONTRESPONDENCE ADDRESS: 169
CORRESPONDENCE ADDRESS: ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: KEALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OSPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rc-Bos/MS-DOS
SOFTWARE: Patentin Nomer: US/08/48,113B
FILING DATE: US-JUN-1995
FILING DATE: US-MX-1995
PRICK APPLICATION NUMBER: US/08/45,691
FILING DATE: 12-MX-1993
PRICK APPLICATION NUMBER: US/07/98,430
FILING DATE: US-MX-1993
PRICK APPLICATION NUMBER: US/07/901,707
FILING DATE: US-DEC-1992
PRICK APPLICATION NUMBER: US/07/901,707
FILING DATE: US-UN-1992
PRICK APPLICATION NUMBER: US/07/901,707
FILING DATE: US-UN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
RECISTRATION NUMBER: 32,918
RECOMMUNICATION INFORMATION:
NAME: MCNICHOLAS, Janet M.
RECISTRATION NUMBER: 312,707-8889
TELECOMMUNICATION INFORMATION:
TELEFRAK: 312/707-8889
TELEFRAK: 212/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11022US07/200-70.P3.C2A
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Sequence 56, Application US/08839765

Patent No. 6146631

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
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                                                                                  COUNTY.

ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/984,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-OF-DEC-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-OF-DEC-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-OF-DEC-1992
PRIOR APPLICATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 20-TO.P4
TELEPHONE: 312/707-9155
TELEPHONE: 312/707-9155
TELEPHONE: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 114; DB 2; Best Local Similarity 100.0%; Pred. No. 1.9e-12; Matches 20; Conservative 0; Mismatches 0;
        500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CHHHASRVARMASDEFPSMC 20
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LENGTH: 20 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-646-360-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
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Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxing Comprising Ribosome-Inactivating TITLE OF SEQUENCES: 173
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: MCANdrews, Held & Malloy, Ltd.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
RICH APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1992
ATMANDER: US 07/787,567
FILING DATE: US NUMBER: US 07/787,567
FILING DATE: US NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE, DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 114; DB 1;
100.0%; Pred. No. 1.9e-12;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; So
Best Local Similarity 100.0%; Pi
Matches 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                          Illinois
                                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-646-360-56
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Gaps

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CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA: BAPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
PRIOR APPLICATION NUMBER: US 07/901,707
PRIOR APPLICATION NUMBER: US 07/901,707
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY.AGENT INFORMATION:
NAME: MCMICADIAB, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/POCKET NUMBER: 200-70.P4
TELECOMMUNICATION INPORMATION:
TELEPHONE: 312/707-9889
TELEPHONE: 312/707-9889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUCTIONS APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-UUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-610-838-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-136-389-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 56, Application US/09136389
Patent No. 6146850
GENERAL INFORMATION
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 114; DB 3; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11022US09/200-70.P3.C3
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ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                        PALCATION NUMBER: US
PRIOR PAPLICATION NUMBER: US
PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERRUCE/DOCKET NUMBER: 32,918
REFERRUCATION INDRER: 32,918
REFERRUCATION INPORMATION:
TELEPHONE: 312/707-9155
                                                                                                         APPLICATION NUMBER: US/08/839,765
PILING DATE: 15-APR-1997
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CHHHASRVARMASDEFPSMC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
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Best Local Similarity 100.0%;
Marches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 500 West
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-839-765-56
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US-09-136-389-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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Gaps
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Batent No. 6376217

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Studinka, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: MCANdrews, Held & Malloy, Ltd.
                                                      ö
100.0%; Score 114; DB 3; Length 20; 100.0%; Pred. No. 1.9e-12; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
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APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lel, Shau-Ping
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                            PILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,918
ATTORNEY/COCKET NUMBER: 31,918
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-8155
TELEPHONE: 312/707-8155
TELEPHONE: 312/707-8165
TELEPHONE: 312/707-8165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 114; DB 4;
100.0%; Pred. No. 1.9e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19221104
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application PC/TUS9209487
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 100.
Matches 20; Conservative
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MOLECULE TYPE: peptide
US-09-711-485-56
                                APPLICATION NUMBER:
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US92-09487-58
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Patent No. 6649742

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 114; DB 3; Length 20; Best Local Similarity 100.0%; Pred. No. 1.9e-12; Matches 20; Conservative 0; Mismatches 0; Indels
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ZIP: 60661
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1992
PRIOR APPLICATION NUMBER: US 07/981,707
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCMACHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9855
TELES: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: peptide US-09-610-838-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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CLASSIFICATION:
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Gaps

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31.6%;
60.0%;
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Best Local Similarity 60.0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 MASDEFPSMC 20
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  1 MAQDAFPNAC 10
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CITY: Palo Alto
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                        CITY: Den
STATE: CC
COUNTRY:
                                                                                 US-08-459-019A-6
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Sequence 6, Application US/08109391A

Sequence 6, Application US/08109391A

Patent No. 5639876

GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.
APPLICANT: Frank, Glenn R.
APPLICANT: Grieve, Robert B.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING NOVEL
TITLE OF INVENTION: PARASITIC HELMINTH PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.6%; Score 36; DB 1; Length 16; Best Local Similarity 60.0%; Pred. No. 14; Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/109,391A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Sheridan Ross & McIntosh
1700 Lincoln St., Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                       1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                  1 CHHHASRVARMASDEFPSMC 20
                REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 3113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELERX: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAK: 303/863-0223
INPORMATION POR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
Noland, Greta E.
                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US92-09487-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1'
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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PRESULT 12

Sequence 6, Application Us/08459019A

Parcent No. 556000

GREECAL MOOWARION

TATLE OF INVENTION: NOVEL PRASTIC HELMINTH P4 PROTEINS

MOMBER OF SEQUENCES: 17

CONTRIST OF INVENTION: NOVEL PRASTIC HELMINTH P4 PROTEINS

MOMBERS TO 10 LINCIA RESET

CONTRIST OF INVENTION: NOVEL PRASTIC HELMINTH P4 PROTEINS

MOMBERS TO 10 LINCIA RESET

CONTRIST OF INVENTION: NOVEL PRASTIC HELMINTH P4 PROTEINS

MOMBERS TO 10 LINCIA RESET

CONTRIST OF INVENTION: NOVEL PRASTIC HELMINTH P4 PROTEINS

CONTRIST OF TO 10 LINCIA RESET

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Sequence 21, Application US/08482304

Patent No. 6060281

GENERAL INFORMATION:
APPLICANT: Grave, Robert B.
APPLICANT: Frank, Glenn R.
APPLICANT: Wishewki, Nancy
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 55
NUMBER OF SEQUENCES: 55
NUMBER OF SEQUENCES: 55
SERRET: 1700 Lincoln Street, Suite 3500
                                                                                                              Query Match
31.6%; Score 36; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score. 36; DB 3; Length 16; Pred. No. 14; 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SISTEM: FUL-DUS, NS-LUCS
OPETWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,304
FILLING DATE:
CLASSIFICATION: 254
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 2618-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-923
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: June 20, 2005, 10:59:06 Job time : 30.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-428A-6
                                                                                                                                                                                                                                                1 MAQDAFPNAC 10
                                                                                                                                                                                                   11 MASDEFPSMC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                           US-08-482-304-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 1; Length 16;
Pred. No. 14;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE:

COMPUTER: IBM PC compatible
COMPOTER: APERICATION DATA:
APPLICATION NUMBER: US/08/460,428A
FILING DATE: 02-UN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-13-3
TELECOMMUNICATION INFORMATION:
TELEFHONE: 303/863-9700
                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-460-428A-6;
Sequence 6, Application US/08460428A;
Patent No. 5912337;
GENERAL INFORMATION:
APPLICANT: Tripp, Cynthia A.;
APPLICANT: Frank, Glenn R.;
APPLICANT: Frank, Glenn R.;
TITLE OF INVENTION: NOVEL PARASITIC HELMINTH:
TITLE OF INVENTION: P22U PROTEINS;
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                           PRILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,257
FILING DATE: 12-JAN-1993
ATTORNAY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 27010-20f;
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Sheridan Ross P.C.
1700 Lincoln St., Suite 3500
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.6%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEC ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 MASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAQDAFPNAC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
US-08-408-120-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဥ
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Wed Jun 22 05:53:28 2005

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 20, 2005, 10:27:32; Search time 23 Seconds (without alignments) 83.667 Million cell updates/sec

US-10-717-243-56

Perfect score:

114 1 CHHHASRVARMASDEFPSMC 20 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

3886 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

his operon leader his operon leader MHC class II histo pufk protein (impo chymotrypsin (EC 3 MHC HLA-DR gamma c hypothetical 2.1K hypothetical 2.1K dihydrolipoamide d tetracenomycin A2 alpha-2-macroglobu his operon leader ribulose-bisphosph his operon leader R-phycoerythrin ga hypothetical prote 24k serine protein hypothetical prote ribosomal protein endo-1,3-beta-gluc 6-phosphofructokin dystrophin-associa hypothetical prote Ig H chain V-D-J r phosphocarrier pro beta-crystallin B2 alpha-conotoxin EI protein F14D16.5 chromogranin-B -Description SUMMARIES H22565 S33001 A61577 S18582 S66635 AB0764 179432 T50757 A61414 I55663 A58589 D49164 S78760 B60763 B86323 JQ2310 JQ2320 S63478 LFECH C90981 A85827 A55149 A14454 PH1637 Length Query Score Result Š

Ig H chain V-D-J r Ig heavy chain C r cytokinin-binding	actin 7 - soybean protein QF200051 - translation elonga	glutathione transf ribosomal protein ribosomal protein	actin 6 - soybean hypothetical prote methylitaconate De	urease (EC 3.5.1.5 T cell receptor be endopeptidase Clp	nucleolin - bovine
PH1592 A37268 A35585	S15755 PA0088 S30608	S55307 S78415 A34835	S15754 G83975 S77901	F49215 S57518 PC1323	802808
000	000	0 0 0	0 0 0	0 0 0	101
100	13 15	16 16 17	. 17	18 18	19
16.7 16.7 16.7	16.7 16.7 16.7	16.7 16.7 16.7	16.7 16.7 16.7	16.7	16.7
19 19	119	19 19	1 1 1 6 1 6 1 6 1 6 1 6 1 6 1 6 1 6 1 6	100	19
30 31 32	33 354 35	36 37 38	39 41 41	4 4 4 2 8 4	45

## ALIGNMENTS

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RESULT	H22565

R-phycoerythrin gamma-C chain - red alga (Gastroclonium coulteri) (fragment) C,Species: Gastroclonium coulteri C,Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 09-Jul-2004

C;Accession: H22565
R;Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin. A;Reference number: A22565; MUID:85182601; PMID:3886644
A;Molecule type: protein
A;Residues: 1-20 < KLO>

A; Cross-references: UNIPROT: Q7M270

C; Superfamily: Aglaothamnion neglectum R-phycoerythrin gamma chain 33

Gaps ö 25.4%; Score 29; DB 2; Length 20; 37.5%; Pred. No. 3.2e+02; rive 3; Mismatches 2; Indels Local Similarity 37.5 Query Match Best Local Si Matches 3;

ö

ઠ 셤 RESULT 2

hypothetical protein - human herpesvirus 4 C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 C;Accession: S33001

R;Farrell, P.J. submitted to the EMBL Data Library, March 1988 A;Reference number: S32973

A; Accession: S33001

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-20 <FAR>

A,Cross-references: UNIPROT: Q9QCF1; EMBL: V01555; NID: 959074; PIDN: CAA24847.1; PID: 9133486

ö 22.8%; Score 26; DB 2; Length 20; 38.5%; Pred. No. 9.6e+02; tive 5; Mismatches 3; Indels 5; Conservative Query Match Best Local Similarity Matches 5; Conserv

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Gaps

SRVARMASDEFPS 18 || : ::|:| |: SRTSSISSNEDPA 20 9 g ò

RESULT 3 A61577 24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)

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Clacesion: AB0764
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Ghurcher, th, T; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A,Atitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A,Reference number: AB0502; MUID:11577608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - spinach (fragments)
C;Species: Spinacia oleracea (spinach)
C;Species: Spinacia oleracea (spinach)
C;Acession: A28965
R;Mulligan, R.M.; Houtz, R.L.; Tolbert, N.E.
Proc. Natl. Acad. Sci. U.S.A. 85, 1513-1517, 1988
A;Title: Reaction-intermediate analogue binding by ribulose bisphosphate carboxylase/oxycetylated proline.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            his operon leader peptide - Escherichia coli (strain K-12)
Cjopecies: Escherichia coli
Cjopecies: Escherichia coli
Cjopecies: Escherichia coli
Cjopecies: Escherichia coli
Cjopecies: Escherichia coli
Cjopecies: Escherichia coli
Cjopecies: D-011-1981 #sequence revision 29-Jul-1981 #text_change 09-Jul-2004
Cjores 29-Jul-1981 #sequence revision 29-Jul-1981 #text_change 09-Jul-2004
Cjores P. Frunziol, R. ja Noscara, P. P. p. Blasi, F.; Bruni, C.B.
Rychede, P.; Frunziol, R.; Bruni, C.B.
Ajritle: Identification, nucleotide sequence and expression of the regulatory region of the Ajritle: Identification, nucleotide sequence and expression of the regulatory region of the Ajritle: Identification, nucleotide sequence and expression of the regulatory region of the symbolecule type: DNA
Ajritle: Identification A03594
Ajritle: Identification A03594
Ajritle: Identification A03594
Ajritle: Identification A03594
Ajritle: Identification Recension Recommendation mechanism for the control of the expi
Ajritle: Lhis protein is involved in the attenuation mechanism for the control of the expi
                                      his operon leader peptide [imported] - Salmonella enterica subsp. enterica serovar Typhi C.Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Residues: 1-13 <PAR>
A,Cross-references: GB:AL513382, PIDN:CAD02432.1, PID:g16503299, GSPDB:GN00176
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.1%; Score 24; DB 2; Length 13; 100.0%; Pred. No. 1.3e+03; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A28965
A;Status: preliminary
A;Molecule type: protein
A;Molecule : 1-15
A;Cross-references: UNIPROT:P00875
C;Keywords: carbon-carbon lyase; carboxy-lyase; chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A28965; MUID:88144466; PMID:3422748
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Best Local Similarity 80...
As Conservative
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Best Local Similarity 100.
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: AB0764
A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 HHH 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: hisL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein K (pufQ 3' region) - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Species: 12-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994
C;Accession: S18582; S32855
R;Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
R;Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.
A;Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg
A;Reference number: S18580; MUID:92140030; PMID:11779756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T.J.; Thirup, S.; Sottr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
S66635
alpha-2-macroglobulin isoform 1 - bovine (fragment)
C;Species: Bos primigenius indicus (zebu cattle)
C;Species: Bos primigenius indicus (zebu cattle)
C;Accession: S6635
R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrn FBBS Lett. 372, 93-95, 1995
A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain of A;Reference number: S66634; MUID:96032553; PMID:7556651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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C;Species: Streptomyces fradiae
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A61577; MUD: 9.J.
Int. J. Biochem. 23, 979-984, 1991
A;Title: Two new extracellular serine proteases from Streptomyces fradiae.
A;Reference number: A61577; MUD: 92155439; PMID:1786859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residudes: 1-18 <SIN>
A;Cross-references: UNIPROT:Q7M198
C;Keywords: extracellular protein; hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 2; Length 18;
Pred. No. 1.2e+03;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 2; 1
Pred. No. 1.4e+03;
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A, Residues: 1-9 < DOL>
A, Cross-references: UNIPROT: Q7M2N8
                                                                                                                                                                                                                                                                                                                                                                                                               21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.9%;
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A,Molecule type: DNA
Residues: 1-20 «HUN»
A,Cross-references: EMBL:X68795
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5
Matches 5; Conservative
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Best Local Similarity 44.4
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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9 HNHVASVLR 17
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A;Accession: A85827
A;Status: preliminary
A;Molecule type: DNA
A;Robicule type: DNA
A;Rosidues: 1-16 <STO>
A;Ross-references: UNIPROT:Q8X8T5; GB:AE005174; NID:g12516199; PIDN:AAG57077.1; GSPDB:GN
A;Experimental source: strain O157:H7, substrain EDL933
A;Genetics:
A;Genetics:
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C;Species: Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: 150557
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2. A;Reference number: 225222; MUID:20115911; PMID:10648776
A;Recession: TSO757
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 6p21.3
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein
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Pred. No. 2e+03;
1; Mismatches 6; Indels
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100.0%; Pred. No. 1.6e+03;
ive 0; Mismatches 0;
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Best Local Similarity 41.7
Matches 5, Conservative
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 44.4
Matches 4; Conservative
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A; Residues: 1-20 <CHO>
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his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RIMD C;Species Escherichia coli
C;Species Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C90981
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A;Tile: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A;Reference number: A99629; MUID:21156231; PMID:111258796
Proc. Natl. Acad. Sci. U.S.A. 75, 4276-4280, 1978
A;Title: Nucleotide sequence of the attenuator region of the histidine operon of Escheri
A;Reference number: I41073; MUID:79033821; PMID:360215
                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:V00285; NID:g41701; PIDN:CAA23550.1; PID:g41702
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC82819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: GB:AE000293; GB:U00096; NID:92367127; PIDN:AAC75079.1; PID:91788329;
A,Experimental source: strain K-12, substrain MG1655
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+03;
tive 0; Mismatches 0;
                                                                                                                    A;Accession: I41073
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reaidues: 1-16 <RES>
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C;Superfamily: his leader peptide
C;Keywords: histidine biosynthesis
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Best Local Similarity 100...
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Best Local Similarity
Matches 3, Conserv
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A;Molecule type: DNA
A;Residues: 1-16 <HAY>
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Gaps 9

Score 22; DB 1; Length 18; Pred. No. 3.8e+03; 4; Mismatches 6; Indels

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C;Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; post P;3/Modified site: 4-hydroxyproline (Pro) #status experimental F;4-10,5-18/Disulfide bonds: #status experimental F;4-10,5-18/Disulfide bonds: #status experimental F;18/Modified site: amidated carboxyl end (Cys) #status experimental
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                                                                                                                                                     Query Match
Best Local Similarity 20.0%;
Matches 4; Conservative
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R;Bhargava, A.K.; Barnard, E.A.
Nol. Evol. 2, 187-198, 1973
A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ A;Reference number: A61414; MUID:76146602; PMID:4807189
A;Accession: A61414
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A,Residues: 1-18 <MAR>
A,Residues: 1-18 <MAR>
A,Cross-references: UNIPROT:P50982
A,Oute: sequence confirmed by chemical synthesis
C,Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt C,Superfamily: alpha-conotoxin
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R;Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.; Biochemitarry 34, 14519-14526, 1995
A;Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nove A;Reference number: A58889; MUID:96062516; PMID:7578057
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C;Genetics:
A;Gene: HLA-DR
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R;O'Sullivan, D.M.; Noonan, D.; Quaranta, V.
J. Exp. Med. 166, 444-460, 1987
A;Title: Four Ia invariant chain forms derive from a single gene by alternate splicing A;Reference number: I55663; MUID:87252940; PMID:3036998
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                                                                                                                                               chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)
C;Species: Chelydra serpentina (snapping turtle)
C;Date: 09-Sep.1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-conotoxin EI - cone shell (Conus ermineus)
C;Species: Conus ermineus (ermine cone)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHC HLA-DR gamma chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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A;Molecule type: protein
A;Residues: 1-20 <BHA>
A;Cross-references: UNIPROT:Q7LZ34
C;Keywords: hydrolase; protein digestion; serine proteinase
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A;Molecule type: mRNA
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Santos-Guerra A.;
"Phylogenetics and Evolution of the Macaronesian Clade of Crassulaceae
Inferred from Nuclear and Chloroplast Sequence Data.";
Syst. Bot. 27:271-288(2002).
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"Characterization of the bilin attachment sites in R-phycoerythrin.";
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                                                                                                                                                                         Score 30; DB 2; Length 13;
Pred. No. 5.4e+02;
2; Mismatches 1; Indels
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                                                                                                          COFB1B6DAD15CB02 CRC64;
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20 AA; 2353 MW; 166FE7DB5F5309DF CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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llarity 37.5%; Pred. No. 1.3e+03;
Conservative 3; Mismatches 2;
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   GO; GO:0009507; C:chloroplast; IEA
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MEDLINE=85182601; PubMed=3886644;
                                                                                                                                                                            26.3%;
                                 Chloroplast.

NON TER
SEQUENCE 13 AA; 1361 MW;
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Chloroplast.
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SEQUENCE
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Matches
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-i. PUNCTION: Major component of a prophage tail sheath (Probable).
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01-NOV-1996 (TYEMBLrel. 01, Last sequence update)
01-NOV-1996 (TYEMBLrel. 01, Last annotation update)
01-NOV-1998 (TYEMBLACA. 08, Last annotation update)
NUD/RPD2 alpha peptide (TYEMBROL).
Name=VD1/RPD2 alpha peptide;
Lymnacae steapnalis (Great pond snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Lymnacoidea, Lymnaeidae; Lymnaea.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Serratia.
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Score 27; DB 2; Length 12;
Pred. No. 1.5e+03;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                               P83375;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Bacteriocin serracin P 43 kDa subunit (Fragment).
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Pred. No. 4.2e+03;
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MEDINE=93351194; PubMed=8348590; Bogerd J., Van Kesteren R.E., Van Heerikhuizen H., Geraerts W.P., Bogerd J., Van Kesteren R.E., Van Heerikhuizen H., Geraerts W.P., Venstra J., Smit A.B., Joosse J.; "Alternative splicing generates diversity of VDI/RPD2 alpha peptides in the central nervous system of Lymnaea stagnalis."; Cell. Mol. Neurobiol. 13:123-136(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=VDJ/RPD2 alpha peptide;
Lymnaea stagnalis (Great pond snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8; Sinha U., Wolz S.A., Lad P.J.; "Two new extracellular serine proteases from Streptomyces fradiae."; Int. J. Biochem. 23:979-984(1991).
                    Interpro; IPR001211; PhospholipaseA2.
Pfam; PF00068; Phospholip A2 1; 1.
Calcium; Direct protein sequencing; Hydrolase; Lipid degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces fradiae.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                       Score 25; DB 1; Length 17; Pred, No. 4.8e+03;
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Pred. No. 5.1e+03;
1; Mismatches 2; Indels
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VDI/RPD2 alpha peptide (Fragment).
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24k serine proteinase (EC 3.4.21.-) (Fragment)
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57.1%;
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                                                                                                                                                                                                                          4; Conservative
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Best Local Similarity
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    subfamily
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SEQUENCE
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Thromb. Res. 70:471-481(1993).
-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=93369790; PubMed=8362372; DOI=10.1016/0049-3848(93)90089-7; Yuan Y., Jackson S.P., Mitchell C.A., Salem H.H.; "Purification and characterisation of a snake venom phospholipase A2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE=93351194; PubMed=8348590;
Bogerd J., Van Kesteren R.E., Van Heerikhuizen H., Geraerts W.P.,
Bogerd J., Van Kesteren R.E., Van Heerikhuizen H., Geraerts W.P.,
Veendtra J., Smit A.B., Joosse J.;
"Alternative splicing generates diversity of VDI/RPD2 alpha peptides
in the central nervous system of Lymnaea stagnalis.";
Cell. Mol. Neurobiol. 13:123-136(1993).
EMBL; S65072; AAB27754.1; -.
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    Gaps
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Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Lymnaeoidea; Lymnaeidae; Lymnaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Elepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophilnae; Austrelaps.
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Pred. No. 4.5e+03;
0; Mismatches 1; Indels
  Indels
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                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VD1/RD2 alpha peptide (Fragment).
Name=VD1/RPD2 alpha peptide;
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  Mismatches
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3, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6523;
                                           CHIHH 4
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Q26322;
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Matches
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SEQUENCE FROM N.A.
MEDLINE=21265430; PubMed=11371582;
Liu J.C., Makova K.D., Adkins R.M., Gibson S., Li W.H.;
Liu J.C., Makova K.D., Adkins R.M., Gibson S., Li W.H.;
"Episodic evolution of growth hormone in primates and emergence of the species specificity of human growth hormone receptor.";
Mol. Biol. Evol. 18:945-953(2001).
                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 16, Last annotation update)
Growth hormone receptor (Fragment)
Papio cynocephalus (Yellow baboon).
Pakaryotes Metazoa; Chordates, Craniata, Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecinae; Papio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 2; Length 20;
Pred. No. 5.7e+03;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Deng X., Yang Y., Liu W.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF416916; AAL14562.1; -.
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20 AA; 2339 MW; 3FC9F94636B38BE7 CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity 33.3%;
Matches 3; Conservative
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9 ILRVFSSDFP 18
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Name=TYR;
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4 STGQFPRVC 12
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NCBL_TaxID=9031;
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"Comparative study of protein profiles on pathogenic and nonpathogenic Naegleria species by 2D-PAGE.";
J. Eukaryot. Microbiol. 0.0-0(2004).
-!- MISCELLANBOUS: On the 2D-gel the determined pI of this protein is:
7.2, its MW is: 92.4 kDa.
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NCBI_TaxID=5763;
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Sukaryota: Pungi, Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Tricholomataceae; Tricholoma.
NCBL_TaxID=40145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of the insertion sites of marY1, the gypsy-type retrotransposon from the ectomycorrhizal basidiomycete Tricholoma matsutake strain Y1, in the genome the fungus based on the inter-retrotransposon amplified polymorphism analysis."; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AB160895; BAD32671.1; ...
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                      Length 19;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Fragment)
                    21.9%; Score 25; DB 2; 1
75.0%; Pred. No. 5.4e+03;
                                                                                                                                                                                                                                                                                                      25-OCT-2004 (Rel. 45, Created)
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Unknown protein NF019 from 2D-PAGE (Fragment).
Naegleria fowleri.
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Query Match
Best Local Similarity 75.ur
and 3; Conservative
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Period 4; Conservative
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8 SRVVKFSIDE 17
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Omura M., Fur
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P83899;
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protein search, using sw model OM protein -

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US-10-717-243-56 Title:

114 1 CHHHASRVARMASDEFPSMC 20 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 seqs, 386760381 residues Searched:

716780 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

genese@2000s:* genese@2001s:* genese@2002s:* genese@2003as:* genese@2003bs:* genese@2004s:* geneseqp1980s:* geneseqp1990s:* 4.0.02

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		sh	ij	11	ţ;	Ö	ic	H	EG	2	en	ge	Ju 1	당	Q	e)	ø	ΕĞ	Ð	(8)	ā	2	Ħ	<b>n</b>	3	#
	· uo	E.coli sh	P. aerugi	Salmonel	D. immit	Peptide	Parasitic	MTN-13/I	KDR & VEG	Cyclic KD	Immunogen	Self-asse	Green flu	Escheric	His tag	Protein	Peptide e	KDR & V	Cyclic	Poly (His)	Sequence	Peptide	Peptide	Peptide	Peptide	Peptide
	Description	Aar37300	Abr82617	Adn61592	Aay88253	Aab08745	Adj87174	Add29094	Adk40590	Adr40808	Aay47525	Abp59407	Adm78554	Aae08870	Aau77664	Aab13448	Aag83124	Adk40464	Adr40682	Aay83783	Aay28952	Aaw88019	Aaw88022	Aaw88020	Aaw88023	Aab73340
	QI	AAR37300	ABR82617	ADN61592	AAY88253	AAB08745	ADJ87174	ADD29094	ADK40590	ADR40808	AAY47525	ABP59407	ADM78554	AAE08870	AAU77664	AAB13448	AAG83124	ADK40464	ADR40682	AAY83783	AAY28952	AAW88019	AAW88022	AAW88020	AAW88023	AAB73340
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	Score	114	45	38	36	36	36	36	36	36	32	35	34	34	34	34	34	34	34	34	33	. 33	33	33	33	33
Result	No.	-	8	c	4	ß	9	7	Φ	თ	10	11	12	13	14	15	16	17	18	. 19	20	21	22	23	24	25

Adro6001 Labelling Aab20206 Histidine Abb64370 L19/HyHEL Adr9009B Bacteriop Aab20300 Histidine Adr90092 Bacteriop Adb8991 Pluoresce Adv35319 Antimicro Add4924 Biopannin Aaw61548 Endoprote Aaw09365 N-termina Abg67008 Streptavi Abd57008 Streptavi Abd57084 Streptavi Abd57084 Streptavi Abd57084 Streptavi Abd57084 Streptavi Abd57084 Streptavi Abd57084 Streptavi Add34592 AKT subst Abd59184 Human gen Aar41770 Specific Aar41770 Specific Adr0559 Novel ssp	Adr90500 H. longic
## ADROGOO1  ### AAB20296  ### AAB20296  ### AAB20300  ### AAB20300  ### AAB20300  ### AAB20319  ### AAB20319  ### AAB20319  ### AAB20319  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20345  ### AAB20334  ### AAB20334	8 ADR90500
2 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	28.1 15
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	45 32

## ALIGNMENTS

AAR37300 standard; protein; 20 AA. AAR37300; RESULT 1 AAR37300

(revised)
(first entry) 25-MAR-2003 13-SEP-1993

E.coli shiga-like toxin segment.

Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; human engineered antibody; variable region; light chain; cell targetting; chimeric antibody; SLT.

Escherichia coli

 .20 /note= "intervening loop includes protease sensitive amino acid sequence" Location/Qualifiers 92WO-US009487 Key Disulfide-bond 04-NOV-1992; WO9309130-A1 13-MAY-1993. 

91US-00787567. 92US-00901707. 04-NOV-1991; 19-JUN-1992;

(XOMA ) XOMA CORP.

SP; Lei Lane JA, Carroll SF, Better MD, Berhard SL,

WPI; 1993-167617/20.

Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.

Example 10; Page 114; 163pp; English.

The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules are antibodies or their fragments, esp. human engineered H65 antibody

ABR82616-17 represent fluorescent labelled peptide substrates used to detect the presence of P. aeruginosa using a protease assay

initiated early enough to prevent more serious infection. Sequences

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Gaps

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Length 19

Score 45; DB 7 Pred. No. 2.1; 2; Mismatches

39.5%; 53.8%;

Similarity 53.8 7; Conservative

Query Match Best Local S

Matches

Sequence 19 AA;

88888

CHHHASRVARMAS 13

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                               sequence gelonin gene fused to an H65 truncated heavy chain gene or an H65 Light chain (kappa) gene. A DNA linker encoding a peptide segment of the E.coli shiga-like toxin was inserted between the gelonin gene and the Ab gene. The resulting immunoconjugates can be used as cytotoxic therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microorganism detection; antimicrobial therapy; DNA metabolism; protease;
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
   Fusion constructs were assembled that included a natural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P. aeruginosa detecting papal modified peptide substrate papa3.
                                                                                                                                                                                                                                                                                                       Length 20;
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                                                                                                                                                                                                                                                                                                100.0%; Score 114; DB 2;
100.0%; Pred. No. 4.7e-12;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 15; Page 48; 84pp; English.
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28-MAY-2002; 2002US-0383847P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                     Sequence 20 AA;
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      fragments.
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Novel isolated mitogen activated protein kinase activated protein kinase polypeptides, useful as therapeutic agents in treating inflammatory based diseases.
                                                                                                                                                                                               mitogen activated protein kinase activated protein kinase 2;
MAP kinase activated protein kinase 2; MK2; drug design; crystallography;
inflammatory disease; antiinflammatory; LSP-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the crystal structures of human mitogen activated protein (MAP) kinase activated protein kinase 2 (MKZ), and the use of these structures in drug design. Also disclosed are the polymucleotide sequence encoding MKZ, a vector comprising the polymucleotide, a transformed host cell transfected or infected with the vector, and a method of producing crystallised MKZ. The crystallised MKZ is useful as a therapeutic agent in treating inflammatory based diseases. The present sequence represents Salmonella typhosa LSP-1 peptide. The peptide is used in the kinetic analysis of MKZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Svenson K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 8; Length 16; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mosyak L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID NO 10; 272pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Underwood KW, Stahl ML,
                                                                        ADN61592 standard; peptide; 16 AA.
                                                                                                                                                         Salmonella typhosa LSP-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.3%;
                                                                                                                                                                                                                                                                                                                                           13-NOV-2002; 2002US-00294027.
                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2002; 2002US-00294027.
                                                                                                                             (first entry)
CHHHASXAAHKSA 13
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UNDERWOOD K V
STAHL M L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-410434/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MOSYAK L.
SVENSON K.
SHANE T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                   Crystal structure;
                                                                                                                                                                                                                                                                                     US2004091872-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16 AA;
                                                                                                                                                                                                                                                          Salmonella sp
                                                                                                                             29-JUL-2004
                                                                                                                                                                                                                                                                                                                 13-MAY-2004.
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Taylor ML;
                                                                                                    ADN61592;
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(STAH/)
(MOSY/)
(SVEN/)
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(TAYL/)
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                                            RESULT 3
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1 MAQDAFPNAC 10
              11 MASDEFPSMC 20
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORTION GENETIES A HOVEL INCIDENCE DETABLISHED THE MILITION GENETIES A HOVEL INCIDENCE OF TOWN (I) (I) (I) is selected from: (a) a NAM comprising a sequence selected from cDNA sequences of Dirofilaria immitis: nDiPLA2-857; onchocerca colvulus: nDVPLA2-450, nDIPLA2-857 and nOVPLA2-557; onchocerca volvulus: nOVPLA2-420, nDVPLA2-154, and nOVPLA2-65 and BENGIA malayi: nBmPLA2(19)-242, nBmPLA2(19)-163, nBmPLA2(25)-255 and nBmPLA2(25)-163; nBmPLA2(19)-242, nBmPLA2(19)-163, nBmPLA2(25)-255 and nBmPLA2(25)-163; nBmPLA2(25)-255 and nBmPLA2(25)-163; nBmPLA2(19)-242, nBmPLA2(19)-163, nBmPLA2(25)-255 and nBmPLA2(25)-163; nBmPLA2(19)-257 encoding a protein comprising at least 15 contiguous Amino acids (aa) that elicits an immune that has at least 5 contiguous amino acids (aa) that elicits an immune tresponse against a protein comprising as sequence selected from the PLA2 proteins (c) a NAM that is complementary to (a) or (b). The products of the invention have antihelminthic activity and can be used in vaccines.

(I) is useful for protecting the animals from diseases caused by parasitic helminth, for preventing the spread of onchocerciasis, heartworm and/or filariasis by administering it to vectors such as mosquitoes, in which the parasitic helminth infections. This sequence reagents for detecting parasitic helminth infections. This sequence represents a Dirofilaria immitis P22U protein tryptic fragment
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New parasitic helminth phospholipase A2-like nucleic acid molecule for protecting animals from diseases caused by parasitic helminth, preventing the spread of onchocerciasis, heartworm and/or filariasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes a novel isolated parasitic helminth nucleic acid
                                                                                                                                                                                                                    PLA2; parasitic helminth, phospholipase A2; antihelminthic; detection; onchocerciasis; heartworm; filariasis; mosquito; diagnostic; vaccine.
  Gaps
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  Indels
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Mismatches
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                                                                                                                                                                                             D. immitis P22U tryptic fragment #1.
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                                                                                                               AAY88253 standard; protein; 16 AA.
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93US-00101283.
94WO-US000679.
94US-00225479.
95US-00408120.
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                                                                                                                                                                  (first entry)
                         7 RVARMASDEFPSM 19
                                        ::|| || || || 4 KLARQASIELPSM 16
 Conservative
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                                                                                                                                                                                                                                                           Dirofilaria immitis.
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                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                12-FEB-1991;
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20-MAR-1995;
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Gaps

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31.6%; Score 36; DB 3; Length 16; 60.0%; Pred. No. 59; 1, Mismatches 3; Indels

Conservative

Query Match Best Local Similarity Matches 6; Conserv

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parasitic helminth phospholipase A2-like proteins useful, for treating or preventing diseases e.g. onchocerciasis, filariasis caused by a parasitic helminth in animals such as dogs, cats, humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AABO8745-61 represent peptides derived from a parasitic helminth phospholipase A2-like protein (PLA2), designated PDiPLA2-150. The enzyme catalyses the hydrolysis of the 2-acyl ester group of sn.3-glycerophospholipids. The polypeptide has a role in lipid metabolism, membrane synthesis, and parasite remodelling and migration. The PLA2 polypeptides are useful for identifying inhibitors. They are also useful for treating or preventing diseases such as onchocerciasis, filariasis caused by a parasitic helminth in animals preferably dogs, cats, humans, ferrets, horses, cattle, sheep, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                       Peptide derived from a helminth phospholipase A2-like protein (PLA2)
                                                                                                                                                                                                          Helminth; phospholipase A2-like protein; PLA2; membrane synthesis; sn-3-glycerophospholipid; lipid metabolism; parasite remodelling; parasite migration; onchocerciasis; filariasis.
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Pred. No. 59;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grieve RB;
AAB08745 standard; peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Col 40; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00654226.
93US-00003257.
93US-00003389.
93US-00101283.
93US-00109391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-US000679.
94US-00225479.
95US-00408120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00483474.
                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wisnewski N, Frank GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 MASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAQDAFPNAC 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-531655/48.
                                                                                                                                                                                                                                                                                                                 Dirofilaria immitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLS ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                         02-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                       US6099843-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                          08-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L2-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-APR-1994
                                                      AAB08745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
ADJ87174
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recombinatorial phage display library.

#O2003074678-A2

Synthetic

12-SEP-2003

01-MAR-2002; 2002US-0361121P. 03-MAR-2003; 2003WO-US006582.

(DYAX-) DYAX CORP.

Ladner RC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition useful for preventing parasitic helminth infection, comprises an excipient and a nucleic acid encoding a protein that binds to immune serum isolated from an animal that is immune to infection by Dirofilaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to parasitic helminth phospholipase A2-like (PLA2) proteins and the nucleic acids encoding them. The invention includes a method for identifying a compound that is capable of inhibiting phospholipase A2 activity of a parasitic helminth, comprising contacting an isolated parasitic helminth PLA2 protein with a putative inhibitory compound under conditions in which, in the absence of the compound, the protein has phospholipase A2 activity and determining if the putative inhibitory compound inhibits the phospholipase A2 activity The composition is useful for protecting an animal from infection caused by a parasitic helminth such as Dirofilaria immitis. This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                       Parasitic helminth; phospholipase A2; PLA2; parasitic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.6%; Score 36; DB 8; Length 16; 60.0%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                         Parasitic helminth PLA-2 related peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a PLA2 related peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 21; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    (COLS ) UNIV COLORADO STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                Frank GR, Wisnewski N;
ADJ87174 standard; peptide; 16 AA
                                                                                                                                                                                                                                                            99US-00391270.
                                                                                                                                                                                                                                                                                           91US-00654226
                                                                                                                                                                                                                                                                                                       93US-00003257
                                                                                                                                                                                                                                                                                                                                                    95US-00482304
                                                                                                                                                                                                                                                                                                                                       95US-00408120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.08;
                                                          06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAQDAFPNAC 10
                                                                                                                                       antiparasitic; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-068618/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    (HESK-) HESKA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16 AA;
                                                                                                                                                                                                  US6673916-B1
                                                                                                                                                                                                                                                            07-SEP-1999;
                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                                                                                           12-FEB-1991;
                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                         12-JAN-1993;
03-AUG-1993;
                                                                                                                                                                                                                              06-JAN-2004
                                                                                                                                                                                                                                                                                                                                       20-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                               Grieve RB,
                              ADJ87174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
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The present invention describes a library of display vectors comprising a plurality of DNA molecules that comprise a general structure: R1-Z-R2, plurality of DNA molecules that comprise a general structure: R1-Z-R2, where R1 and R2 is a constant region that includes a cleavage site for a restriction endonuclease. Also described: (1) obtaining a binding peptide, comprising: (a) selecting for plage in the above library, where a displayed peptide binds to a target of interest; (b) obtaining RF DNA for the selected phage; (c) cleaving the library RF DNA tragments for the selected RF DNA tragments; (e) cligating the mixed fragments; (e) ligating the mixed fragments; (f) introducing the ligated fragments into cells, such that phage displaying a new library are produced; and (g) cobtaining the binding peptide, (2) producing a modular phage display cobtaining the binding peptide; (2) producing a modular phage display library. The methods are useful for obtaining a recombinatorial phage display a modular phage display library, and producing a recombinatorial phage display containing a pinding peptide, producing a modular phage display library, and producing a recombinatorial phage display containing a pinding peptide, producing a modular phage display library. The library of display vectors is useful in isolating binding percent for a target molecule. The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDR & VEGF/KDR complex binding peptide of an MTN13 peptide library ID241.
                                                                                                                                                                                                                                                                                                                                                                   늉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endothelial cell; vacular endothelial growth factor; VEGF; receptor tyrosine kinase; VEGF-2; kinase domain region; KDR; foetal liver kinase-1; flk-1; VEGF/KDR complex; angiogenesis; neoplastic tumnour; radiotherapeutic; malaria; HIV; SIV infection; simian haemorrhagic fever virus; enterchaemorragic Escherichia coli infection; protozoacidal; anti-HIV; virucidal; antibacterial; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                 New modular recombinatorial display libraries comprising a plurality (
DNA molecules, useful for isolating binding polypeptides for a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.6%; Score 36; DB 7; Length 19; 83.3%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 71;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 29; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADK40590 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
Best Local Similarity 83.33,
Best Local Similarity 63.33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                         WPI; 2003-779023/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CHHHAS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHHHIS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                             nolecule
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display vector library; binding peptide; modular phage display library;

MTN-13/I KDR binding peptide SEQ ID NO:29.

15-JAN-2004 (first entry)

ADD29094
ID ADD;
XX
AC ADD;
XX
DT 15-0
XX
XX
XX
AX
AX
AX
A161

ADD29094;

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ADD29094 standard; peptide; 19

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This invention relates to novel peptides useful for detecting and targeting primary receptors on endothelial cells that bind vacular endothelial growth factor (VEGF). Specifically, it refers to detecting the receptor tyrosine kinase identified as VEGF-2, which is also kown as kinase domain region (KDR) and foetal liver kinase-1 (flk-1). The present invention describes the involvement of the VEGF/KDR complex as important in angiogenesis, and that VEGF/KDR complex binding polypeptides can be used for imaging neoplastic tumours. Purthermore, these compositions are useful for targeting radiotherapeutics to specific sites for treating diseases associated with KDR activation, which include malaria, HIV, SIV infection, simian haemorrhagic fever virus and enterohaemorragic Escherichia activities including protozzacidal, anti-
                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide that binds to vascular endothelial growth factor receptor -2, useful for diagnosis and treatment of e.g. tumors, and its conjugates with therapeutic or imaging agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyclic KDR/ VEGF binding peptide of the secondary MTN13 library Seq 241.
                                                                                                                                                                                                                                                           Sato AK, Sexton DJ, Ladner RC, Dransfield DT, Swenson RE;
Marinelli ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A;
Pochon S, Bussat P, Arbogast C, Pillai R, Fan H, Linder KE, Song
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virucidal, antibacterial and cytostatic. This peptide sequence is affinity binding peptide of KDR and the VEGF/KDR complex, part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase domain region; KDR; vascular endothelial growth factor; VEGF; VEGF receptor 2; VEGFR2; foetal liver kinase 1; flk-1; angiogenesis; neoplastic tumour; malaria; HIV infection; SIV infection; similan haemorrhagic fever virus infection; enterohaemorrhagic Escherichia coli infection; cytostatic; antiangiogenic; antimalarial; anti-HIV; virucidal; antibacterial; MTN13 library; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 7; Length 19;
Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the MTN13 peptide library of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 79; SEQ ID NO 241; 350pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR40808 standard; peptide; 19 AA.
                                                                                                           03-MAR-2003; 2003WO-US006731
                                                                                                                                              01-MAR-2002; 2002US-0360851P.
15-JAN-2003; 2003US-0440411P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                                    (DYAX-) DYAX CORP.
(BRAC ) BRACCO INT BV.
                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-779009/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3est_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHIHHAS 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHHHIS 9
                                     WO2003074005-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                  Nanjappan P;
                                                                        12-SEP-2003
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR40808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Kinase domain region (KDR) to vascular endothelial growth factor
(VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide
climers and multimeric complexee that bind with high affinity to KDR (also
known as the VEGF receptor 2 (VEGFR2) and detail liver kinase 1 (flk.1))
or the VEGF/KDR complex, and as such due to the involvement of VEGF and
CC KDR in angiogenesis these binding peptides can be used for imaging
important sites of angiogenesis, as well as in targeting therapeutics to
such sites. The present invention describes these peptides as useful for
promoting or inhibiting angiogenesis and pathogenic conditions associated
thereof such as neoplastic tunours. Furthermore, these binding peptides
are useful for treating malaria, HIV infection, SIV infection, simian
hadmorrhagic fever virus infection and enterohaemorrhagic Escherichia
coli infection. Accordingly, they exhibit cytostatic, antiangiogenic,
antimalarial, anti-HIV, virucidal and antibacterial activities. In
particular, they inhibit VEGF activation of its receptor (i.e. KDR), and
enable efficient detection, imaging and localisation of activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated polypeptide having ability to bind to kinase domain region or vascular endothelial growth factor/kinase domain region complex, useful in inhibiting vascular endothelial growth factor activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic peptide having a human leukocyte antigen binding motif #2136.
                                                                                                                                                                                                                                                                                                                                                      Sato AK, Sexton DJ, Dransfield DT, Ladner RC, Arbogast C;
Bussat P, Fan H, Khurana S, Linder KE, Marinelli ER, Nanjappan P;
Nunn A, Pillai R, Pochon S, Ramalingam K, Shrivastava A, Song B;
Swenson RE, Von Wronski MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial cells exhibiting upregulated KDR expression. This peptide sequence is a high affinity KDR and VEGE/KDR cyclic binding peptide belonging to the secondary MTN13 library of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel isolated peptides that can bind to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.6%; Score 36; DB 8; Length 19; 83.3%; Pred. No. 71; cive 0; Mismatches. 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 241; 470pp; English.
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY47525 standard; peptide; 14 AA.
                                                                                                                                                                                                                  15-JAN-2003; 2003US-0440411P.
                                                                                                                                                                                                                                  03-MAR-2003; 2003US-00382082.
03-MAR-2003; 2003WO-US006731.
                                                                                                                                                                         11-SEP-2003; 2003WO-US028787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                         Key
Disulfide-bond 4..16
                                                                                                                                                                                                                                                                                                                 (BRAC ) BRACCO INT BV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinase domain region
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-580734/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                              (DYAX-) DYAX CORP
                                                                                              WO2004065621-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CHHHAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-1999
                                                                                                                                      05-AUG-2004.
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY47525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
AAY47525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
BXXXXX
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having a human major histocompatibility complex (MHC) Class I (also known as human newlocyte antigen (HLA)) binding motif. The immunogenic peptides as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allale (i.e. HLA-A subtypes HLA-A-I, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T ceal response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in therefore useful therapoutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to licit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytocoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above
                                                                                                                                                                                                                                                                                                                                                                                                                                               New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to AAY48214 represent specifically claimed immunogenic peptides
                 Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AlDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Self-assembling oligopeptide; dipolar; nanotube; nanostructure; drug delivery; carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 2; Length 14;
Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                          Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Self-assembling di-block oligopeptide AH20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Celis E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 113; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP59407 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                          Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.7%;
                                                                                                                                                                                                                                                           98WO-US005039.
                                                                                                                                                                                                                                                                                               98WO-US005039
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                                                                                            vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                    (BPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-551214/46.
                                                                                                                                                                                                                                                                                                                                                                        Sette A, Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14 AA;
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                           13-MAR-1998;
                                                                                                                                                                                  W09945954-A1
                                                                                                                                                                                                                                                                                               13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2003
                                                                                                                                                                                                                      16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9:
                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP59407;
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The present invention relates to self-assembling dipolar oligopeptides and di-and tri-block peptide copolymers. The dipolar oligopeptides have and di-and tri-block peptide copolymers. The dipolar oligopeptides have ability to self assemble to form stabble ananotubes. The self-assembled nanostructure have the ability to entrap and deliver molecular systematic design, modification and synthesis, can be subjected to extensive molecular modelling and simulations before synthesis; can be highly purified to be mono-dispersed macreials; combinatorial approach can be employed to systematically characterize these co-polymers at various ratio, and can be synthesized in vitro or in vivo. The nanotubes fuse with the lipid bilayers and do not deform the cells as liposomes do. The oligopeptides can be used in a self-assembled nanostructue (e.g. nanotube) for delivering drug into a cell and as a carrier for biologically active materials. The present sequence is one such di-block oligopeptide
                                                                                                                                                                                                                                                                  New dipolar oligopeptides in a self-assembled nanostructure useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.7%; Score 35; DB 6; Length 20; 50.0%; Pred. No. 1.1e+02; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fluorescence; Aequorea green fluorescent protein; GFP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Green fluorescent protein phosphorylation motif #36.
                                                                                                                                                                      (MASI ) MASSACHUSETTS INST TECHNOLOGY
                                                                                                                                                                                                                                                                                                               Claim 17; Page 21; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM78554 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AURO-) AURORA BIOSCIENCES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-00129192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-2002; 2002US-00293580.
                                                                                                          10-JUL-2002; 2002WO-US021757.
                                                                                                                                       10-JUL-2001; 2001US-0304256P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Best Local Similarity 50.0°
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 HHHASRVARMAS 13
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                                                                                                                                                                                                    Zhang S, Vauthey S;
                                                                                                                                                                                                                                 WPI; 2003-267944/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003170767-A1.
                                             WO2003006043-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 AA;
                                                                                                                                                                                                                                                                                drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-2003.
                                                                           23-JAN-2003
                Synthetic.
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Gaps

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Disclosure; SEQ ID NO 51; 52pp; English
                                                                                                                                                                                    AAE08870 standard; peptide; 15 AA.
                                                                                                                                        29.8%;
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                                                                                                                                                                                                    15-NOV-2001 · (first entry)
                                                                                                                                                6; Conservative
                                                                                                                                                        2 HHHASRVAR 10
                                                                                                                                                                σ
       WPI; 2003-863757/80.
                                                                                                                                            Local Similarity
                                                                                                                                                                1 HHHRSRPKR
                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                           WO200157065-A2.
                                                                                                                                 Sequence 9 AA;
                                                                                                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                            AAE08870;
                                                                                                                                         Query Match
                                                                                                                                                 Matches
                                                                                                                                                                             RESULT 13
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03-FEB-2000; 2000GB-00002492. 04-FEB-2000; 2000US-0180326P. 03-UJU-2000; 2000GB-0016346. 07-ANG-2000; 2000GB-0019362.

(DIVE-) DIVERSYS LTD

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The invention relates to a chimeric folded protein domain derived from a repertoire of chimeric proteins. The chimeric protein comprises two or more sequence segments derived from parent amino acid sequence that are non-homologous. The chimeric protein is useful in vaccination against one or more of the amino acid sequences from which the chimera is derived, for administration to a human for therapeutic purposes, and for use in a commercial product to which humans are exposed. The chimeric protein is useful as improved enzyme inhibitors, and to avoid sensitisation in thumans (for e.g. enzymes and washing powders). The present sequence is N-terminal His-tag peptide sequence of Escherichia coli cold shock protein (CspA) used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel chimeric folded protein domain, useful in vaccination, is derived from a repertoire of chimeric proteins and comprises two or more sequence segments derived from parent non-homologous sequences.
                                                                                                  Chimeric folded protein domain derived from repertoire of chimeric proteins useful therapeutically, comprises two or more sequence segments derived from parent amino acid sequence that are non-homologous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a chimaeric folded protein domain, when derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from a repertoire of chimaeric proteins comprises two or more sequence segments derived from parent amino acid sequences that are non-homologous. Also included are nucleic acids encoding the chimaeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CspA; chimaeric folded protein domain; His tag; cold shock protein; vaccine; asthma; proteolysis resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 4; Length 15;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                             Example 16; Page 49; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 14; Page 63; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU77664 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2001; 2001WO-GB003508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2000; 2000GB-00019362.
02-FEB-2001; 2001GB-00002678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIVE-) DIVERSYS LTD.
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                                                  WPI; 2001-529779/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHHGSRL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 HHHASRV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   His tag peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200212277-A2.
Riechmann L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU77664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU77664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                         activity, comprising a fluorescent protein moiety and at least one exogenous substrate recognition motif for an activity, where the exogenous substrate recognition motif for an activity, where the fluorescent protein moiety and where the fluorescent protein moiety and where the fluorescent compound state in response to the activity, and where the fluorescent compound exhibits a different fluorescent property in the two states under comparing conditions. The activity is an enzymatic activity, preferably a kinase, phosphatase, proteins, glycosplation or farmaser transferase activity. The fluorescent protein moiety comprises an Aequorea-related fluorescent protein preferably comprising the mutations in GFP mutant K8, where at least one substrate recognition motif for an activity is within the first 20, more preferably the first 10 amino acids of the amino the first 20, more preferably the first 10 amino acids of the amino condition is acid quenching. The moiety preferably comprises a poly-lys region and a protein-protein interaction domain and is membrane bound. The quenching condition accomplision motif for a serine/threomine specific protein kinase, protein kinase A, protein kinase I or II or MAP kinase activated protein kinase. The protein kinase activated protein kinase. The protein kinase activated protein kinase. The present sequence represents a phosphorylation compound is used to detect enzymatic activities in biological samples. The present sequence represents a phosphorylation compound of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                               A fluorescent compound comprising a fluorescent protein moiety and a ubstrate recognition motif for an activity, which exhibits a change in fluorescence in response to the activity, used to detect enzyme activity in biological samples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli cold shock protein (CspA) N-terminal His-tag peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                           invention relates to a fluorescent compound for detecting an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric folded protein, vaccine; therapeutic; enzyme inhibitor; washing powder; cold shock protein; CspA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 7; 1
Pred. No. 1.8e+06;
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Gaps

proteins encoded by the nucleic acid sequences. The encoded proteins comprise an immunogenic portion of a Chlamydia antigen. The encoded proteins are useful for the serodiagnosis and treatment of Chlamydia infection. Chlamdiae are intracellular bacterial pathogens that are responsible for a wide variety of human infections. C. trachomatis infection is one of the most common sexually transmitted diseases and can infection is one of the most common sexually transmitted diseases.

lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. Trachoma due to ocular infection with C. trachomatis is the leading cause of preventable blindness worldwide. C. pneumonia is a major cause of acute respiratory tract infections in humans and is a laso thought to play a role in the pathogenesis of atherosclerosis and coronary heart disease. The present sequence is a protein isolated in the present invention

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proteins His-2f3 and His-1c2 were used for immunisation of a rabbit to analyse, if resulting antisera from the immunisation of a rabbit to crossreactive with CspA. The animals were then challenged with an injection of folded cold shock protein (CspA) to see if a specific anticaph incommunisation of a manalyses of the rabbit immune response involving T cell mediated help was established during immunisation. The analyses of the rabbit immune response showed, that immunisation with both 2f3 and 1c2 raised antisera highly reactive with their respective antigen as they bound phage displaying the chimaeric proteins strongly after the second, third and fourth vaccination. Crossreactivity with CspA was observed. The protein domain is useful in vaccination against parent proteins from which the chimaera is derived, for administration to a human for therapeutic purposes and for use in commercial product to which humans are exposed. The protein domains are useful for treating asthma and in immunisation. The chimaeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protease enzymes and is not immunogenic or weakly immunogenic, and hence suitable for therapeutic purposes and to avoid sensitisation in humans. The present sequence is a His tag which is added to chimaeric proteins of the invention to aid protein purifaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     folded protein domain is resistant to in vivo or in vitro proteolysis by
   protein domains and a method of producing the protein domains. Chimaeric
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                       Gaps
                       ;
Score 34; DB 5; Length 15;
Pred. No. 1.2e+02;
1; Mismatches 1; Indels
 29.8%;
                       Conservative
          Local Similarity
Query Match
Best Local S
Matches 5
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HHHGSRL 14 HHHASRV 8 N ω g ઠે

Protein encoded by C. trachomatis clone 3-G3-10. AAB13448 standard; peptide; 18 AA. (first entry) 02-FEB-2001 AAB13448; RESULT 15 AAB13448

LID AAB1

AAC AAB1

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Chlamydial infection; sexually transmitted disease; pelvic inflammatory disease; PID; tubal obstruction; infertility; trachoma; blindness; acute respiratory tract infection; atherosclerosis; coronary heart disease; antibacterial.

Chlamydia trachomatis.

WO200034483-A2

15-JUN-2000.

99WO-US029012. 08-DEC-1999; 08-DEC-1998;

98US-00208277. 99US-00288594. 99US-00410568. 99US-00426571. 01-OCT-1999;

(CORI-) CORIXA CORP.

Jen S, Fling SP, Skeiky YAW, Probst P, Bhatia A, WPI; 2000-431303/37.

Stromberg EJ

Example 1; Page 114; 256pp; English

Isolated polypeptide for diagnosis and treatment of Chlamydia infection comprises immunogenic portion of Chlamydia antigen, which comprises amino acid sequence encoded by polynucleotide sequence.

The present invention relates to new nucleic acid sequences and the

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Pred. No. 1.5e+02;
0; Mismatches 8;
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Job time : 64.5 sece
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Best Local Similarity
7; Conserve
                                                                                                             Sequence 18 AA;
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Scoring table:

Searched:

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Perfect score:

Sequence:

OM protein

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Sequence 4, Appli
Sequence 8, Appli
Sequence 5, Appli
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Sequence 32, Appli
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Sequence 26, Appl
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Sequence 26, Appl
Sequence 377, App
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Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTER ILLINGS
COUNTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPAtible

COMPUTER: IBM PC COMPATIBLE

COMPUTER: PATENT PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
; US-10-342-331-11

7 US-10-58-752-12

1 US-10-743-649-4

5 US-10-743-649-8

5 US-10-743-649-8

6 US-10-743-649-8

1 US-10-743-649-8

1 US-10-743-649-8

1 US-10-155-419-5

1 US-10-104-381-32

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2 US-10-808-131-24

2 US-10-808-131-24

2 US-10-808-131-31

3 US-10-808-131-31

4 US-10-808-133-172-16

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PPPLICATION NUMBER: US/08/646,360
PPLING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
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APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
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Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 173
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           Sequence 56, Appl
Sequence 16, Appl
Sequence 29, Appl
Sequence 241, App
Sequence 51, Appl
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                                                                                                                                                                                             June 20, 2005, 10:46:29; Search time 104 Seconds (without alignments) 73.842 Million cell updates/sec
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| cgn2 6/ptodata 2/pubpaa | PCT NEW PUB.ppp:*
| cgn2 6/ptodata 2/pubpaa | USO6 NEW PUB.ppp:*
| cgn2 6/ptodata 2/pubpaa | USO7 NEW PUB.ppp:*
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-717-243-56
US-10-294-027-10
US-10-378-557-29
US-10-661-156-241
US-10-1293-832-53
US-10-293-841-132-8
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US-10-661-156-115
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Maximum Match 100%
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Result Š.

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i. Sequence 29, Application US/10378557
i. Publication No. US20030186223A1
i. GENERAL INFORMATION:
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; Sequence 10, Application US/10294027
; Publication No. US20040091872A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CHHHASRVARMASDEFPSMC 20
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| NAME/KES: MISC FEATURE
| OTHER INFORMATION: LSP-1 peptide
US-10-294-027-10
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ORGANISM: Salmonella typhosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 KLARQASIELPSM 16
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                                                                                                                                                                                                                                                                                                                                                                    Local Similaricy
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Best Local Similarity
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Matches
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Sequence 56, Application US/005054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Srephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
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100.0%; Score 114; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.2e-11;
Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-00v-2003
CLASSIFICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-AAY-1993
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 03-DEC-1992
APPLICATION NUMBER: US 07/901,707
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MCANDTews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
                  FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCANICATION:
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8189
TELEFAX: 312/707-8189
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                             | LENGTH: 20 amino acids | TYPE: amino acids | TYPE: amino acid | TOPUCOY: linear | MOLECULE TYPE: peptide | SEQUENCE DESCRIPTION: SEQ ID NO: 56: US-10-127-890-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CHHHASRVARMASDEFPSMC 20
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                                                                                                                                                                                                                                                                                TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60661
COMPUTER READABLE FORM:
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APPLICANT: Teach, Mark L.
APPLICANT: Stach, Mark L.
APPLICANT: Stach, Mark L.
APPLICANT: Stach, Mark L.
APPLICANT: Shane, Tristine
APPLICANT: Shane, Tania
APPLICANT: Shane, Tania
APPLICANT: Taylor, Meggin L.
TITLE OF INVENTION: CRYSTAL STRUCTURES OF MK2 AND USES THEREOF
FILE REPRENCE: 2366/77
CURRENT FILING DATE: 2003-11-13
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 16
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NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEFAX: 650 388-1248
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TITLE OF INVENTION: MODULAR RECOMBINATORIAL DISPLAY
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 3421.1013-001
CURRENT APPLICATION NUMBER: US.10378,557
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/361,121
                                                                                                                                                                                                                                                                                                                                                                        1 100.0%; Score 114; DB 17;
Similarity 100.0%; Pred. No. 9.2e-11;
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SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acide

TYPE: amino acide

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-10-717-243-56
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Pred. No.
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us-10-717-243-56.closed.rapb

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1 HHHRSRPKR
4 CHHHIS 9
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APPLICANT: Song, BO
APPLICANT: Swenson, Rolf E.
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
TITLE OF INVENTION: Their Use in Diagnosis and Therapy
FILE REPERENCE: D0617-70012030
CURRENT APPLICATION NUMBER: US/10/661,156
CURRENT FILING DATE: 2003-03-13
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR PILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-03
PRIOR FILING DATE: 2003-03-15
PRIOR FILING DATE: 2003-01-15
NUMBER OF SEQ ID NOS: 617
SOFTWARE: FESTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.6%; Score 36; DB 17; Length 19; Best Local Similarity 83.3%; Pred. No. 1.3e+02; Matches 5; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                         31.6%; Score 36; DB 14; Length 19; 83.3%; Pred. No. 1.3e+02;
                                                                                                                                                           ; OTHER INFORMATION: Selected library sequence US-10-378-557-29
                                                                                                                                                                                                                                                                  0; Mismatches
            NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 241, Application US/10661156
Publication No. US20050100963A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nunn, Adrian
Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Library Isolate US-10-661-156-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sexton, Daniel J.
Dransfield, Daniel T.
Ladner, Robert C.
Arbogast, Christophe
Bussat, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
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                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                  5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sudha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sato, Aaron K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fan, Hong
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
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LENGTH: 19
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APPLICANT:
APPLICANT:
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Gaps

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CHIHIAS 6

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APPLICANT: Autora Biosciences Corporation
APPLICANT: Autora Biosciences Corporation
APPLICANT: Cubitt, Andrew B.
TITLE OF INVENTION: Fluorescient Sensors of Post-Translational Modifications
FILE REPERENCE: AURO1270 (08366/031001)
CURRENT APPLICATION NUMBER: US/10/293,580
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US/09/129,192
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 74
SEQ THANKE: Patentin version 3.0
SEQ ID NO 51
LENGTH: 9
Sequence 53, Application US/10192832

Esquence 53, Application No. US20030176335A1

Sequence 100. US20030176335A1

GENERAL INFORMATION:

TITLE APPLICANT: VAUTHEY, SYLVAIN

TITLE REPRENCE: MTV-043.01

CURRENT PAPLICATION NUMBER: US/10/192,832

CURRENT FILING DATE: 2002-07-10

PRIOR FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 53

LENGTH: 20
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Pred. No. 2e+02;
2; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-293-580-51; Application US/10293580; Publication No. US20030170767A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 8, Application US/09841132; Patent No. US20020061848A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: cyclin A-CDK2 US-10-293-580-51
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.7%;
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ORGANISM: Artificial sequence
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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US-09-841-132-8
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APPLICANT:
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Publication No. US20040234536A1
SEGRERAL INFORMATION:
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: LOURGES: 210121.469C10
CURRENT APPLICATION NUMBER: US/10/872,155
CURRENT FILING DATE: 2000-07-20
FRIOR PELLING DATE: 2000-07-20
FRIOR PAPLICATION NUMBER: 09/598,419
FRIOR APPLICATION NUMBER: 09/556,877
FRIOR APPLICATION NUMBER: 09/556,877
FRIOR APPLICATION NUMBER: 09/426,571
FRIOR PILING DATE: 1999-12-03
FRIOR PILING DATE: 1999-12-03
FRIOR APPLICATION NUMBER: 09/426,571
FRIOR APPLICATION NUMBER: 09/426,571
FRIOR APPLICATION NUMBER: 09/426,571
FRIOR PILING DATE: 1999-10-01
FRIOR PILING DATE: 1999-10-01
FRIOR FILING DATE: 1999-110-01
FRIOR FILING DATE: 1999-12-03
FRIOR FILING DATE: 1999-12-03
FRIOR FILING DATE: 1999-12-03
FRIOR PILING DATE: 1999-12-03
FRIOR FILING DATE: 1999-12-03
FRIOR PILING DATE: 1999-12-03
                 APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SSCFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
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46.7%; Pred. No. 2.6e+02;
trive 0; Mismatches 8,
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                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Chlamydia trachomatis
US-09-841-132-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 HHASRVARMASDEFP 17
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APPLICANT: Bhatia, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7, Conserve
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RESULT 10 .US-10-661-156-115

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Sequence 12, Application US/09809517A

Facent No. US20020034733A1

GENERAL INFORMATION:
FALL INFORMATION:
FAPPLICANT: Lohning, Cortinna
TITLE OF INVENTION:
FILE REFERENCE: MORPHO/11

CURRENT APPLICATION NUMBER: US/09/809,517A

FILE REFERENCE: MORPHO/11

CURRENT PELING DATE: 1999-07-20

FRIOR PELICATION NUMBER: EP 99114072.4

FRIOR PELICATION NUMBER: EP 00103551.8

FRIOR FILING DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin version 3.0

SEQ ID NO 12

LENGTH: 7
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illarity 50.0%; Pred. No. 2.6e+02;
Conservative 1; Mismatches 4.
Sequence 115, Application US/10661156 Publication No. US20050100963A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pillai, Radhakrishna
Pochon, Sibylle
Ramalingam, Kondareddiar
Shrivastava, Ajay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Library Isolate US-10-661-156-115
                                                                                                                                                                                                                                                                                                   Fan, Hong
Khurana, Sudha
Linder, Karen E.
Marinelli, Edmund R.
Nanjappan, Palaniappa
                                                                                            APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogaek, Christophe
APPLICANT: Bussat, Philippe
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ORGANISM: Artificial Sequence
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                                                                                                                                               ; OTHER INFORMATION: Description of Artificial Sequence: synthetic module WS-10-658-752-12
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                                                                                                                                                                                                                                      Length 7;
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                                                                                                                                                                                                                                 Similarity 100.0%; Score 33; DB 17; 1 Similarity 100.0%; Pred. No. 1.6e+06; 4; Conservative 0; Mismatches 0;
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FILE REFERENCE: 2370-63
CURRENT PEDLICATION NUMBER: US/10/743,649
CURRENT PELING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US/9/964,444
PRIOR FILING DATE: 2000-09-18
PRIOR PELING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 52
SEQ ID NO 4
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Publication No. US20040208849A1
GENERAL INFORMATION:
ITILE OF INVENTION: ONCOLYTIC VIRUS
FILE REFERENCE: 2370-63
CURRENT FILING DATE: 2003-12-22
PRIOR APPLICATION NUMBER: US/09/664,444
PRIOR FILING DATE: 2000-09-18
FRIOR PILING DATE: 1999-09-17
PRIOR FILING DATE: 1999-09-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10743649
Publication No. US20040170607A1
GENERAL INFORMATION:
                                                                  LENGTH: 7
TYPE: PRT
OKGANISM: artificial sequence
FEATURE:
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
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US-10-743-639-4
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APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: Novel methods for displaying (poly) peptides/proteins on bacteriog
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/10/658,752
CURRENT PILING DATE: 2003-09-10
PRIOR FILING DATE: 2001-03-15
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
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APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOWSTRA, JAN B.
APPLICANT: WRITEN, MARC W.T.
APPLICANT: WRITEN, MRC W.T.
APPLICANT: WRITEN, MRC W.T.
APPLICANT: WRITEN, MRC W.T.
APPLICANT: WRITEN, MRC W.T.
APPLICANT: WRITEN, MRC W.T.
APPLICANT: WRITEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE ENTLSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: SILVER HALIDE ENTLSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: PREPARATION THEREOF
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TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION: PREPARATION THEREOF
TITLE OF INVENTION NUMBER: US/03-01-15
PRIOR FILING DATE: 1998-12-23
PRIOR FILING DATE: 1998-12-23
                                              ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-12
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                                                                                                                                        28.9%; Score 33; DB 9; Length 7; 100.0%; Pred. No. 1.6e+06; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/10342331 Publication No. US20030229205A1 GENERAL INFORMATION:
TYPE: PRT ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
                                                                                                                                     Query Match 28.9
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-743-639-4
                                                                                              Query Match 28.9%; Score 33; DB 16; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 4; Conservative 0; Mismatches 0; Indels
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1 CHHH 4
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Search completed: June 20, 2005, 11:15:08 Job time : 105 secs

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LENGTH: 20 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
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US-07-988-430-58
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Sequence 5860, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                 June 22, 2005, 07:01:48; Search time 41 Seconds (without alignments) 36.414 Million cell updates/sec
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'cgn2_6/ptodata1/iaa/5A_COMB.pep:*
'cgn2_6/ptodata1/iaa/5B_COMB.pep:*
'cgn2_6/ptodata1/iaa/6A_COMB.pep:*
'cgn2_6/ptodata1/iaa/6B_COMB.pep:*
'cgn2_6/ptodata1/iaa/BTCOMB.pep:*
'cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata1/iaa/backfiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-328-352-5860
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US-08-425-336-56
US-08-4477-484B-56
US-08-646-360-56
US-08-646-360-56
US-09-136-389-56
US-09-11485-56
US-09-711-485-56
US-09-711-485-56
US-09-711-485-56
US-09-314-477-21
US-08-318-77-21
US-08-318-77-21
US-08-318-77-21
US-08-314-477-21
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US-08-314-477-37
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                             114
1. CHHHASRVARMASDEFPSMC 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                       Run on:
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APPLICANT: Berthard, Susan L.
APPLICANT: Berthard, Stephen F.
APPLICANT: Berthard, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STREET: Street
CUNTRY: USA
                           2, Appli
6, Appli
1, Appli
25, Appl
25, Appl
39, Appl
39, Appl
28104, A
                                                                                                                                                              24440, Ap 3910, Ap 49, App1 35, App1 35, App1 35, App1 35, App1
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                                   US-08-816-977-6
US-09-334-477-6
US-08-180-7618-1
US-08-816-977-25
US-09-334-477-25
US-09-334-477-39
US-09-252-991A-28104
US-09-252-991A-24440
US-09-107-522A-3910
US-09-107-522A-3910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATM: US/07/988,430
FILING DATE: 19921209
                                                                                                                                                                                                      US-09-334-477-49
US-08-816-977-35
US-09-334-477-35
                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIPACATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UTN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 3133
TELECOMMUNICATION INFORMATION:
TELEFONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application US/07988430 Patent No. 5416202
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## Sequence 56, Application US/08488113B
| Patent No. 5744580
| GENERAL INFORMATION
| APPLICANT: Carroll, Stephen F. APPLICANT: Carroll, Stephen F. APPLICANT: Studnika, Gary M. TITLE OF INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INVENTION: Processes INCANDAGENESSE: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES: ADDRESSES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 10-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AREAT INVERMATION:
REGISTRATION NUMBER: US 07/787,567
FILING DATE: 10-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US 04-NOV-1991
ATTORNEY/AREAT INVERMATION:
REGISTRATION NUMBER: US 07/787,567
FILING DATE: US 04-NOV-1991
ATTORNEY/AREAT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 56
SEQUENCE CHARACTERISTICS:
TOWNTH: 20 amino acids
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Matches 20; Conserve
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US-08-477-484B-56
   US-08-488-113B-56
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                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                        Query Match 100.0%; Score 114; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 1.9e-12; Matches 20; Conservative 0; Mismatches 0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 12-AAX-1993
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US/07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS THOMES BATTON NUMBER: US/07/87,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS THOMES BATTON NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION NUMBER: 31394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 114; DB 1;
100.0%; Pred. No. 1.9e-12;
tive 0; Mismatches 0;
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US-08-425-336-56
; Sequence 56, Application US/08425336
; Patent No. 5621083
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                                                                                                                                                                                                                                                            1 CHHHASRVARMASDEFPSMC 20
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INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 312/474-6300
312/474-0448
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; MOLECULE TYPE: peptide
US-08-425-336-56
MOLECULE TYPE: peptide
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Best Local Similarity
Matches 20; Conserv
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STATE: Illinois
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US-07-988-430-58
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                                  Gaps
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0
100.0%; Score 114; DB 1; Length 20; 100.0%; Pred. No. 1.9e-12;
                                Indels
                                0; Mismatches
                                                                                                                                                                               ; Sequence 56, Application US/08477484B; Patent No. 5756699; GENERAL INFORMATION: Marc D. APPLICANT: Carroll, Stephen F.
```

RESULT 3

```
ADDRESSEE: McAndrews, Held & Malloy, Ltd..
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
CATE: Illinois
COUNTRY: USA
                                                                                                         500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Scc.
100.0%; Pred. No.
0; Mismatches
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Patent No. 6146631
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CHHHASRVARMASDEFPSMC 20
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-646-360-56
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COMPUTER READABLE FORM:
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AFFLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: MACAdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-646-360-56

Sequence 56, Application US/08646360

Patent No. 5837491

PAPLICANT: Better, Marc D.

APPLICANT: Better, Marc D.

APPLICANT: Garroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proceins
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/425,336
FILING DATE: 18-ARR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,707
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INCORMATION:
REGISTRATION NUMBER: 32.91
ATTORNEY/AGENT INCORMATION:
NAME: MCNICHOLAS Janet M.
REGISTRATION NUMBER: 32.91
ATTORNEY/AGENT INCORMATION:
NAME: MCNICHOLAS JANET M.
REGISTRATION NUMBER: 32.91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A TELECOMMUNICATION INFORMATION: TELEPHONE: 312/707-8889 TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.9e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Best Local Similarity 100.0%; Pr
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INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   ZIP: 60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-477-484B-56
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Gaps
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APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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COMPUTER BADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DAY-1993
PRIOR APPLICATION NUMBER: US 07/901,707
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: US-UN-1991
ATPONENTS/AGENT INFORMATION:
NAME: WCANICADLES: Janet M.
REGISTRATION NUMBER: US 07/907,567
ATTONENTS/AGENT INFORMATION:
NAME: WCANICADLES: Janet M.
REGISTRATION NUMBER: 32,918
RESERRENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
TELEFRAX: 312/707-8155
TTELEPHONE: WASABATION
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Gaps
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US-09-610-838-56

Sequence 56, Application US/09610838

Sequence 56, Application US/09610838

Patent No. 6376217

APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating

TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
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500 West Madison Street, 34th floor
                                                                                                               PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY.1994
FILING DATE: 12-MAY.1994
PRIOR APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY.1994
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY.1993
PRIOR APPLICATION DATA: 05-DEC.1992
PRIOR APPLICATION NUMBER: US 07/986,430
FILING DATE: 05-DEC.1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUM.1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV.1991
ATTORNEY,AGENT INFORMATION:
NAME: MCMA.CAO.189
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
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INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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Best Local Similarity
Matches 20; Conserva
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Patent No. 6146850
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinika, Gary M.
TITLE OF INVENTION: Immunitoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proceedins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: 32,918
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICADIAS, JANET M:
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 312/707-9155
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHOME: 312/707-9155
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136.389
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ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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CITY: Chicago
STATE: Illinois
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US 08/064,691
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Best Local Similarity
Matches 20; Conserva
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| Sequence 56, Application US/09711485
| Patent No. 6649742
| GENERAL INFORMATION:
| APPLICANT: Better, Marc D.
| APPLICANT: Studnika, Garroll, Stephen F.
| TILLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
| TITLE OF INVENTION: Droteins
| TITLE OF INVENTION: Proteins
| NUMBER OF SEQUENCES: 169
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: McAndrews, Held & Malloy, Ltd.
| STREET: 500 West Madison Street, 34th floor
| CITY: Chicago |
| STATE: Illinois
| CONNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
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COMPUTE: TOTO!

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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100.0%; Pred. No. 1.9e-12;
ative 0; Mismatches 0;
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA: 18-MAY-1994
PRIOR APPLICATION DATA: 12-MAY-1993
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA: 18-MAY-1993
PRIOR APPLICATION NUMBER: US 07/984,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: 32,918
REFRERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
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LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-09-610-838-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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APPLICANT: Berthard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PRESENTED FOR COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
CITY: Chicago
COUNTRY: USA
                                                                                                                                                                                                                                                                                             NAME: MONICACATA MANAGEM.

NAME: MONICACATA MANAGEM.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3

TELECOMMUNICATION INFORMATION:
TELEFAX: 312/707-9889

TELEFAX: 312/707-9155

TELEFAX: 312/707-9155

TELEFAX: 312/707-9155

INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 114; DB 4;
illarity 100.0%; Pred. No. 1.9e-12;
Conservative 0; Mismatches 0;
FILING DATE: 12-MAY-1993
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/988,430
FILING DATE: 09-DEC-1992
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/901,707
FILING DATE: 19-UNN-1992
FRIOR APPLICATION NUMBER: US 07/917
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT: 10FORWATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 58, Application PC/TUS9209487
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CHHHASRVARMASDEFPSMC 20
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APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MOROAN, ALICE ER
APPLICANT: MOROAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECIRSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DESPROY DISK
COMPUTER: PER PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
TITLE OF INVENTION: Verotoxin-Induced Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                         ; Sequence 73, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 CHHHASRVARMASDEFPSMC 283
264 CHHHASRVARMASDEFPSMC 283
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Patent No. 6080400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BORUCKI, ANDREA TREGISTRATION NUMBER: 33651
REPRENCE/DOCKET NUMBER: 3827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               E: ANDREA T. BORUCKI
9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 315 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T.
STREET: 9330 ZIONSVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                        INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Matches 20; Conserv
                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as
                                                                                    US-08-485-286-73
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US-08-816-977-2
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY:
STATE:
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Sequence 73, Application US/08378761A
Sequence 73, Application US/08378761A
Sequence 73, Application US/08378761A
Sequence 73, Application US/08378761A
Septicant: Norgan, Alice ER
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                   100.0%; Score 114; DB 5; Length 20; 100.0%; Pred. No. 1.9e-12;
                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: DEP COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILLING DATE: 26-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 114; DB 1; Best Local Similarity 100.0%; Pred. No. 4.8e-11; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHHHASRVARMASDEFPSMC 20
                                                                              TELEFAX: (312)
TELEFAX: (312)
TELER: 25-3856
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
LENGTH: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELECTION INFORMATION: TELECOMMUNICATION: TELECHONE: (317) 337-4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 73:
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                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 20; Conservative
  Noland, Greta E.
                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                                                                                                                                                                                                        PCT-US92-09487-58
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US-08-378-761A-73
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                                                                                                                                                                                                                                                                                                                                   Query Match
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; Sequence 21, Application US/09334477
                      INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 323 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 16
US-09-334-477-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 315;
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COMPUTER READABLE FORM:
MEDIUM TYPER Flopmy disk
COMPUTER: 19M PC compatible
COMPUTER: 19M PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-Jun-1999
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09334477
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Byrne, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTOREY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELECPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/816,977
                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                        California
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 CHIHASRVARMASDEFPSMC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CHHHASRVARMASDEFPSMC 20
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                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 315 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
San Francisco
                                                         ZIP: 94104
                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-334-477-2
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Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 114; DB 3;
100.0%; Pred. No. 4.9e-11;
iive 0; Mismatches 0;
                                                                                                                                            Query Match
100.0%; Score 114; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.8e-11;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Byrne, Lisa M.
APPLICANT: Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment O
TITLE OF INVENTION: Verotoxin-Induced Disease
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-334-477-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 CHHHASRVARMASDEFPSMC 283
                                                                                                                                                                                                                                                                               264 CHHHASRVARMASDEFPSMC 283
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/08816977 Patent No. 6080400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MACKLIGHL, Kamrin T.
REGISTRATION NUMBER: 38,230
REFRENCE/DOCKET NUMBER: OPHD.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                             1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CHHHASRVARMASDEFPSMC 20
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION POR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STRET: 220 Montgomery Street, Suite 2200
STRET: Prancisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <UNknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-Qy-3-3-4,77-7
Sequence 37, Application US/09334477
Patent No. 6652857
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 CHHHASRVARMASDEFPSMC 294
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SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 705-84:
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 326 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                 APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
TITLE OF INVENTION: Vervention And Treatment Of Verotoxin-Induced Disease
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSER: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/08816977
Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
APPLICANT: Byrne, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of TITLE OF INVENTION: Verotoxin-Induced Disease NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: 220 Montgomery Street, Suite 2200
STREET: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                           STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                       CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                           NUMBER OF SEQUENCES:
         ; Patent No. 6652857
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
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US-08-816-977-37
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Gaps
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100.0%; Score 114; DB 3; Length 326; 100.0%; Pred. No. 5e-11; tive 0; Mismatches 0; Indels 0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
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linear
                                                               60606-6402
    Chicago
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                                                                                                                                                                                                                                                                                                Sequence 251, Application US/08621803
Patent No. 5861802
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Pusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT:
BETTEL:
MATC D.
TILLE OF INVENTION: Methods for Recombinant Microbial Production of
TILLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                             100.0%; Score 114; DB 4; Length 326; 100.0%; Pred. No. 5e-11; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
STREET:
STREET:
STREET:
STATE: 111inois
CITY: Chicago
STATE: 111inois
COUNTRY: United States of America
ZIP: 6606-6402
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PRADABLE FORM:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 114; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.1e-11;
Matches 20; Conservative .0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 251, Application US/09217352
Patent No. 6274344
                                                                                                                                                                              275 CHHHASRVARMASDEFPSMC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 CHHHASRVARMASDEFPSMC 296
                                                                                                                                              1 CHHHASRVARMASDEFPSMC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 312/474-6300
312/474-0448
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amino acid
                                                                                 Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-621-803-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-09-217-352-251
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US-09-334-477-37
                                                                 Query Match
                                                                                        Best Loc
Matches
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Gaps
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NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
Illinois
: United States of America
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6080400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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Best Local Similarity 100.
Matches 20, Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                      US-08-816-977-33
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                                                                                                                                                                                   Length 690;
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                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
FILING DATE: IG-Jun-1999
CLASSIFICATION: <u >Unknown></u>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Prevention And Treatment Of Verotoxin-Induced Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/816,977
FILING DATE: «UNKINOWIN-
ATTORNEY/AGENT INFORMATION:
NAME: MACKALGHT, Kamrin T.
REGISTRATION NUMBER: 38,230
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                         639 CHIHIASRVARMASDEFPSMC 658
                                                                                                                                                                                                                                                                                                                                                                                   US-09-334-477-47; Sequence 47, Application US/09334477; Patent No. 6652857; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Williams, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Byrne, Lisa M.
Pugh, Charles S.G.
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STATE: California
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COMPUTER READABLE FORM:
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TELEFAX: (415) 397-8338
INFORMATION FOR ESD ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 690 amino acids
TYPE: amino acid
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Best Local Similarity 100.0
Matches 20; Conservative
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                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-816-977-47
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC Compatible
COMPUTER: EN PC Compatible
OPERATIONS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,977
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INPORMATION:
NAME: MACKLight, Kamrin T.
REFERENCE/DOCKET NUMBER: 38,230
REFERENCE/DOCKET NUMBER: 38,230
TELEPHONE: (415) 705-8410
Sequence 33, Application US/08816977

Patent No. 6080400
GENERAL INFORMATION:
APPLICANT: Williams, James A.
APPLICANT: Byrne, Lisa M.
TITLE OF INVENTION: Prevention And Treatment Of TITLE OF INVENTION: Prevention And Treatment Of CONTRESPONDENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Prevention And Treatment Of Verotoxin-Induced Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
COUNTRY: United States of America
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APPLICANT: Williams, James A. Byrne, Lisa M. Byrne, Lisa M. Byrne, Lisa M. Byrne, Lisa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 CHHHASRVARMASDEFPSMC 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
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Matches 20; Conservative
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CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/334,477

FILING DATE: 16-Jun-1999

CLASSITATONIN: <URKNOW:

PRIOR APPLICATION NAME:

APPLICATION NAME:

APPLICATION NAME:

APPLICATION NAME:

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Search completed: June 22, 2005, 07:12:06 Job time : 42 secs

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Sequence 3, Appli Sequence 20, Appli Sequence 194718, Sequence 10140, Sequence 11679, Sequence 11679, Sequence 10325, A Sequence 1004, Ap Sequence 1004, Ap Sequence 1004, Ap Sequence 1100, Ap Sequence 1100, Ap Sequence 116625, Sequence 11851, A Sequence 11851, A Sequence 18851, A Sequence 21435, Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 28, Appli Sequence 39, Appli

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Sequence 56, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                            6 US-01-09-05-021-3

6 US-10-408-76-8A-20

7 US-10-437-953-194718

6 US-10-437-963-194718

5 US-10-437-963-194718

5 US-10-437-95-200140

5 US-10-428-152A-66424

6 US-10-425-115-220907

US-09-925-29-1004

US-09-925-29-1004

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US-09-37-758A-28

US-09-37-758A-28

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US-09-37-758A-28
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US-09-344-882-26
4 US-10-293-865-26
5 US-10-437-963-106650
US-09-334-477-49
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 US-10-127-890-56
44444
877444
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                                                                                                                                                   Sequence 56, Appl
Sequence 56, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 2, Appli
                                                                                                                 June 20, 2005, 10:13:56; Search time 108.5 Seconds (without alignments) 70.780 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications AA+ 1807 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1807 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1807 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1806 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1806 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1807 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1808 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1808 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1809 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1809 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1809 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1809 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1809 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1809 PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1811) NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1810B PUBCOMB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pep: + (gnz_6/ptodata/2/pubpaa/1860 NEW PUB. pe
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1 US-10-17-243-56

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1 US-09-334-477-21

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1 US-09-334-477-47

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                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                           1714042 seqs, 383979560 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                       114
1 CHHHASRVARMASDEFPSMC 20
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Gapop 10.0', Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Database :

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993

Sequence 21, Appl Sequence 37, Appl Sequence 251, App Sequence 47, Appl Sequence 33, Appl Sequence 237717,

US-10-425-115-237717

100.0 100.0 100.0 42.1

Score

Result Š.

Sequence 26, Appl Sequence 26, Appl Sequence 106650, Sequence 49, Appl

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Best Loca
Matches
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Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 20;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18 NOV-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 12-APR-1997
APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/980,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-DEC-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 114; DB 14; Best Local Similarity 100.0%; Pred. No. 9.2e-11; Matches 20; Conservative 0; Mismatches 0;
               FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAWE: MCAICAD18s, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 312/707-9155
TELEFAX: 650 388-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear; MOLECULE TYPE: peptide; SEQUENCE DESCRIPTION: SEQ ID NO: 56: US-10-127-890-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 56, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CHHHASRVARMASDEFPSMC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-717-243-56
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APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: MRTHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARES PATENTION TOWN. 2.0
SEQ ID NO 37
LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: McDonald, John R.
APPLICANT: McDonald, John R.
APPLICANT: Coggine, Philip
TITLE OF INVENTION: MCTHON AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
CURRENT PILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                     Length 20;
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                     REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 114; DB 17; 100.0%; Pred. No. 9.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 114; DB 9;
Pred. No. 1.6e-09;
                                                                                                       TELEFRAX: 312/707-9155
TELER: 650 389-1248
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TYPE: amino acid
FYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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; Sequence 37, Application US/10375209A

; Publication No. US20030215421A1

; GENERAL INFORMATION:
NAME: McNicholas, Janet M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-792-793A-37; Sequence 37, Application US/09792793A; Sequence 37, Application US/09792793A; Patent No. US20020168370A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 CHHHASRVARMASDEFPSMC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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TYPE: PRT
COGANISM: Shigella dysenteriae
US-10-375-209A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Shigella dysenteriae
US-09-792-793A-37
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tes 20; Conservat
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Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                       US-10-717-243-56
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RESULT 7
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Query Match 100.0%; Score 114; DB 15; Length 293; Best Local Similarity 100.0%; Pred. No. 1.6e-09; Matches 20; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                Sequence 2, Application US/09334477
Patent No. US2002012658A1
GENERAL INFORMATION: Williams, James A.
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pyrne, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 114; DB 9;
100.0%; Pred. No. 1.7e-09;
7ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
COUNTRY: United States of America
ZIP: 94104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/09334477
Patent No. US20020012658A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 CHHHASRVARMASDEFPSMC 283
                                                                                                          242 CHHHASRVARMASDEFPSMC 261
                                                                                   1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 315 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 20; Conserv
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Gaps
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                                                                                                                                                                                                                                   COMPUTER READMALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OFFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vergion #1.30
CURRENT APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: "ATTEMPTED BY M. Byrne, Lisa M. Byrne, Lisa M. Byrne, Charles S.G. TITLE OF INVENTION: Prevention And Treatment Of Verotoxin-Induced Disease
TITLE OF INVENTION: Prevention And Treatment Of Verotoxin-Induced Disease
                                           NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE Medden & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREFT: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 114; DB 9; 100.0%; Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/BOCKET NUMBER: 0PHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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APPLICATION NUMBER: US/09/334,477
FILING DATE: 16-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States of America
                                                                                                                                                                                          COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37, Application US/09334477
Patent No. US20020012658A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 CHHHASRVARMASDEFPSMC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Williams, James A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CHHHASRVARMASDEFPSMC 20
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COMPUTER READABLE FORM:
                                                                                                                                                                     STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 20; Conservative
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Query Match
Best Local Similarity
Matches 20; Conserv
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US-09-334-477-47
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Patent No. US20020006638A1
GENERAL INPORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Geretein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
CITY: Chicago
CONTYRY: United States of America
CONTYRY: United States of America
ZIP: 6006-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRINT APPLICATION DATA:
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 114; DB 9;
100.0%; Pred. No. 1.7e-09;
tive 0; Mismatches 0;
           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/816,977
FILING DATE: «Unknown:
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: 08/810
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: Amino acids
TYPE: Amino acids
TOPPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
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NOLECULE TYPE: procein
SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/621,803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447
  CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 CHHHASRVARMASDEFPSMC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 332 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 251:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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  Length 332;
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                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
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Pugh, Charles S.G.
TITLE OF INVENTION: Prevention And Treatment Of
                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Prevention And Treatment Of
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                               Verotoxin-Induced Disease
ch 100.0%; Score 114; DB 9; Similarity 100.0%; Pred. No. 1.8e-09; 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 114; DB 9;
100.0%; Pred. No. 3.8e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/816,977
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-334-477-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16-Jun-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                  Sequence 47, Application US/09334477;
Patent No. US20020012658A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Byrne, Lisa M.
Pugh, Charles S.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09334477; Patent No. US20020012658A1; GENERAL INFORMATION:
APPLICANT: Williams, James A.
                                                                                                                    277 CHHHASRVARMASDEFPSMC 296
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INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 690 amino acids
                                                                                            1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CHHHASRVARMASDEFPSMC 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Anou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 224605
LENGTH: 74
                                                                                                                                                                                                                                        APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 40168
LENGTH: 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
COGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-C46914_1.pep
US-10-767-701-40168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: PAT_MRT3847_44849C.1.pep
US-10-424-599-224605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.2%; Score 47; DB 15;
50.0%; Pred. No. 11;
tive 3; Mismatches 5
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GENERAL INFORMATION:
                                                                                                                                                       Sequence 40168, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/09962021
; Patent No. US20020106737A1
; GENERAL INFORMATION:
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                            |||| :|:: |:|
82 CHHHLARLSGSATD 95
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Best Local Similarity 50.0
Matches 8; Conservative
  1 CHHHASRVARMASD
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-424-599-224605
                                                                                                            RESULT 12
US-10-767-701-40168
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US-09-962-021-3
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: ADOU, Yinha
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 237717
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                                                                                                                                                                          COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenten Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,477
                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: MRT4577_148383C.1.pep
US-10-425-115-237717
Verotoxin-Induced Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAVE: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: OPHD-02450
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 709 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-334-477-33
                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 16-Jun-1999
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/816,977
FILING DATE: «Unknown»
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657 CHHHASRVARMASDEFPSMC 676
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                        NUMBER OF SEQUENCES: 49
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Best Local Similarity 50.0
Matches 7; Conservative
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ORGANISM: Zea mays
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41.2%; Score 47; DB 9; Length 135;
Best Local Similarity 44.4%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Indels
                                                                                                                                                                                       ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020106737A1 g180233
US-09-962-021-3
          APPLICANT: Goli, Surya K.
TITLE OF INVENTION: HUMAN SOM1 PROTEIN HOMOLOG
FILE REFERENCE: PF-0170-2 CON
CURRENT APPLICATION NUMBER: US/09/962,021
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-10-408-765A-20
Sequence 20, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        1 CHHHASRVARMASDEFPS 18
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58 CAHHLIRLLKCKRDSFPS 75
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58 CAHHLIRLLKCKRDSFPS 75
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4°
Matches 8; Conservative
                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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Search completed: June 20, 2005, 10:40:19 Job time: 109.5 secs

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                                                                       (without alignments)
80.181 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                             June 20, 2005, 10:00:54 ; Search time 24 Seconds
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                               283416 segs, 96216763 residues
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                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                             Listing first 45 summaries
                                                                                                                          CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A28626
XUBPH9
JN0725
F91000
H85845
A53887
T08577
T33763
A346583
A34653
D95853
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A32360
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E90779
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Gapop 10.0 , Gapext 0.5
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1: pir1:*
2: pir2:*
3: pir3:*
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43	42	36.8	398	100	F98338	fosmidomycin resis	resis	
4 4 5	4 4	36.8	404	7 ~	AB03/6 JC5041	probable membrane fosmidomycin resis	norane n resis	
					ALIGNMENTS			
RESULT 1								
Azoszo Nigella toxin chain A precurso	xin c	hain A	A precursor	80r	יוים - Shigella dysenteriae	iae		
N; Contains:	rRNA	N-glyc	osidae		EC 3.2.2.22)			
C;Species: C;Date: 05-	Feb-1	11a aya 999 #se	quence	re	666	#text_change 09-Jul-2004	-2004	
C, Accession R, Strockbin	1: A28	626; SO A.; Jac	4021 kson,	Σ.	Sung, L.M.; Holmes,	R.K.; O'Brien,	A.D.	
A; Title: Cl	oning	and se	quenci	gi	J. Bacceriol. 1/0, 1116-1122, 1988 A;Title: Cloning and sequencing of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga a section of the genes for Shiga and Shiga and Shiga a section of the genes for Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and Shiga and	ga toxin from Shigella		dysenteriae ty
A; Contents:	Type	1 3818 1 3818		10	:00737100 <i>i</i> ENTD:2030	0.73		
A; Molecule	type:	DNA						
A, Residues: A, Cross-ref	1-31 erenc	5 <str> es: UNI</str>	PROT:C	9X8	z		347.1; 1	PIDN:AAA98347.1; PID:g152785
R, Kozlov, Y Dokl. Bioch	.V.;	Kabishe 95, 216	v, A.F	198	Fedchenko, V.I.; Baev,	v, A.A.		
A; Title: Cl A: Reference	onino.	and pr er: S04	imary 021	вtr	11a	toxin genes.		
A, Accession	1: S04	021	-					
A, Residues:	1-31	5 < KOZ>		:				
A,Cross-ref C:Genetics:	erenc	es: EME	L:X075	93;	NID:946946			
A, Gene: stx	cA heter	ohexame	يد مو	9	A;Gene: stxA C:Comolex: heterohexamer of one A chain and five B c	chains (see PIR:XVEBBD)	BBD)	
C, Function:		,	, ;	}	)	}		
A; Descripti C; Superfami	on: ly: S	ydrolyz hiqella	es the	z d	;Description: hydrolyzes the N-glycosidic bond of a ;Superfamily: Shiqella toxin chain A	lc adenine	in 285 1	rrna
C; Keywords:	cyto	toxin;	glycos	ida	Keywords: cytotoxin; glycosidase; hexamer; hydrolase; RNA	Be; RNA binding		
F;23-315/Pr	oduct	Shige	lla to	xin	chain A #status pre-	dicted <mat></mat>		-
Query Match Best Local Matches 2	ch 1 Sim: 20;	Similarity 100 0; Conservative	vat	100.0%; 100.0%; ive	; Score 114; DB 1; ; Pred. No. 1.2e-10; 0; Mismatches 0;	Length 315; Indels 0;	Gaps (	0;
ò	E-	CHHHASRVARMASDEFPSMC	RMASDE	FPS	MC 20			
Dp 5	264 CHI		RVARMASDEFI	FPS				
1								

Shiga-like toxin chain A precursor - phage H19B C;Species: phage H19B A;Note: host Escherichia coli C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004 C;Accession: A27052 R;Calderwood, S.B.; Auclair, F.; Donohue-Rolfe, A.; Keusch, G.T.; Mekalanos, J.J.

RESULT 2 XUBPH9

Best Local Similarity Matches 20; Conserv

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Query Match

A; Molecule type: DNA A; Residues: 1-315 <CAL>

Genetics:

Accession: A27052

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## Residues: 23-51;62-76;107-132,'XX',135-136;183-192;202-224,'XX',227-241;276-282,291-294

## Reperimental source: strain 0157:H7

CyGenetics:

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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85845
R;Perna, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shiga toxin I subunit A precursor [imported] - Escherichia coli (strain O157:H7, substrai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CjAccession: F91000
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom A;Reference number: A99629; MUD:21156231; PMID:11258796
A;Status: preliminary
A;Status: preliminary
A;Residues: preliminary
A;Residues: 1-315 <HAY>
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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A;Reteronce number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85845
A;Accession: H85845
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-315 <STO>
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100.0%; Score 114; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0;
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C;Superfamily: Shigella toxin chain A
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C;Superfamily: Shigella toxin chain A
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Matches 20; Conservative
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A; Cross-references: EMBL: 236901; NID: 9535089; PIDN: CAA85370.1; PID: 9535089
A; Experimental source: serotype OX3:H8
R; Tako, T.; Tanabe, T.; Hong, Y.M.; Shimonishi, Y.; Kurazono, H.; Yutsudo, T.; Sasakawa Microb. Pathog. 5, 357-369, 1988
A; Title: Identity of molecular structure of Shiga-like toxin I (VT1) from Escherichia co
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A; Residues: 1-315 <PAT'>
A; Residues: 1-315 <PAT'>
A; Experimental source: serotype O111:H(-)
R; Paton, A.W.; Beutin, L.; Paton, J.C.
R; Paten, A.W.; Beutin, L.; Paton, A.C.
A; Title: Heterogeneity of the amino-acid sequences of Escherichia coli Shiga-like toxin
A; Reference number: 153932; MUID:95189106; PMID:7883188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence of a variant Shiga-like toxin type-I operon of Escherichia coli O111:H
A;Reference number: JN0725; MUID:93328129; PMID:8335264
                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P08026; GB:M16625; NID:g215043; PIDN:AAA98099.1; PID:g21504
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C;Species: Escherichia coli
C;Decies: 14-Jul-1994 #sequence revision 14-Jul-1994 #text change 09-Jul-2004
C;Accession: JN0725; I53932; I68041; I68043; C61473; A61473; B47254; S47256; S47258
R;Patcon, A.W.; Paton, J.C.; Goldwater, P.N.; Heuzenroeder, M.W.; Manning, P.A.
Gene 129, 87-92, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                       A;Title: Nucleotide sequence of the Shiga-like toxin genes of Escherichia coli
A;Reference number: A27052; MUID:87260808; PMID:3299365
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Accasidues: 1-170, '52,172-248,'E',250-315 <PATI>
A;Cross-references: EMBL:236899; NID:g534987; PIDN:CAA85366.1; PID:g534988
A;Experimental source: serotype 048:H21
A;Note: submitted to the EMBL Data Library, August 1994
A;Accession: 168041
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;RCOSS-references: EMBL:336900; NID:9533054; PIDN:CAA85368.1; PID:9538055
A;Experimental source: serotype 0111:H(-)
A;Note: submitted to the EMBL Data Library, August 1994
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C,Superfamily: Shigella toxin chain A
C,Superfamily: Shigella toxin chain A
E,P-22-Domain: signal sequence #status predicted <81G>
F,1-22-Domain: signal sequence #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; Score 114; DB 1; Length 315; Similarity 100.0%; Pred. No. 1.2e-10; 20; Conservative 0; Mismatches 0; Indels (
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A;Status: preliminary; translated from GB/EMBL/DDBJ
               4364-4368, 1987
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A, Experimental source: strain 0157:H7
. Natl. Acad. Sci. U.S.A. 84,
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Reference number: A61473

Molecule type: DNA

A,Accession: I53932 A,Status: prelimina

A;Accession: A61473 A;Status: preliminary

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A;Cross-references: UNIPROT:Q9TVW1; EMBL:AF100675; PIDN:AAC69004.1; GSPDB:GN00022; CESP:) A;Experimental source: strain Bristol N2; clone Y55H10A C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F11C1.210 - Arabidopsis thaliana
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana 04-Feb-2000 #text_change 09-Jul-2004
Cispecies: M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; Mayesubitted to the Protein Sequence Database, December 1999
A;Reference number: Z23007
A;Reference number: Z23007
A;Reference number: Z23007
A;Residues: 1-2152 - EBAR>
A;Residues: 1-2152 - EBAR>
A;Residues: 1-2152 - CBAR>
A;Residues: 1-2153 - CBAR>
A;Residues: 1-2153 - CBAR>
A;Residues:
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C;Species: Homo sapiens (man)
C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 09-Jul-2004
C;Accession: A34653
R;Wong, Y.C.; Tsao, S.W.; Kakefuda, M.; Bernal, S.D.
Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. Biochem. A;Title: cDNA cloning of a novel cell adhesion protein expressed in human squamous carcir A;Reference number: A34653; MUID:90147818; PMID:2302251
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C;Keywords: cell adhesion
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A;Introns: 53/3; 411/2; 1479/3; 1543/2; 1592/3; 1659/1; 1750/1; 1965/3
A;Note: F11C1.210
                                                                                                                                                     AjGene: CESP:YSSH10A.1
Ajmap postition: 4
AjIntrons: 29/2; 57/1; 95/3; 233/1; 319/3
CjSuperfamily: Caenorhabditis elegans hypothetical protein YSSH10A.1
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                                                                                                                                                                                                                                                                                                                                       43.9%; Score 50; DB 2; Length 451; 58.8%; Pred. No. 3.2; ive 3; Mismatches 4; Indels
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Pred. No. 2.9;
2; Mismatches 8; Indels
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43.0%; Score 49; DB
Best Local Similarity 41.2%; Pred. No. 23;
Matches 7; Conservative 5; Mismatches
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151 HEKSSRVKRVATDEFNS 167
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131 HHVEKVATLRGEDFPSL 147
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 58.8'
Matches 10; Conservative
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A; Residues: 1-135 < WON>
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A;Status: preliminary
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Shiga-like toxin I A chain precursor - phage 933J
C;Species phage 933J
C;Species phage 933J
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: A53887
C;Accession: A53887
Microb. Pathog. 2, 147-153, 1987
A;Title: Nucleotide sequence analysis of the structural genes for Shiga-like toxin I encapaceasion: A53887; MUD:89180929; PMID:333796
A;Reference number: A53887
A;Accession: A53887
A;Accession: A53887
A;Accession: A53887
A;Accession: A53887
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C;\species: Arabidopsis thaliana (mouse-ear cress)
C;\species: 11-\Jun-1999 #sequence_revision 11-\Jun-1999 #text_change 09-\Jul-2004
C;\scalabaran, M.; Zimmermann, W.; \text{Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May Babaran, M.; Reference number: 216442
A;\scenesion: T08577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-315 <JAC>
A;Cross-references: UNIPROT:P08026; GB:M19473; NID:g215072; PIDN:AAA98151.1; PID:g215073
C;Superfamily: Shigella toxin chain A
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A;Residues: 1-365 <BEV>
A;Cross-references: UNIPROT:Q9T035; EMBL:AL050351; GSPDB;GN00062; ATSP:T22F8.190
A;Experimental source: cultivar Columbia; BAC clone T22F8
C;Genetics:
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A;Map position: 4
C;Superfamily: conserved hypothetical protein containing F-box amd Kelch domains
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33763
R;Antoniou, B.; Smith, A.; Gibson, A.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid Y55H10A.
A;Reference number: Z21402
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100.0%; Score 114; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 20; Conservative 0; Mismatches 0;
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A;Molecule type: DNA
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                                               CHIHHASRVARMASDEFPSMC 20
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C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 160446; 157048; $31420
R;Patch, A.W.; Patch, J.C.; Heuzenroeder, M.W.; Goldwater, P.N.; Manning, P.A.
Microb. Pathog. 13, 225-236, 1992
A;Title: Cloning and nucleotide sequence of a variant Shiga-like toxin II gene from Esche A;Reference number: 160446; MUID:93180660; PMID:1291844
A;Accession: 160446 MUID:93180660; PMID:1291844
A;Actus: translated from GB/EMBL/DDBJ
A;Actus: translated from GB/EMBL/DDBJ
A;Actus: 1.319 <ARS>
A;Reference number: 1.319 <ARS>
A;Reference number: 1.319 <ARS>
A;Accession: 15, 77-82, 1993
A;Title: POlymerase chain reaction amplification, cloning and sequencing of variant Esche A;Accession: 157048
A;Accession: 157048
A;Accession: 157048
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N.Alternate names: PN 4-oxidase; pyridoxin 4-oxidase
C;Species: Microbacterium luteolum YK-1
C;Date: BNOv-2002 #sequence_revision 18-Nov-2002 #text_change 21-Apr-2003
C;Accession: JC7855; PC7192
R;Kaneda, Y.; Ohnishi, K.; Yagi, T.
Biosci. Biotechnol. Biochem. 66, 1022-1031, 2002
A;Title: Purification, Molecular cloning, and characterization of pyridoxine 4-oxidase fine the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the
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A; Molecule type: 2-20; 348-364 < KA2>
A; Residues: 2-20; 348-364 < KA2>
C; Comment: This enzyme that is an FAD-dependent enzyme and a monomeric protein belongs to ors to form pyridoxal and hydrogen peroxide or reduced forms of the acceptors. This enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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C;Species: Mycobacterium leprae
C;Bate: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S72759; T1014
R;Smith, D.R.; Robison, K.
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C;Superfamily: Shigella toxin chain A
C;Keywords: cytotoxin
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Pred. No. 16;
0; Mismatches (
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A, Residues: 1-197, 'G', 199-319 <RE2>
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A;Residues: 1-507 <KAN>
A;Cross-references: DDBJ:AB049341
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C;Keywords: oxidoreductase
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A:Molecule type: DNA
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A:Molecule type: DNA
A:Experimental source: strain 1021, megaplasmid pSymB
A:Experimental source: strain 1021, megaplasmid pSymB
A:Experimental source: strain 1021, megaplasmid pSymB
A:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Pederspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A; Tile: The composite genome of the legume symbiont Sinorhizobium meliloti.
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C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Accession: D95853
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
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A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2931
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Score 47; DB 2; Length 252; Pred. No. 5.4; 1; Mismatches 7; Indels

41.2%;

Conservative

Query Match Best Local Similarity Matches 9; Conserv

A; Contents: annotation

A; Genome: plasmid

A; Gene: SMb20092 C;Genetics:

à g Length 196; Indels

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B

Score 46; DB Pred. No. 6; 0; Mismatches

40.48;

Conservative

Query Match Best Local Similarity 9; Conserv?

A; Residues: 1-196 <STO>

A, Status: preliminary A, Molecule type: DNA

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RESULT 13

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Shiga-like cytotoxin subunit A - Escherichia coli N;Alternate names: shiga-like toxin II variant chain C;Species: Escherichia coli

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submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid B1496.
A; Reference number: $72695
A; Accession: $122759
A; Accession: $122759
A; Molecule type: DNA
A; Residues: 1-254 *SMI-
A; Cross-references: UNIPROT:Q49688; EMBL:U00013; NID:g466868; PIDN:AAA17126.1; PID:g4668
B; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
A; Residues: 1-254 *BML Data Library, September 1997
A; Recence number: 216918
A; Recession: T11014
A; Residues: 1-254 *PAR>
A; Rosidues: 1-254 *PAR>
A; Cross-references: EMBL:299125; NID:g2398683; PIDN:CAB16173.1; PID:g2398708
C; Genetics:
A; Gene: MLCL536.29C
A; Start codon: GTG
Ouery Match
Best Local Similarity 45.5%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 4; Indels 6; Gaps 2;
A; Mismatches 10; CohHCPVSHVA----EEFPELC 213
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Search completed: June 20, 2005, 10:14:36 Job time : 25 secs

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01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Shiga-like toxin I subunit A precursor (EC 3.2.2.22) (Verotoxin subunit A) (SLT-I) (rRNA N-glycosidase).
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
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Calderwood S.B., Auclair F., Donohue-Rolfe A., Keusch G.T.,
Mekalanos J.J.;
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58.860 Million cell updates/sec
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1.CHHHASRVARMASDEFPSMC 20
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2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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"Cloning and sequencing of the genes for Shiga toxin from Shigella dysenteriae type 1.\,";
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QGLDT4;
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MEDLINE-88139166; PubMed-2830229;
Strockbine N.A., Jackson M.P., Sung L.M., Holmes R.K., O'Brien A.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific adenosine on the 28S rRNA.
-!- SUBUNIT: The Shiga-like toxins contain a single A subunit and
multiple copies of B subunit.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
                                                                                                                                                                                                                                                                            MEDLINE=88190113; PubMed=3357883;
Hovde C.J., Calderwood S.B., Mekalanos J.J., Collier R.J.;
"Evidence that glutamic acid 167 is an active-site residue of Shiga-
                                                                                                                                                                                                                                                                                                                                                                                                                                     subunits.
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at
                                                                                                                                                                      "Nucleotide sequence and promoter mapping of the Escherichia coli
Shiga-like toxin operon of bacteriophage H-19B.";
J. Bacteriol. 169:4313-4319(1987)
                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 85:2568-2572(1988).
-1- FUNCTION: The A subunit is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ol-MAR-1989 (Rel. 10, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Shiga toxin A-chain precursor (EC 3.2.2.22) (rRNA N-glycosidase).
Name=STXA;
  'Nucleotide sequence of the Shiga-like toxin genes of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                    SEQUENCE FROM N.A.
MEDLINE-87308020; PubMed=3040689;
de Grandis S., Ginsberg J., Toone M., Climie S., Friesen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 315;
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100.0%; Pred. No. 3e-10;
ive 0; Mismatches 0; Indels
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PIR; A53887; A53887.
InterPro; IPR01574; RIP.
PEam; PF00161; RIP; 1.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 315 Shiga-like toxin I subunit
189 189
315 AA; 34799 MW; 8B993DF7A8E58F30 CRC64;
                                          Proc. Natl. Acad. Sci. U.S.A. 84:4364-4368(1987)
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P10149;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
SUBUNIT: Shiga toxin contains a single A-chain and five copies of B-chain.
                                                                                                                                                                                                                                                    MEDLINE=89006281; PubMed=3049254; DOI=10.1016/0378-1119(88)90398-8; Kozlov Y.V., Kabishev A.A., Lukyanov E.V., Bayev A.A.; "The primary structure of the operons coding for Shigella dysenteriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal
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                                                                                    Kozlov Y.V., Kabishev A.A., Fedchenko V.I., Bayev A.A.; "Cloning and primary structure of Shigella toxin genes."; Dokl. Biochem. 295:744-749(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Shiga toxin-like subunit A precursor.
                                                                                                                                                                                                                                                                                                                                               toxin and temperature phage H30 shiga-like toxin."; Gene 67:213-221(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiga toxin A-chain.
By similarity.
T -> S (in Ref. 3).
A -> P (in Ref. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Bacteriol. 170:1116-1122(1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 AA; 34813 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M24352; AAA26538.1; -. EMBL; M23980; AAA72732.1; -. InterPro; IPR001574; RIP.
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189
67
190
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Gaps

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0; Mismatches
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nes 20; Conservative
  Conservative
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                                                                                                              PRELIMINARY;
                                                                                                                                                                                                   Bacteriophage Lahn1.
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SEQUENCE FROM N.A.
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                                                                                                                                     05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q779K4;
05-JUL-2004
                                                                                                                                                              05-JUL-2004
20;
                                                                                                                                                                                         Name=stx1A;
                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                              0777W4
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  Matches
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Q779K4
                                                                                      RESULT 6
                                                                                                   0777W4
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1. J. Bacteriol. 185:396-371(2003).
2. -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
2. -1- SIMILARITY: Belongs to the ribosome-inactivating protein family.
3. BMBL; APPONSIS3; BAC77588.1; -1.
3. GO; GO:0016787; F:hydrolase activity; IEA.
3. GO; GO:0017148; F:nydrolase activity; IEA.
3. GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.
3. GO; GO:0009405; P:pathogenesis; IEA.
3. InterPro; IPR001574; RIP.
3. RAM: PROSITE; PS00275; SIRP; 1.
3. Hydrolase; Protein synthesis inhibitor; Toxin.
3. SEQUENCE 315 AA; 34813 MW; 8A423DF7ABFSBF30 CRC64;
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                                                                                 J. Bacteriol. 170:1116-1122(1988).

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein.family. EMBL; M19473; AAA98151.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro: IPRO01574; RIP.
                      SEQUENCE FROM N.A. MEDINE-88139166; PubMed=2830229; Strockbine N.A., Jackson M.P., Sung L.M., Holmes R.K., O'Brien A.D.; Cloning and sequencing of the genes for Shiga toxin from Shigella dysenteriae type 1.";
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Stx1 phage;
MEDLINB=22697399; PubMed=12813092;
DOI=10.1128/JB.185.13.3966-3971.2003;
Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T., Takeda Y., Yamasaki S.;
"Genome analysis of a novel Shiga toxin 1 (Stx1)-converting phage which is closely related to Stx2-converting phages but not to other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stx1 converting bacteriophage.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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                                                                                                                                                                                                                                                                 Shiga toxin-like subunit A. 8B993DF7A8E58F30 CRC64;
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PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Protein synthesis inhibitor; Signal; Toxin.
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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Pred. No. 3e-10;
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                                                                                                                                                                                                                                                                                                                                                                       264 CHHHASRVARMASDEFPSMC 283
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Microb. Pathog. 2:147-153(1987)
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                                                                                                                                                                                                                                                                              SEQUENCE 315 AA; 34799 MW;
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1 Similarity 100.0%;
20; Conservative 0
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Best Local Similarity
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q776E8;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shigella sonnei bacteriophage 7888.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
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SEQUENCE 315 AA, 34813 MW, 8A423DF7ABF58F30 CRC64,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                      (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from enterohaemorrhagic Escherichia coli.";
Thesis (2000), Department of Veterinary Medicine,
Justus-Liebig-University, D-35392 Giessen, Germany.
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                                                                                                                                                           315 AA
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PROSITE; PS00275; SHIGA RICIN; 1.
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                                          264 CHHHASRVARMASDEFPSMC 283
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1 CHHHASRVARMASDEFPSMC 20
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PRELIMINARY;
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PROSITE; PS00275; SHI
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                                                                                                                                                               Escherichia coli.
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                     Q8L170
Q8L170;
01-OCT-2002
                                                                                                                                                                                                                                                                                       STRAIN=HI-A;
                                                                                                                                          Name=stx1A;
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047638;
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                                                                       Creuzburg K.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28 rRNA.
              DOI=10.1128/IAI 69.12.7588-7595.2001;
Strauch E., Lurz R., Beutin L.;
"Characterization of a Shiga toxin-encoding temperate bacteriophage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Generic structure and chromosomal integration site of the cryptic Shiga toxin 1-converting prophage CP-1639."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 315;
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Creuzburg K., Koehler B., Hempel H., Schreier P. Jacobs E.,
Schmidt H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                           Pfam; PP00161; RIP; 1.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Protein synthesis inhibitor; Toxin.
SEOUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfan, PF001G1, RIP; 1.
PROSITE, PS00275; SHIGA_RICIN; 1.
Hydrolase; Protein synthesis inhibitor; Toxin.
SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-5010-2004 (TrEMBLrel. 27, Created)
05-5010-2004 (TrEMBLrel. 27, Last sequence update)
05-5010-2004 (TrEMBLrel. 27, Last annotation update)
Shiga toxin 1 Stx1, A-subunit.
Name=stx1A; ORENames=EC_CP1639_35;
                                                                                                                                                                                                                                                                                                                                                                                                         Score 114; DB 2;
Pred. No. 3e-10;
); Mismatches (
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100.0%; Pred
0; F
MEDLINE=21562619; PubMed=11705937
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Best Local Similarity 100.
Matches 20; Conservative
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RESULT 9

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STRAIN=HI-A;
Asakura H., Makino S., Kobori H., Shirahata T., Ikeda T., Takeshi K.;
"Phylogenetic Diversity and Similarity of Active Sites of Shiga toxin (Stx) in Shiga toxin-producing Escherichia coli (STEC) isolates from
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GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
InterPro; IPR001574; RIP.
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"Detection and long-term existence of Shiga toxin (Stx)-producing
Escherichia coli in sheep.";
Microbiol. Immunol. 42:683-688(1998).
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Enterobacteriaceae; Escherichia.
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Abakura H., Makino S., Kim S., Allano M.R., Kuri A., Watarai M.,
Shirahatea T.,
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Ikeda T., Takeshi K.;
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315 AA; 34756 MW; 1E1F9146E3421149 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
SIT-1 A subunit coding region.
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    315 AA.
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Enterobacteriaceae; Escherichia
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Best Local Similarity
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STRALI-SESCOYPRO 011:H-;
MEDLINE-95189106; PubMed=7883188; DOI=10.1016/0378-1119(94)00777-P;
Paton A.W., Beutin L., Paton J.C.;
"Heterogeneity of the amino-acid sequences of Escherichia coli Shiga-,
like toxin Lype-I operons.";
Gene 153:71-74(1995).
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                                                                             GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
InterPro; PR001574; RIP.
Pfam; PF00161; RIP; 1.
PROSITE; PS00275; SHIGA RICIN; 1.
SEQUENCE 315 AA; 34885 MW; 8A423E94CBF6EC50 CRC64;
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GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
InterPro; IPR001574; RIP.
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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Enterobacteriaceae; Escherichia.
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PROSITE; PS00275; SHIGA_RICIN; 1.
SEQUENCE 315 AA; 34843 MW; CE4BE03E7FF59B3F CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Shiga-like toxin type-I alpha subunit precursor.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
SLT-I A subunit coding region.
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EMBL; Z36899; CAA85366.1; -. HSSP; Q9FBI2; 1DM0.
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1es 20; Conservative
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STRAIN=CB7888;
MEDLINE=99247285; PubMed=10232325; DOI=10.1016/S0140-6736(99)00961-7;
MEDLINE=99247285; PubMed=10232325; DOI=10.1016/S0140-6736(99)00961-7;
Blutin L., Strauch B., Fischer I.;
"Isolation of Shigella sonnei lysogenic for bacteriophage encoding gene for production of Shiga toxin.";
Lancet 353:1498-1498(1999).
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"Sequence of a variant Shiga-like toxin type-I operon of Escherichia coli 0111:H-."; Gene 129:87-92(1993).
                                                                                                                                                                                                                                                                                                                                           Potential.
Shiga-like toxin type-I subunit alpha.
2DDF149B7BF5995C CRC64;
                                                                                            EMBL; L04539; AAA71893.1; -.
PIR; JN0725; JN0725.
HSSP; QSPB12; 1DM0.
GO; GO:0010598; F:RNA N-glycosylase activity; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
InterPro; IPR001574; RIP.
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GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
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(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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PROSITE; PS00275; SHIGA RICIN; 1.
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MEDLINE=99170895; PubMed=10071501;
Iwasa M., Makino S., Asakura H., Kobori H., Morimoto Y.;
"Detection of Escherichia coli O157:H7 from Musca domestica (Diptera:
Muscidae) at a cattle farm in Japan.";
J. Med. Entomol. 36:108-112(1999).
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MEDLINE-21445868; PubMed=11561972;
Asakura H., Makino S., Kobori H., Watarai M., Shirahata T., Ikeda T.,
                                                                                                                                                                                                         Unkmeir A., Schmidt H.;
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EMBL, AJ271153; CAC05622.1;
GO; GO:0030598; F:RNA N-glycosylase activity; IEA.
GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.
InterPro; IPR001574; RIP.
                                   Shigella dysenteriae.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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"Detection and long-term existence of Shiga toxin (Stx)-producing
Bscherichia coli in sheep.";
Microbiol. Immunol. 42:683-688(1998).
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Enterobacteriaceae, Escherichia.
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MEDLINE=99074174; PubMed=9858463;
Asakura H., Makino S., Shirahata T., Tsukamoto T., Kurazono H.,
Ikeda T., Takeshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Shiga toxin 1 A-subunit (Shiga-like toxin 1 A-subunit) (Stx1A
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Name=stx1 A-subunit; Synonyms=stx-1 A subunit, stx1, stx1A;
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PROSITE; PS00275; SHIGA_RICIN; 1.
SEQUENCE 315 AA; 34822 MW; 897E3DF7ACB58P30 CRC64;
                                                                                                                               SEQUENCE FROM N.A.
STRAIN=H2765-39/81,
MEDLINE-20407286; Pubwed=10948097;
DOI=10.1128/IAI.68.9.4856-4864.2000,
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01-MAR-2002 (TrEMBLrel. 20, Last seq
25-OCT-2004 (TrEMBLrel. 28, Last ann
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 Shiga toxin A protein.
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Best Local Similarity
                     Name=shiga toxin A;
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                                                                                               NCBI_TaxID=622;
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Submitted (ARR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AB083044; BAC.

EMBL; AB083044; BAC.

GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.

GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.

InterPro; IPRO01574; RIP.

PROSITE; PS00161; RIP; 1.

PROSITE; PS00275; SHIGA_RICIN; 1.

SRQUENCE 315 AA; 34844 MW; 91588DF7ABF58F31 CRC64;
                                                                                                                                                                                                                           PDB; 1DM0; X-ray; A/L=-...

PDB; 1R4Q; X-ray; A/L=-...

GO; GO:0030599; F:RRM N-glycosylase activity; IEA.

GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

INCAFPC; IFR001574; RIP.

PFam; PF00161; RIP; 1.
                                                                                                                                 McDonough M.A., Butterton J.R., "Spontaneous tandem amplification and deletion of the shiga toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Shiga toxin 1 variant A subunit.
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Last annotation update)
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Mol. Microbiol. 34:1058-1069(1999).
EMBL; AF153317; AAF28121.1; -.
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                                                                                           STRAIN=type 1;
MEDLINE=20063152; PubMed=10594830;
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                 Enterobacteriaceae; Shigella
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                                                                         SEQUENCE FROM N.A.
                                     NCBI_TaxID=622;
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01-MAR-2001 (
01-MAR-2004 (
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Matches
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Q9FB12
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Q7WZI7

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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Shiga toxin I subunit A (Shiga-like toxin I subunit A encoded within prophage CP-933V) (Shiga toxin I subunit A).
Name=stxlA; OrderedLocusNames=EC82974, Z3344;
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MEDLINE=20564182; PubMed=11111050; DOI=10.1016/S0378-1119(00)00416-9;
YOKOYAMA K., Makino K., Kubota Y., Watanabe M., Kimura S.,
Yutendo C.H., Kurokawa K., Ishii K., Hatfori M., Abe H., Iida T.,
Yamamoto K., Hayashi T., Yasunaga T., Honda T., Sasakawa C.,
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GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA
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Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                       Unkmeir A., Schmidt H.;
"Structural analysis of phage-borne stx genes and their flanking sequences in shiga toxin-producing Escherichia coli and Shigella dysenteriae type 1 strains.";
Infect. Immun. 68:4856-4864 (2000).
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                                                                                                                                                                        SEQUENCE FROM N.A. SYS21, and FD930; STRANN=C984, EX201, EX921, and FD930; Yu J.Y., Gorn H.G., Kang Y.H., Kim E.C., Sohn C.K., Lee submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                               Sou-ichi M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                        Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 315 AA; 34813 MW; 8A423DF7ABF58F30 CRC64;
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100.0%; Pred. No. 3e-10;
ive 0; Mismatches 0;
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DOI=10.1128/IAI.68.9.4856-4864.2000;
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EMBL; AF461166; AAM70031.1; -.
EMBL; AF461169; AAM70035.1; -.
EMBL; AF461172; AAM70043.1; -.
EMBL; A751325; CACO5535.1; -.
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Matches 20; Conservative
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PIR; H85845; H85845.
HSSP; Q9FBI2; 1DM0.
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PIR; F91000; F91000
[4]
SEQUENCE FROM N.A.
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                                                                                              STRAIN-GPU96MM;
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                                                                                                                                                                                                                                                          SEQUENCE
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AJ487680; CAD32216.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=0157:H7 / RIMD 0509952 / EHEC;
MRDLLINE=21156211; PubMed=11258796;
MRDLLINE=21156211; PubMed=11258796;
MRDLLINE=21156211; PubMed=11258796;
Han C.-G., Ohtenbo E., Nakayama K., Murata T., Tanaka M., Tobe T., ilda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H., Complete genome sequence of enterohemorrhagic Escherichia coli (Complete genome sequence of enterohemorrhagic scherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                           "Complete nucleotide sequence of the defective Sakai-VT1 prophage carrying the shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak.";
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GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
InterPro; IPR001574; RIP.
                                                                                                                                                                     SEQUENCE FROW N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11205551; DOI=10.1038/35054089;
MEDLINE=21074935; PubMed=11205551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glaener J.D.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
Welch R.A., Blattner F.R.;
Welche Sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
NCBL_TaxID=196242;
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Recktenwald J., Schmidt H.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS00275; SHIGA_RICIN; 1.
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EMBL, AP000400, BAB19590.1; -.
EMBL; AE005442; AAG57228.1; -.
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                                                                                                                         Gene 258:127-139(2000)
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Best Local Similarity
Matches 20; Conserv
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25-OCT-2004
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DR EMBL; AJ556162; CAD88841.1; -.

DR GO; GO:0030598; F:RRNA N-glycosylase activity; IEA.

DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

DR InterPro; IPR001574; RIP.

DR Pfam; PF00161; RIP; 1.

DR PROSITE; PS00275; SHIGA RICIN; 1.

KW Hydrolase; Protein synthesis inhibitor; Toxin.

SQ EQUENCE 315 AA; 34813 WW; 8A423DF7ABF58F30 CRC64;

Query Match 100.0%; Score 114; DB 2; Length 315;

Best Local Similarity 100.0%; Pred. No. 3s-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY I CHHAASRVARMASDEFPSMC 20

COS CHHAASRVARMASDEFPSMC 283
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Search completed: June 22, 2005, 07:08:29 Job time: 176 secs

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June 22, 2005, 06:53:33; Search time 163 Seconds (without alignments) 47.455 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Title:	US-10-717-243-56
Perfect score:	114
Sequence:	1 CHHHASRVARMASDEFPSMC 20
Scoring table: BLOSUM62	BLOSUM62
Gapop 10	Gapop 10.0 , Gapext 0.5
Searched:	2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: Minimum DB seq.length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

το.	Description	Aar37300 E.coli sh	Aaw58827 Shiga tox	Aay39393 Shiga-lik	Aay69046 Amino aci		Aaw21702 Shiga-lik	Aaw25139 SLT-1 (a	Aay96681 E. coli v	Aau77817 E. coli v	Adc00545 Enterohae	Adh34319 Verotoxin	Aaw25786 Phage H19	Aaw06407 Histidine	Aay96686 Recombina	Aau77822 HIS-tagge	Aaw06413 Flag tag/		Flag	Aaw29294 BPI pepti	Aar13118 Shiga-lik	*Aay55891 E.coli ba			Aau77830 MBPNVT1-A	Aaw06411 Maltose h
SUMMARIES	ID	AAR37300	AAW58827	AAY39393	AAY69046	AAW06403	AAW21702	AAW25139	AAY96681	AAU77817	ADC00545	ADH34319	AAW25786	AAW06407	AAY96686	AAU77822	AAW06413	AAY96692	AAU77828	AAW29294	AAR13118	AAY55891	AAY78591	AAY96694	AAU77830	AAW06411
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d	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	.100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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08 3 AAY96690 08 5 AAU77826 35 7 ADJ68214 35 7 ADS6298 35 7 ADS6989 36 6 ABU38500 04 7 ABR82811 19 7 ABR82312 25 7 ABR34573 25 7 ABR34573 25 7 ABR34573 37 7 ABC9229 44 3 AAS7966 37 7 ADJ69294 37 7 ADJ69294 38 2 AAW60837 38 5 AAW60837 38 5 AAW97643 97 2 AAW07643	13088 13088 13088 13088 13088 1337 1337 144 1588 177 177 177 177 177 177 177 177 177 1	Aay96690 MBP-VT-1 Aau77826 MBPNVT1-A Adj68214 Human hea		Abo69919 Pseudomon Abr82617 P. aerugi Aag59236 Arabidops	Ada34573 Acinetoba Abo79520 Pseudomon Ads21292 Bacterial	Aab53464 Human col Aam79060 Human pro Adj69294 Human hea	Aaw60837 Human SQM Abg72567 Human cel Aaw58829 Shiga tox Aaw07643 Mutant Sh Aaw07641 Mutant Sh
008 008 008 008 008 008 008 008		AAY96690 AAU77826 ADJ68214	ADE95989 ADK14898 ABU38500	ABO69919 ABR82617 AAG59236	ADA34573 ABO79520 ADS21292	AAB53464 AAM79060 ADJ69294	AAW60837 ABG72567 AAW58829 AAW07643 AAW07641
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## ALIGNMENTS

Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; human engineered antibody; variable region; light chain; cell targetting; chimeric antibody; SLT. AAR37300 standard; protein; 20 AA. E.coli shiga-like toxin segment. (revised)
(first entry) Escherichia coli. 25-MAR-2003 13-SEP-1993 AAR37300; RESULT 1 

Key Disulfide-bond

91US-00787567. 92US-00901707. 92WO-US009487 04-NOV-1992; 04-NOV-1991; 19-JUN-1992; WO9309130-A1 13-MAY-1993.

SP; Lei Lane JA, Carroll SF, Better MD, WPI; 1993-167617/20. Berhard SL,

(XOMA ) XOMA CORP.

Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo.

Example 10; Page 114; 163pp; English.

The invention covers analogues of the plant type I RIP gelonin which have a non-naturally occurring Cys residue in a position which enables the analogue to be conjugated via a disulphide linkage to a molecule which specifically binds to a target cell. Pref. target-cell binding molecules are antibodies or their fragments, esp. human engineered H65 antibody

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AAY39393;
            AAY39393
ID AAY3
  RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Shiga toxin (Stx) peptides (AAWS8827-WS8830) were histine-tagged to simplify and expedite purification. Non toxic Shiga toxoids, Fusion proteins of Hist-tagged Shiga toxins/toxoids and antibodies can be used in the treatment, diagnosis or prevention of infections mediated by toxins of the Stx family. These are associated with haemorrhagic colitis and the
fragments. Fusion constructs were assembled that included a natural sequence gelonin gene fused to an H65 truncated heavy chain gene or an H65 Light chain (kappa) gene. A DNA linker encoding a peptide segment of the E.coli shiga-like toxin was inserted between the gelonin gene and the Ab gene. The resulting immunoconjugates can be used as cytotoxic therapeutic agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purification and isolation of histidine-tagged Shiga toxins - useful in vaccines against haemorrhagic colitis and haemolytic uremic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                life-threatening sequela, haemolytic uremic syndrome. Shiga antibodies are also useful for the treatment, diagnosis and prevention of disease and infections by pathogenic Escherichia coli
                                                                                                                                                                                                                                                                                                                             Histine-tag; toxoid; antibody; treatment; diagnosis; prevention; Stx; haemorrhagic colitis; haemolytic uremic syndrome.
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                                                                                                       Length 20;
                                                                                                                              Indels
                                                                                                      100.0%; Score 114; DB 2;
100.0%; Pred. No. 4.7e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
                                                                                                                                                                                                                                                                                                         Shiga toxin type 1 mature A subunit
                                                                                                                                                                                                                                    AAW58827 standard; peptide; 293 AA
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                                                                                                                                                                                                                                                                                (first entry)
                                                                                                 Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Obrien AD, Schmitt CK;
                                                                                                                                                                                                                                                                                                                                                                 Shigella dysenteriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-207390/18.
N-PSDB; AAV11400.
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Matches 20; Conserv
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                                                                                  Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                       WO9811229-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1997;
                                                                                                                                                                                                                                                                                18-AUG-1998
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                                                                                                                                                                                                                                                           AAW58827;
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                                                                                                                                                                                                              RESULT 2
                                                                                                                                                                                                                          AAW58827
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CHHHASRVARMASDEFPSMC 261

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This is the Shiga-like toxin (SIT) subunit A amino acid sequence. SIT is a bacterial toxin related to the Shiga toxin (ShT). SIT and ShT have the smallest known B subunit of all AB toxins, and the A subunit has identical catalytic activity as the corresponding subunit in ricin. The B subunit amino acid sequences are used in the methods of the invention, which relates to the creation of a library of microorganism clones producing mutant proteins which are then screened for their ability to specifically bind to and kill carget cell. AAY3393-Y3389 and AAY43001-Y33024 are examples of mutant B subunit identified by the methods of the invention. The B subunit of the toxin has high binding specificity, and therefore mutant versions of the B subunit identified by the methods of the specific cell. Cytotoxic mutant proteins identified by the method can be used to identify therapeutic proteins and medicaments having binding specificity for a target cell. The cytotoxic mutants can also be used to construct diagnostic probes for detecting the presence of cell surface markers. These medicaments can be used to target medicines to target
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                                                                                                                                                                                                                                                       Shiga toxin; ShT; Shiga-like toxin; SLT; A subunit; B subunit; ricin; microorganism clone; combinatorial library; therapeutic protein; medicament; target cell; binding specificity.
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AAY39393 standard; protein; 293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 1a; 61pp; English.
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                                                                                                                                                                                                  Shiga-like Toxin 1, A subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-CA001137.
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                                                                                                                                                                                                                                                                                                                                                                                                  Shigella dysenteriae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gariepy J, Bray MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-590695/50
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-1998;
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XZXXX
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coli verotoxin (VT) can be used to treat intoxicated adults and children with enteric bacterial infections. They may also be used as prophylactics e.g. as a vaccine, against diarrhoeal disease or the development of extra-intestinal complications of 8 coli infection, especially haemolytic traemic syndrome. The antitoxin can also be used to detect 8. coli VT in a sample. The VT is recombinant, preferably a fusion protein containing a non-VT protein sequence and part of the 8 coli VTI or VT2 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pro-Ribosome Inactivating Protein, proRIP; peptide linker; cancer, inactivation; eukaryotic ribosome, alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                                                                                                                                                                                                                                                                                                 Compsn. contg. neutralising antitoxin against E.coli vero-toxin - used t
treat intoxicated individuals, and as a prophylactic against diarrhoeal
disease or extra-intestinal complications of E.coli infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compositions containing neutralising antitoxin against one or more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145. .155
/note= "Position of possible insertion of internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 114; DB 2; Length 315; 100.0%; Pred. No. 9.8e-11; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                        Stafford DC, Padhye NV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 51; 101pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shiga-like toxin (SLT-1) RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-00378761.
                                                                                                                                                    95US-00410058,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-00535636
                                                                                                                                                                                               (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (revised)
                                                                                                                                                                                                                                                                                   1996-505779/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage H-19B.
                                                                                                                                                                                                                                                                                                        N-PSDB; AAT42649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUN-1990;
                      WO9630043-A1
                                                                                                                                                                                                                                        Carroll SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-2003
25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5635384-A
                                                                  03-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW21702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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AAW21702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an exemplary cell toxin, which can be incorporated into the conjugates of the invention. The specification describes a conjugate, comprising a targeted agent and a chemokine receptor ligand. The conjugate binds to a chemokine receptor resulting in internalisation of the targeted agent in cells bearing the receptor. The conjugates are used for formulating a medicament or for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders associated with inflammatory responses resulting from activation; proliferation and migration of immune effector cells. The disorders or disease states comprise secondary tissue damage such as central nervous system (CNS) injury, CNS inflammatory diseases, neurodegenerative disorders, heart disease, inflammatory eye diseases, inflammatory bowel diseases, inflammatory joint diseases, inflammatory kidney or renal diseases, inflammatory lung diseases, inflammatory nasal diseases, inflammatory thyroid disease such as thyroiditis, or cytokineregulated cancers
                                           Chemokine receptor; ligand; inflammatory response; immune effector cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new therapeutic agent comprising a conjugate for treating secondary tissue damage and other disease conditions like Alzheimer's disease, stroke, Parkinson's disease and atherosclerosis.
                                                             secondary tissue damage; central nervous system injury; shiga; CNS inflammatory disease; neurodegenerative disorder; heart disease; inflammatory bowel disease; PCR primer; inflammatory powel disease; inflammatory ioint disease; inflammatory kidney; renal disease; inflammatory iung disease; inflammatory nasal disease; inflammatory thyroid disease; cytokine-regulated cancer; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine; haemolytic uraemic syndrome; detection.
sequence of exemplary cell toxin shiga toxin A-chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 114; DB 3
Pred. No. 9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Verotoxigenic E. coli toxin (VT1) subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 67; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 CHHHASRVARMASDEFPSMC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW06403 standard; protein; 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                   99WO-CA000659
                                                                                                                                                                                                                                                                                                                                                                                            98US-00120523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coggins PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        (OSPR-) OSPREY PHARM LID
                                                                                                                                                                                                                 Shigella dysenteriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 293 AA;
                                                                                                                                                                                                                                                             WO200004926-A2
                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcdonald JR,
                                                                                                                                                                                                                                                                                                                                                   21-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1997
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  acid
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RESULT 5

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Claim 2; Col 113-116; 121pp; English.
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                                                                                                                                                                                                         264 CHHHASRVARMASDEFPSMC 283
                                                                                                                                                                                                   1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                               90US-00535636.
92US-00987927.
95US-00378761.
09-DEC-1992; 92US-00987927
                                                                                                                                                                                                                                                                                                                                                                     95US-00485286
                                                                                                                                                                                                                                                              (revised)
(first entry)
                                                                                                                                                                                  Best Local Similarity 100.
Matches 20; Conservative
                      Morgan AER,
                                WPI; 1997-309831/28
          (DOWC ) DOWELANCO,
                                                                                                                                                                  Sequence 315 AA;
                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1992;
26-JAN-1995;
                                                                                                                                                                                                                                                             25-MAR-2003
02-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                               US5646026-A
                                                                                                                                                                                                                                                                                                                                                         08-JUL-1997
                                                       sednences.
                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                   AAW25139;
                                                                                                                                                                             Query Match
                     Hey TD,
                                                                                                                                                                                                                             RESULT 7
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which was engineered to contain a selectively removable internal peptide
which was engineered to contain a selectively removable internal peptide
thinker sequence separating the alpha and beta units of the RIP. When
separated the two units regain activity and are capable of inactivating
cukaryotic ribosomes and hence preventing protein production. Many
different RIPs may be produced with an internal linker including maize
and in the construction of therapeutic toxins targeted to
specific cells such as tumour cells via the attachment of a targeting
colypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy
(see U5486903). There is interest in expressing RIP recombinantly in
chost eukaryotic cells, because of the capacity to provide correct post-
translational processing. However, RIPs effectively inhibit protein
synthesis in eukaryotic cells resulting in cell death. Since the inactive
RIP proteins are not cytotoxic to eukaryotic cells, they can be
recombinantly expressed in such cells and then converted to active RIP
                                                                                                             DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food; recombinant production; screening; dairy; anti-bacterial; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 114; DB 2;
100.0%; Pred. No. 9.8e-11;
iive 0; Mismatches 0;
                                                                                                                                                                                                                 Claim 4; Col 115-116; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96681 standard; protein; 315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. coli verotoxin 1 subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-00410058.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
                        Hey TD, Morgan AER,
                                                                WPI; 1997-362934/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 315 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6080400-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY96681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY9668:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                         The sequences given in AAW21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proRIP of the invention. The proRIP has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein carbosomes, but can be converted by removal of the linker into a protein carbosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidase activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 288 RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected Toells. The inactive proRIP proteins make it possible to provide protein synthesis inhibitors with uses in practical and improved ways not before possible. The RIP can be used to make cytotoxic conjugates. Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                     Inactive precursor of maize ribosome-inactivating protein - also chimeric ribosome-inactivating protein precursors containing internal linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Apporin; SLT-1; Luffin A; MAP; Ricin A-chain; Asporin; SLT-1; Luffin B; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; thraspeutic roxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 114; DB 2; Length 315; 100.0%; Pred. No. 9.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLT-1 (a ribosome inhibitory protein) inactive precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                            Walsh TA
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Gaps

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Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial infections, comprises expression vector encoding bacterial toxin.

(DOWC ) DOWELANCO.

Williams JA, Byrne LM;

WPI; 2000-451195/39. N-PSDB; AAA51194.

Example 6; Col 69-71; 83pp; English. 

The invention relates to antitoxin therapy for humans and other animals.

The invention relates to antitoxin therapy for humans and other animals.

C Antitoxins which neutralize the pathologic effects of Escherichia coli

Coxins are generated by immunization of avian hosts with recombinant

C toxin fragments. The recombinant E. coli verotoxin (VT) is a fusion

protein comprising a non-verotoxin protein (especially an affinity tag)

C fused to a pórtion of the VT-1 or VT-2 sequence. The VT B chains are

Small proteins (approximately 8 kDa), so use of a small affinity tag was

CC small proteins (approximately 8 kDa), so use of a small affinity tag was

preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates

Single step affinity purification of subunits from periplasmic extracts.

CHOWEVER, the popor recovery of his-ragged VT-1 A and VT-2 A chains,

C HOWEVER, the to poor recovery of the VT-2 B subunit, strict uninduced

C conferraten. Due to the toxicity of the VT-2 B subunit, strict uninduced

C promocre control is necessary to permit cell viability. Bacterial host

C cells expression a recombinant expression vector encoding a polyhistidine

CC cells expressing a recombinant expression vector encoding a polyhistidine

CC closen from pET24hisVT2BL- and pET24VT2B, where "L+"

CC closen from pET34hisVT2BL- and pET24VT2B, where "L+"

CC indicates that the vector encodes the mature form of the protein and

CL "-" indicates that the vector encodes the mature form of the protein.

CT he bacterial cell is capable of expressing large quantities (40 mg/1) of

CT The bacterial toxins in environmental samples including soil, water,

C dairy processing instruments

CC dairy processing instruments

Sequence 315 AA;

Gaps ö Length 315; Indels ; 100.0%; Score 114; DB 3; 100.0%; Pred. No. 9.8e-11; 0; Mismatches 20; Conservative Query Match Best Local Similarity Matches

ਠੇ g AAU77817 standard; protein; 315 AA

AAU77817;

05-JUN-2002 (first entry)

E. coli verotoxin VT1-A chain protein.

antibacterial; haemostatic; vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome; Verotoxin; VT1-A; antitoxin; antidiarrheal; thrombotic thrombocytopenic purpura. 

Escherichia coli.

JS2002012658-A1

31-JAN-2002.

99US-00334477 16-JUN-1999; 97US-00816977. 13-MAR-1997;

(WILL/) WILLIAMS J A. (BYRN/) BYRNE L M. (PUGH/) PUGH C S G. Pugh CSG; Williams JA, Byrne LM,

WPI; 2002-205094/26. N-PSDB; ABK11775.

New recombinant expression vector encoding affinity tag and Escherichia coli type 1 or type 2 verotoxin, useful for treating or preventing

This invention relates to a recombinant expression vector encoding an affinity tag and protein comprising at least a portion of a bacterial coxin consisting of Escherichia coli type 1 or type 2 verocoxin. The expression vector can be used to produce recombinant verotoxin protein which can be used to create a vaccine against diseases caused by E. coli such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins are useful for treating humans and animals intoxicated with a bacterial coxin, particularly E. coli verotoxin. The antitoxins may also be used in the preventative treatment and in diagnostic assays to detect the treatment and in diagnostic assays to detect the complex are useful as immunogens for the production of vaccines.

The prevence of a troxin in a sample. The polypeptides derived from E. coli cortoxins are useful as immunogens for the production of vaccines.

The prevence of a trisk of diarrhoeal disease or a trisk of developing extractine thrombotic thrombocytopenic purpura. The present sequence syndrome, thrombotic thrombocytopenic purpura. The present sequence represents the E.coli verotoxin protein VTI-A used to create the diseases due to E. coli verotoxins and in producing vaccines Example 6; Page 38-39; 98pp; English. expression vectors of the invention 

Sequence 315 AA;

Gaps 0 Length 315; Indels 100.0%; Score 114; DB 5; 100.0%; Pred. No. 9.8e-11; ive 0; Mismatches 0; Query Match
Best Local Similarity 100.
Matches 20; Conservative

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RESULT 10 ADC00545

ADC00545 standard; protein; 315 AA ADC00545;

(first entry 14-DEC-2003 Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 590.

Escherichia coli; 0157:H7

JP2002355074-A.

10-DEC-2002

24-JAN-2002; 2002JP-00015959.

24-JAN-2001; 2001JP-00112010

(UYTS-) UNIV TSUKUBA

Enterohemorragic Escherichia coli O157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell. 

Claim 3; SEQ ID NO 590; 2067pp; Japanese.

The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the invention.

Sequence 315 AA;

(first entry)

(revised)

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New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a trans-location domain
                                                                   Shiga-like toxin; slt-A gene; hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 8A-C; 30pp; English.
                                             Phage H19B shiga-like toxin.
                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-470103/43.
N-PSDB; AAT91637.
                                                                                                                      Bacteriophage H-19B.
                                                                                                                                                                                                                                                                                                         (SERA-) SERAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                       of a protein.
                                                                                                                                                                                            04-AUG-1993;
                                                                                                                                                                                                                                25-APR-1985;
07-JUN-1985;
                                                                                                                                                                                                                                                                                  27-JUN-1991;
                                                                                                                                              US5668255-A.
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                     27-MAR-1998
17-0CT-2003
           25-MAR-2003
                                                                                                                                                                     16-SEP-1997
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                                                                                                                                                                                                                                                                      4-JUN-1990
                                                                                                                                                                                                                                                                                                                                  Murphy JR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to attenuated verotoxins (VTs) comprising mutations in one or more of the regions spanning residues 167-172 or 202-207 of the mature verotoxin A subunit. The invention also relates to the mutant verotoxin A subunit and the DNA encoding it; anticancer agents containing verotoxin A subunit and a ligand, especially troponin I, which binds to a cancer cell; a fusion gene encoding the mutant A subunit and verotoxin a subunit and vectors encoding the mutant A subunit/troponin I subunit, or the fusion gene encoding the mutant verotoxin A subunits, fusion proteins, and polymuciacides encoding the useful in the treatment of cancer. The present sequence represents the A subunit
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Attenuated verotoxin controls tumor growth for treatment of cancer
                                                                                                                                                                                                                                          Attenuated verotoxin; attenuated VT; mutant A subunit; troponin I; fusion protein; cancer; cytostatic; verotoxin 1; VT1; A subunit.
                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 114; DB 7; Length 315; 100.0%; Pred. No. 9.8e-11; tive 0; Mismatches 0; Indels (
           Length 315;
                                  Indels
          100.0%; Score 114; DB 7;
100.0%; Pred. No. 9.8e-11;
iive 0; Mismatches 0;
                                                                                                                                             ADH34319 standard; protein; 315 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 3; 56pp; Japanese.
                                                                       264 CHHHASRVARMASDEFPSMC 283
                                                          1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                         03-FEB-2003; 2003WO-JP001043
                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2002; 2002JP-00026577
                                                                                                                                                                                                                      Verotoxin 1 (VT1) A subunit
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                 Escherichia coli; 0157:H7.
                     Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in the treatment of coof verotoxin 1 (VT1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-646309/61.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshida H, Liu X;
                                                                                                                                                                                                                                                                                                                                                                                                         (YOSH/) YOSHIDA H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 315 AA;
                                                                                                                                                                                                                                                                                                         WO2003066854-A1.
                                                                                                                                                                                            11-MAR-2004
                                                                                                                                                                                                                                                                                                                                 14-AUG-2003
                                                                                                                                                                    ADH34319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
           Query Match
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85US-00726808. 85US-00742554. 89US-00456095.

84US-00618199

90US-00538276.

93US-00102387.

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This protein comprises the Escherichia coli phage H19B Shiga-like toxin.

UNA (see AAT91637) encoding the A subunit of the Shiga-like toxin was

UNA (see AAT91637) encoding the A subunit of the Shiga-like toxin was

UNA (see AAT91637) encoding the A subunit of the Shiga-like toxin was

UNA (SLTA-DTB'-LIZ) gene that was expressed in E. coli. The hybrid protein of

Can be isolated and used to treat conditions involving over-production of

Can be bearing ILZ receptors, such as certain T-cell lymphomas and organ

CC cells bearing ILZ receptors, resulting in cessation of protein synthesis and

CC death of target cells. Claimed hybrid proteins comprise a translocation

CC domain and a cell binding domain from e.g. a hormone, growth factor or

protein toxin. The hybrid molecules can be used for the delivery of

agents (e.g. therapeutic genes, toxins, detectable labels) into cells.

CC protein toxin. The hybrid molecules can be used for the delivery of

agents (e.g. therapeutic genes, toxins, detectable labels) into cells.

CC protein toxin relatively low doses, since a high proportion of the

cubecules can be manufactured as a single hybrid recombinant protein,

CC molecules can be manufactured as a single hybrid recombinant protein,

CC permitting reproducibility, consistency, and the precise control of

CC composition. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 114; DB 2; Length 316; 100.0%; Pred. No. 9.8e-11; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW06407 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 CHHHASRVARMASDEFPSMC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CHHHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
AAW06407
ID AAW06
XX
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Gaps

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AAW25786 standard; protein; 316 AA.

AAW25786

RESULT 12
AAW25786
ID AAW25
XX
AC AAW25

ద 8

us-10-717-243-56.open.rag

AAW06407;

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The invention relates to antitoxin therapy for humans and other animals.

Antitoxins which neutralize the pathologic effects of Escherichia coli
coxins are generated by immunization of avian hosts with recombinant
coxins are generated by immunization of avian hosts with recombinant
coxins are generated by immunization of avian hosts with recombinant
coxins are generated by immunization of avian hosts with recombinant
coxins are generated by immunization of sequence. The VT is a fusion
protein comprising a non-verotoxin protein (especially an affinity tag)
complement of the VT-1 or VT-2 sequence. The VT B chains are
considered (i.e. polyhistidine). A polyhistidine affinity tag facilitates
ingle step affinity purification of subunits from periplasmic extracts.
However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains,
conference control is necessary to permit cell viability. Bacterial host
colls expression of malcose binding protein (MBP) fused subunit, strict uninduced
promoter control is necessary to permit cell viability. Bacterial host
colls expressing a recombinant expression vector encoding a polyhistidine
affinity tag and a portion of the VT-2 B chain are claimed. The vector is
chosen from pgr14hisVT2BL. and pgr24ATSB, where "L"
cindicates that the vector encodes the mature form of the protein and
"L" indicates that the vector encodes the mature form of the protein and
"L" indicates that the vector encodes the mature form of the protein and
"L" indicates that the vector encodes the mature form of the protein
conferial cell is capable of expressing large quantities (40 mg/1) of
VT-2B. The toxins are useful for immunizing non-mammals and for detecting
conferial cannonemental samples including soil, water,
industrial samples, biological samples and samples obtained from detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial infections, comprises expression vector encoding bacterial toxin.
                                                    316. .323
/label= Polyhistidine_affinity_tag
                           /label= Verotoxin-1_subunit_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Col 89-90; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                       97US-00816977
                                                                                                                                                                                                                                                                                        95US-00410058
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                                                                                                                                                                                                                                                                                                                                          (OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                              Williams JA, Byrne LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-451195/39.
N-PSDB; AAA51208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 323 AA;
                                                                                                                                                                                                                                       13-MAR-1997;
                                                                                                                                                                                                                                                                                        24-MAR-1995;
                                                                                                                                 US6080400-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU77822
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions containing neutralising antitoxin against one or more E. coli verotoxin (VT) can be used to treat intoxicated adults and children with enteric bacterial infections. They may also be used as prophylactics e.g. as a vaccine, against diarrhoeal disease or the development of extra-intestinal complications of E.coli infection, especially haemolytic uraemic syndrome. The antitoxin can also be used to detect E. coli VT in a sample. The VT is recombinant, preferably a fusion protein containing a non-VT protein sequence and part of the E.coli VTI or VT2 sequence. This is a histidine tagged version of subunit A of VTI as expressed from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Compsn. contg. neutralising antitoxin against E.coli vero-toxin - used t
treat intoxicated individuals, and as a prophylactic against diarrhoeal
disease or extra-intestinal complications of E.coli infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                 Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine; haemolytic uraemic syndrome; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; recombinant production; screening; dairy; anti-bacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                   Histidine tagged verotoxigenic E. coli toxin (VT1) subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 114; DB 2; Length 323; 100.0%; Pred. No. 1e-10; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant E. coli VT-1 A-polyhistidine fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 61-62; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Padhye NV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96686 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHHHASRVARMASDEFPSMC 283
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                                              25-FEB-1997 · (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carroll SB, Stafford DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-505779/50.
N-PSDB; AAT42663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector pET-23b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyhistidinē.
                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-1995;
                                                                                                                                                                                                                                                                                      WO9630043-A1
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Verotoxin; VT1-A; antitoxin; antidiarrheal; antibacterial; haemostatic; vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome;
                                           Gaps
                                         ö
; Score 114; DB 3; Length 323;
; Pred. No. 1e-10;
0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                       HIS-tagged E. coli VT-1A verotoxin protein.
                                                                                                                                                                                                 AAU77822 standard; protein; 323 AA.
                                                                                                  264 CHHHASRVARMASDEFPSMC 283
                                                                            1 CHIHASRVARMASDEFPSMC 20
                                                                                                                                                                                                                     ZZXEXEXEX
ZZXZ
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Location/Qualifiers

Synthetic.

Chimeric.

Key

264

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RESULT 14

AAY96686;

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Compositions containing neutralising antitoxin against one or more E. coli verotoxin (VT) can be used to treat intoxicated adults and children with enteric bacterial infections. They may also be used as prophylactics e.g. as a vaccine, against diarrhocal disease or the development of extra-intestinal complications of E.coli infection, especially haemolytic uraemic syndrome. The antitoxin can also be used to detect E. coli vr in a sample. The VT is recombinant, preferably a fusion protein containing a non-VT protein sequence and part of the E.coli VTI or VT2 sequence. This
                                                                                                                                                                                                                                                                                                                                                Compsn. contg. neutralising antitoxin against E.coli vero-toxin - used to treat intoxicated individuals, and as a prophylactic against diarrhoeal disease or extra-intestinal complications of E.coli infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food; recombinant production; screening; dairy; anti-bacterial; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 114; DB 2; Length 326; 100.0%; Pred. No. 1e-10; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34. .326
/label= Mature_verotoxin-1_subunit_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is a flag tag/VT1 A subunit fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLAG tag-VT-1 subunit A fusion protein.
                                                                                                                                                                                                                                              Padhye NV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY96692 standard; protein; 326 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 79; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 CHHHASRVARMASDEFPSMC 294
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                                                                                                                                                                                                        (OPHI-) OPHIDIAN PHARM INC
                                                                                                                                                                                                                                              Carroll SB, Stafford DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                     WPI; 1996-505779/50.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer; FLAG tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 326 AA;
                                                                                                                                                                                                                                                                                                            N-PSDB; AAT42673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1997;
                                        WO9630043-A1
                                                                                                                         25-MAR-1996;
                                                                                                                                                               24-MAR-1995;
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                                                                                03-0CT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY96692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY96692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a recombinant expression vector encoding an affinity tag and protein comprising at least a portion of a bacterial toxin consisting of Escherichia coli type 1 or type 2 vertoxin. The expression vector can be used to produce recombinant vertotoxin protein which can be used to create a vaccine against diseases caused by E. coli such as vertoxin haemorrhagic cystitis and balantitis. The antitoxins are useful for treating humans and animals intoxicated with a bacterial toxin, particularly E. coli vertocoxin. The antitoxins may also be used in the preventative treatment and in diagnostic assays to detect the correction at example. The polypeptides derived from E. coli vertocoxins are useful as immunogens for the production of vaccines, including multivalent vaccines and antitoxins, which can be administered to a subject at risk of diarrhoeal disease or at risk of developing extractinestinal complications of E. coli infections, e.g. haemolytic uremic syndrome, thrombocytopenic purpura. The present sequence represents the HIS tagged E.coli VTI-A verotoxin protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant expression vector encoding affinity tag and Escherichia coli type 1 or type 2 verotoxin, useful for treating or preventing diseases due to E. coli verotoxins and in producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine; haemolytic uraemic syndrome; detection.
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                                                                                                                     316. .323
/note= "C terminal peptide with HIS tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flag tag/VT1 A subunit fusion protein.
thrombotic thrombocytopenic purpura.
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW06413 standard; protein; 326 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 48-49; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pugh CSG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHHHASRVARMASDEFPSMC 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pre-
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                                                                                                                                                                                                                                                                   99US-00334477.
                                                                                                                                                                                                                                                                                                          97US-00816977
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Byrne LM,
                                                                                                                                                                                                                                                                                                                                                WILLIAMS J A.
BYRNE L M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-205094/26.
N-PSDB; ABK11789.
                                                                                                                                                                                                                                                                                                                                                                                           PUGH C S G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 20; Conserv
                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 323 AA;
                                                                                                                                                                                   US2002012658-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Williams JA,
                                                                                                                                                                                                                                                                                                            13-MAR-1997;
                                                                                                                                                                                                                                                                 16-JUN-1999;
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                                                                                                                                                                                                                           31-JAN-2002
                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW06413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                (WILL/)
(BYRN/)
                                                                                                                                                                                                                                                                                                                                                                                             (PUGH/)
                                                                                                                   Peptide
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The rigg cay is received between the order in the pFlag-1 vector.

ECORI/Xhol A subunit PCR fragments were cloned into identically cleaved pragation to principle in the pragation of pragatic vector and synchronic protein contains the N-terminal 8 amino acid flag tag, for secretion of A subunit fusion proteins. After secretion the periplasmic protein contains the N-terminal 8 amino acid flag tag, followed by 4 vector-encoded amino acids fused to the recombinant A subunit. When B chains are small proteins (approximately 8 kba), so use of a small affinity tag was preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates single step affinity purification of subunits from periplasmic extracts. However, due to poor recovery of his-tagged vrome periplasmic extracts. However, due to poor recovery of his-tagged vrome periplasmic extression of MBP fused subunits was undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced promoter control is necessary to permit cell viability. Bacterial host cells expressing a recombinant expression vector encoding a polyhistidine affinity tag and a portion of the VT-2 B chain are claimed. The vector is chosen from prizythisyT2BL-, prizzthisyT2BL- and pBT24VT2B, where "L+" indicates that the vector encodes the proprien form of the protein and "L-" indicates that the vector encodes the mature form of the protein and "L-" indicates that the vector encodes the mature form of the protein and "L-" indicates that the vector encodes the mature form of the protein and bacterial cell is capable of expressing large quantities (40 mg/l) of VT-2B. The toxins are useful for immunizing non-mammals and for detecting bacterial samples, biological samples and samples obtained from protein and and protein and protein and protein samples, biological samples and samples obtained from from the protein and protein and protein and protein samples, biological samples and samples and samples obtained from from the protein and protein and protein and protein samples, biological sampl
                                                                                                                                                                                                                                                            Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial infections, comprises expression vector encoding bacterial toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           verotoxin (VT) types 1 and 2 subunit A were cloned into pFLAG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The flag tag is located between the OmpA secretion signal sequence and
                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Col 119-122; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dairy processing instruments
                                   (OPHI-) OPHIDIAN PHARM INC.
                                                                                              Williams JA, Byrne LM
                                                                                                                                                             WPI; 2000-451195/39.
N-PSDB; AAA51218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coli
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Gaps ö 100.0%; Score 114; DB 3; Length 326; 100.0%; Pred. No. 1e-10; ive 0; Mismatches 0; Indels ( Conservative Similarity Sequence 326 AA; Mar Local Sa Query Match Matches

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275 CHHHASRVARMASDEFPSMC 294 20 1 CHHHASRVARMASDEFPSMC g

AAU77828 standard; protein; 326 AA AAU77828; RESULT 18 

(first entry) 05-JUN-2002

Flag tag/VT1 fusion protein.

Verotoxin; antitoxin; antidiarrheal; antibacterial; Flag tag/VT1; haemostatic; vaccine; haemorrhagic cystitis; balantitis; haemolytic uremic syndrome; thrombotic thrombocytopenic purpura.

Escherichia coli. Synthetic

JS2002012658-A1.

31-JAN-2002

99US-00334477. 16-JUN-1999;

This invention relates to a recombinant expression vector encoding an affinity tag and protein comprising at least a portion of a bacterial coxin consisting of Escherichia coli type 1 or type 2 verocoxin. The expression vector can be used to produce recombinant verotoxin protein which can be used to create a vaccine against diseases caused by E. coli such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins are useful for treating humans and animals intoxicated with a bacterial coxin, particularly E. coli verotoxin. The antitoxins may also be used in the preventative treatment and in diagnostic assays to detect the treatment are useful as immunogens for the production of vaccines. Correctoxins are useful as immunogens for the production of vaccines, including multivalent vaccines and antitoxins, which can be administered to a subject at risk of diarrhoeal disease or at risk of developing extractines. Incomplications of E. coli infections, e.g. haemolytic uremic syndrome, thrombotic thrombocytopenic purpura. The present sequence represents the Flag-tag/VTI fusion protein of the invention. This fusion protein of the recombinant New recombinant expression vector encoding affinity tag and Escherichia coli type 1 or type 2 verotoxin, useful for treating or preventing diseases due to E. coli verotoxins and in producing vaccines. Example 6; Page 64-65; 98pp; English. Pugh CSG; 275 CHHHASRVARMASDEFPSMC 294 1 CHHHASRVARMASDEFPSMC 20 97US-00816977 proteins of the invention 20; Conservative Williams JA, Byrne LM, WILLIAMS J A. WPI; 2002-205094/26. N-PSDB; ABK11799. BYRNE L M. PUGH C S G. Best Local Similarity Matches 20; Conserv Sequence 326 AA; 13-MAR-1997; (BYRN/) (PUGH/) Query Match WILL/) 셤 ଚ

Gaps ; 100.0%; Score 114; DB 5; Length 326; 100.0%; Pred. No. 1e-10; ive 0; Mismatches 0; Indels

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RESULT 19 AAW29294

AAW29294 standard; protein; 332 AA. 20-APR-1998 (first entry) AAW29294;

BPI peptide fusion protein pING3793 vector construct protein.

Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA, vector.

Pectobacterium carotovorum. Homo sapiens. Synthetic 

25-SEP-1997

WO9735009-A1.

97WO-US005287. 18-MAR-1997;

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17-JUN-1995;
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15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-1999.
                                  Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY55891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY55891
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                  Lusion protein and is suitable for introduction into a bacterial host.

It were to comprises: (a) DNA encoding at least one cationic
bactericidal/permeability increasing peptide (BPI), (b) DNA encoding at least one cationic
carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
coarrier protein, and (b) The present sequence represents the protein
from the pING3793 vector construct which codes for a BPI fusion protein.
The peptides have many uses including the treatment of bacterial and
cumpal infections. BPI peptides also bind to endotoxins and heparin,
neutralising their effects. The peptides have further been shown to
inhibit anglogenesis (partly due to heparin-binding activity). The fusion
proteins have been found to be expressed in large amounts without
significant proteolysis, and in some cases are actually secreted from the
chost cells. This allows the indirect production of anti-microbial BPI
                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                   Recombinant production of bactericidal/permeability increasing protein -
by expression as a fusion protein in microbial host cells, then cleaving
the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybrid; fusion; membrane translocation; binding region; HIV; infection; toxin; steroid; hormone; monoclonal antibody; antigen; diphtheria; exotoxin; phenylketonuria; cholera; interleukin; IL-2; protease; epidermal growth factor; rcin; tetanus; hexosaminidase; Shiga-like toxin A; SLT-A; ligand; insulin; nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 114; DB 2; Length 3 100.0%; Pred. No. 1e-10; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by stop codon"
                                                                                                                                                 Example 1; Page 148-150; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR13118 standard; protein; 409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                277 CHHHASRVARMASDEFPSMC 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-00456095.
 96US-00621803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shiga-like toxin subunit A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
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Best Local Similarity 100.0
Matches 20; Conservative
                                                                   WPI; 1997-480215/44.
                     (XOMA ) XOMA CORP
                                                                               N-PSDB; AAT86332
                                                                                                                                                                                                                                                                                                                                                            Sequence 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae
22-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1989;
14-JUN-1990;
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                                             Setter MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the binding domain of a cell-binding ligand, allowing binding of the mol. to an animal cell; (2) a portion (B) of a translocation domain of a and protein able to translocate (C) across the cell cytopland; membrane, and and (3) a portion (C) which is to be introduced into the cell. (A) derived from a steroid or polypeptide hormone, a single-chain analogue of a monoclonal antibody able to bind an antigen expressed on the cell surface, or a polypeptide toxin. (B) is derived from a toxin (e.g. diphtheria toxin or Pseudomonas exotoxin (A) may be derived from insulin, interleukins 2, 3 or 6 or epidermal growth factor. Suitable enzymes in (C) include cholera toxin, ricin, tetanus toxin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hexosamininidase A, protease, muclease, SLT-A, etc. Specified examples are CT-A/DT-B'/IL-2, SLTA/DT-B'/IL-2, HIVP-BP/DT-B'/IL-2, and the phenylalanine hydroxylase-DT-B' or their biologically active mutants. (GT-A= cholera toxin, DT-B' = truncated diphtheria toxin, SLTA= Shiga-like toxin A, HIVP-BP= HIV protease binding protein. See also AAQ12710-12. (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant, hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain, botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                             Hybrid molecules for targetting chemical entity to cell - have membrane trans-locating and cell binding-regions and used to treat HIV infection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybrid molecules are produced by covalently linking (1) a portion (A) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 114; DB 2; Length 4
100.0%; Pred. No. 1.3e-10;
ive. 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.coli bacteriophage H19B Shiga-like toxin A subunit.
                                                                                                                                                                                                                                                                                                     trans-locating and cell binding-regions genetic enzyme-deficiency disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by TGA"
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 8(1-3); 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 CHEHASRVARMASDEFPSMC 283
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Best Local Similarity lvv..
20; Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                                                                              WPI; 1991-222845/30.
N-PSDB; AAQ12711.
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(SERA-) SERAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 409 AA;
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The intring your not a certification of a naturally occurring protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein to coxin, and phtherial toxin, botulinum neurotoxin, richi, cholera toxin, LT toxin, Ghiga-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the E.coli bacteriophage H19B Shiga-like toxin A subunit sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate therapy to affected cells, allowing them to function properly and alleviate or cure the disease. The hybrid is affected cells an enzyme supplying the missing function, to supplementing cellular levels of a particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adjocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral cinfections such as detected believed on 17-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to a recombinant DNA molecule encoding a hybrid cein comprising three parts: (a) the first part comprises a portion of binding domain of a cell-binding polypeptide ligand allowing the
                                                                                                                                                                                                                                                                                                       Recombinant DNA molecule encoding a three part hybrid protein used in the treatment of Aids and genetic deficiency diseases.
                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 8; 31pp; English
85US-00726808.
85US-00742554.
85US-0075695.
90US-00538276.
91US-00722484.
                                                                                                                                                                                                                                      WPI; 1999-632431/54.
N-PSDB; AAZ30662.
                                                                                                                                                     (SERA-) SERAGEN INC.
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25-APR-1985;
07-JUN-1985;
22-DEC-1989;
                                                                                                              04-AUG-1993;
                                                                 14-JUN-1990;
                                                                                          27-JUN-1991;
                                                                                                                                                                                               Murphy JR;
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Gaps ö Length 409; 0; Indels Query Match 100.0%; Score 114; DB 2; Best Local Similarity 100.0%; Pred. No. 1.3e-10; Matches 20; Conservative 0; Mismatches 0;

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AAY78591 standard; protein; 409 AA. 

AAY78591;

(revised) 06-AUG-2003 05-MAY-2000

(first entry)

E. coli bacteriophage H19B shiga-like toxin amino acid sequence.

Shiga-like toxin, hybrid protein, translocation domain, cell destruction, cell binding domain, genetic deficiency disease, cell targetting, cancer, adipocyte, enzyme delivery, anti-viral, HIV.

Bacteriophage H-19B.

Location/Qualifiers

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/label= Unknown
/note= "Encoded by TGA"
                                      85US-00726808.
85US-00742554.
85US-0075695.
90US-00538276.
91US-00722484.
                            95US-00479510
                                   84US-00618199
Misc-difference 317
                            07-JUN-1995;
                                                        04-AUG-1993;
                                                 14-JUN-1990;
27-JUN-1991;
              US6022950-A.
                     08-FEB-2000.
                                      25-APR-1985;
07-JUN-1985;
                                             2-DEC-1989
                                   07-JUN-1984
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(SERA-) SERAGEN INC

Murphy JR;

WPI; 2000-160390/14

N-PSDB; AAZ90018

New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer and HIV infections

Example 3; Fig 8; 32pp; English.

This sequence represents the bacteriophage H19B shiga-like toxin protein sequence. The toxin can be included in the hybrid protein of the sequence. The toxin can be included in the hybrid protein of the hybrid protein comprises a first part which is a portion of the binding domain of a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell-binding ligand, effective to portion of a translocation domain of diphtheria toxin) the second part comprises a chemical entity to be introduced into the cell. The third part comprises a chemical entity to be introduced into the cell, where each of the first and third part is nonnative with respect to naturally occurring protein, and the covalent bond attaching the second and third part is cleavable. The toxin represented by the present sequence can form part of the third portion of the hybrid contein. The cell binding domain binds to a specific cell and the protein. The cell binding domain binds to a specific cell and the correst to the cytosel. The third part of the protein, linked to the translocation domain through a cleavable bond, can then carry out its function. The hybrid molecules are useful for treating genetic deficiency diseases by delivering to affected cells an enzyme supplying the missing function, to supplement cellular levels of a particular enzyme or a carce precursor or cofactor, to direct toxins or other poisons to infected cells, and to counteract viral infections such as HIV by infected colls, on 06-AUG-2003 to correct OS field.)

Sequence 409 AA;

Gaps ö Length 409; Indels 100.0%; Score 114; DB 3; 100.0%; Pred. No. 1.3e-10; ive 0; Mismatches 0; 100.0%; 20; Conservative Query Match Best Local Similarity Matches

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RESULT 23

AAY96694 standard; protein; 690 AA AAY96694 ID AAY9 XX Verotoxin, VT2-A, antitoxin, antidiarrheal, antibacterial, haemostatic, vaccine, haemorrhagic cystitis, balantitis, MBPNVT1-A, haemic syndrome, thrombotic thrombocytopenic purpura.

Escherichia coli

Synthetic.

US2002012658-A1.

31-JAN-2002

MBPNVT1-A fusion protein #2.

(first entry)

05-JUN-2002

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Gesigned to allow expression of the native proteins as C-terminal fusions to a periphasmically-secreted version of maltose binding protein (WBP).

To a periphasmically-secreted version of maltose binding protein (WBP).

To a periphasmically-secreted version of maltose binding protein (WBP).

To the chains are small proteins (approximately 8 kDa), so use of a small affinity tag was preferred (i.e. polyhistidine). A polyhistidine affinity tag facilitates single step affinity purification of submits from periphasmic extracts. However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains, expression of MBP fused submits was undertaken. Due to the toxicity of the VT-2 B submit, strict uninduced promoter control is necessary to permit call viability. Bacterial host calls expressing a recombinant expression vector encoding a polyhistidine affinity tag and a portion of the VT-2 B chain are claimed. The vector is chosen from periodes the preprotein form of the protein and "L-" indicates that the vector encodes the mature form of the protein and "L-" indicates that the vector encodes the mature form of the protein and "L-" indicates that the vector encodes the mature form of the protein The bacterial call is capable of expressing large quantities (40 mg/l) of VT-2B. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial infections, comprises expression vector encoding bacterial toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             toxins are useful for immunizing non-mammals and for detecting bacterial toxins in environmental samples including soil, water, industrial samples and samples obtained from food and dairy
                                                                                                                          VT-1; verotoxin; antitoxin therapy; fusion protein; affinity tag; food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                             recombinant production; screening; dairy; anti-bacterial; vaccine; primer; maltose binding protein; MBP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 114; DB 3; Length 690; 100.0%; Pred. No. 2.3e-10; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 7; Col 133-138; 83pp; English.
                                                                               MBP-VT-1 subunit A fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHIHASRVARMASDEFPSMC 658
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                                                                                                                                                                                                                                                                                                                                                                          97US-00816977.
                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00410058
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OPHI-) OPHIDIAN PHARM INC.
                                        26-SEP-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams JA, Byrne LM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 processing instruments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-451195/39.
N-PSDB; AAAS1226.
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les 20; Conserv
                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 690 AA;
                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAR-1995;
                                                                                                                                                                                                                                                                                         US6080400-A.
                                                                                                                                                                                                                                                                                                                                 27-JUN-2000.
                                                                                                                                                                                                                            Synthetic.
Chimeric.
AAY96694;
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This invention relates to a recombinant expression vector encoding an affinity tag and protein comprising at least a portion of a bacterial toxin consisting of Escherichia coli type 1 or type 2 verotoxin. The expression vector can be used to produce recombinant verotoxin protein which can be used to create a vaccine against diseases caused by E. coli such as verotoxin haemorrhagic cystitis and balantitis. The antitoxins are useful for treating humans and animals intoxicated with a bacterial toxin, particularly E. coli verotoxin. The antitoxins may also be used in the preventative treatment and in diagnostic assays to detect the preventative treatment and in diagnostic assays to detect the presence of a toxin in a sample. The polypeptides derived from E. coli verotoxins are useful as immunogens for the production of vaccines, verotoxins may also be used in considerable manual disease or at risk of developing extracting multivadent vaccines and antitoxins, which can be administered to a subject at risk of diarrhoeal disease or at risk of developing extractines in the mombalic thrombocytopenic purpura. The present sequence represents the MBPNVT1-A protein #2 of the invention. This fusion protein associated to facilitate purification of the recombinant proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant expression vector encoding affinity tag and Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli type 1 or type 2 verotoxin, useful for treating or preventing diseases due to E. coli verotoxins and in producing vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 690;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maltose binding protein/VT1 A subunit fusion protein.
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100.0%; Pred. No. 2.3e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 72-73; 98pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                   Pugh CSG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   639 CHHHASRVARMASDEFPSMC 658
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                                                                                                                                                                                                                                                                                             97US-00816977.
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                                                                                                                                                                                                                                                                                                                                                                                               Williams JA, Byrne LM,
                                                                                                                                                                                                                                                                                                                             WILLIAMS J A.
BYRNE L M.
PUGH C S G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ABK11957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 690 AA;
                                                                                                                                                                                                                                                                                             13-MAR-1997;
                                                                                                                                                                                                                                                           16-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW06411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 8
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(PUGH/)
                                                                                                                                                                                                                                                                                                                           (MILL/)
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AAU77830 standard; protein; 690 AA

RESULT 24

AAU77830

AAU77830 ID AAU7 XX AC AAU7

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US2002012658-A1
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                                                                                    13-MAR-1997;
                                                                                                                        24-MAR-1995;
                                         27-JUN-2000.
  US6080400-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU77826;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Compositions containing neutralising antitoxin against one or more E. coli verotoxin (VT) can be used to treat intoxicated adults and children with enteric bacterial infections. They may also be used as prophylactics e.g. as a vaccine, against diarrhoeal disease or the development of extra-intestinal complications of E.coli infection, especially haemolytic uraemic syndrome. The antitoxin can also be used to detect E. coli VT in a sample. The VT is recombinant, preferably a fusion protein containing a non-VT protein sequence and part of the E.coli VTI or VT2 sequence. This is a maltose binding protein/VTI A subunit fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsn. contg. neutralising antitoxin against E.coli vero-toxin - used to treat intoxicated individuals, and as a prophylactic against diarrhoeal disease or extra-intestinal complications of E.coli infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VT-1; verotoxin; antitoxin therapy, fusion protein; affinity tag; food, recombinant production; screening; dairy; anti-bacterial; vaccine; primer; maltose binding protein; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                   Verotoxin; Escherichia coli; enteric infection; diarrhoea; vaccine; haemolytic uraemic syndrome; detection.
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/label= Maltose_binding_protein/
/note= "Acts as an affinity tag"
416.708
/label= Mature_verotoxin-1_subunit_A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 114; DB 2;
100.0%; Pred. No. 2.4e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 6; Page 70-72; 101pp; English
                                                                                                                                                                                                                                                                                                                                 Padhye NV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY96690 standard; protein; 708 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBP-VT-1 subunit A fusion protein.
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                                                                                                                                                                                                        96WO-US004093.
                                                                                                                                                                                                                                               95US-00410058
                                                                                                                                                                                                                                                                                        (OPHI-) OPHIDIAN PHARM INC.
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                                                                                                                                                                                                                                                                                                                               Carroll SB, Stafford DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-505779/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT42671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 708 AA;
                                                                                                                                                                                                      25-MAR-1996;
                                                                                                                        WO9630043-A1
                                                                                                                                                               03-OCT-1996.
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Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY96690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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Gesigned to allow expression of the native proteins as C-terminal fusions designed to allow expression of the native proteins as C-terminal fusions to a periplaamically-secreted version of maltose binding protein (MBP).

The vector contains an engineered factor Xa cleavage site, which permits the removal of the affinity tag (i.e. MBP) from the fusion protein after purification. VT B chains are small proteins (approximately 8 kDa), so the of a small affinity tag was preferred (i.e. polyhistidine affinity tag and interest single step affinity purification of subunits from periplasmic extracts. However, due to poor recovery of his-tagged VT-1 A and VT-2 A chains, expression of MBP fused subunits was undertaken. Due to the toxicity of the VT-2 B subunit, strict uninduced promoter control is necessary to permit cell viability. Bacterial host cells expressing a recombinant expression vector encoding a polyhistidine cells expressing a recombinant expression vector encoding a polyhistidine chosen from pET24hisVT2BL- and pET24VT2B, where "L+" indicates that the vector encodes the mature form of the protein and "L-" indicates that the vector encodes the mature form of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bacterial toxins in environmental samples including soil, water, industrial samples, biological samples and samples obtained from food and
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial cell for recombinantly expressing bacterial toxins in large quantities useful for immunization and treatment of bacterial infections, comprises expression vector encoding bacterial toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The bacterial cell is capable of expressing large quantities (40\ \text{mg/l}) of VT-2B. The toxins are useful for immunizing non-mammals and for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Verotoxin; VT2-A; antitoxin; antidiarrheal; antibacterial; haemostatic; vaccine; haemorrhagic cystitis; balantitis; MBPNVT1-A; haemotytic uremic syndrome; thrombotic thrombocytopenic purpura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 114; DB 3;
Pred. No. 2.4e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 6; Col 105-110; 83pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CHHHASRVARMASDEFPSMC 20
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97US-00816977.
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                                                                                                                                                             OPHI-) OPHIDIAN PHARM INC.
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MY 11-JAN-2002.

MY 16-JUN-1999; 99US-00314477.

MY 11-MAR-1997; 97US-00816977.

MY 11-MAR-1997; 97US-00816977.

MY (WILL) WILLIAMS J A.

PA (WILL) WILLIAMS J A.

PA (WILL) PUGH C S G.

MY 12 2002-205094/26.

MY 12 2002-205094/26.

MY 12 2002-205094/26.

MY WP1; 2002-205094/26.

MY 12 2002-205094/26.

MY 12 2002-205094/26.

MY 12 2002-205094/26.

MY 12 2002-205094/26.

MY 12 2002-205094/26.

MY 2 MAR-11997.

MY 2 ABX11797.

MY 12 2002-205094/26.

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SQ Sequence 708 AA;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.4e-10;
Matches 20; Conservative 0; Mismatches 0; Indels

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0; Gaps

Search completed: June 22, 2005, 07:11:20 Job time : 166 secs

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Sequence 2, Application US/08425336 Patent No. 5621083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,98:
REFERENCE/DOCKET NUMBER: 3135
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , TOPOLOGY: linear
, MOLECULE TYPE: protein
US-08-425-336-2
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                 RESULT 1
US-08-425-336-2
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                                                                June 20, 2005, 09:35:58; Search time 30 Seconds (without alignments) 624.564 Million cell updates/sec
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Sequence 2, App
Sequence 247, 1
Sequence 2, App
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Sequence 2, Ag
Sequence 247,
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-477-484B-2
US-08-641-8010-2
US-08-611-8010-2
US-09-136-389-2
US-09-136-389-2
US-09-610-838-2
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US-09-610-838-2
US-09-610-838-2
US-09-610-838-1
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US-09-645-6038-2
US-08-488-113B-108
US-08-488-113B-108
US-08-46-36-108
US-08-646-36-108
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US-08-425-336-109
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Maximum Match 100%
Listing first 45 summaries
                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1287
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Match Length
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Maximum DB seq length: 251
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GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                          Sequence 1
Sequence 1
Sequence 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: DECOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILLING DATE: 18-APR-1995
CLASSIFICATION: 530
        US-08-488-113B-105
US-08-488-113B-105
US-08-488-113B-105
US-08-477-484B-103
US-08-477-484B-104
US-08-477-484B-105
US-08-477-484B-105
US-08-477-484B-105
US-08-46-360-104
US-08-646-360-105
US-08-646-360-105
US-08-646-360-105
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US-08-839-765-103
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                                                                                                                                                    US-08-839-765-104
                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDADDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                             Gaps
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Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                     100.0%; Score 1287; DB 1; Length 251; 100.0%; Pred. No. 8.6e-125; tive 0; Mismatches 0; Indels 0
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MEDIUM TYPE: RIOPPY disk
COMPUTER: IND PC compatible
COMPUTER: IND PC compatible
COMPUTER: IND PC compatible
COMPUTER: IND PC compatible
COMPUTER: IND PC compatible
COMPUTER: IND PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/425,336
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 12-AMY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: US 08/064,691
FILING DATE: US 09/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
COTY: Illahois
COUNTRY: USA
                                             TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
  312/707-8889
                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 251; Conservative
                             312/707-9155
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                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
TELEPHONE: 31
                                                                                                                                                                                                                                    US-08-488-113B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-477-484B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Better, Marc D.
APPLICANT: Studinka, Gary
APPLICANT: Studinka, Gary
APPLICANT: Studinka, Gary
TITLE OF INVENTION: Inmunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
COUNTRY: 500 West Madison Street, 34th floor
CITY: Chicago
STAFE: Illinisis
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                          Query Match 100.0%; Score 1287; DB 1; Length 251; Best Local Similarity 100.0%; Pred. No. 8.6e-125; Matches 251; Conservative 0; Mismatches 0; Indels 0
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APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY FORENT INFORMATION:
NAME: MCNIcholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION 530
PRIOR APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ALLKFVDKDPK 251
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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RESULT 5
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Patent No. 5837491
PAPPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                 FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICADIAS, Janet M.
REGISTRATION NUMBER: 32,918
REPERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1287; DB 1; Best Local Similarity 100.0%; Pred. No. 8.6e-125; Matches 251; Conservative 0; Mismatches 0;
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ELLOATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
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STREET: 500 West Madison Street, 34th floor
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
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ZIP: 60661
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                    TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      251 amino acid
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                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                            amino acid
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STATE: Illinois
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US-08-646-360-2
                                                                                                                                                                                                                                                                                                                      LENGTH:
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Patent No. 5851802
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
MATC D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of TITLE OF INVENTION: Pusion Proteins and BPI-Derived Peptides NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6100 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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PRIOR PAPELICATION DATA:
PRIOR DATE: 12-MAY-1994
PRIOR APPLICATION NUMBER: 9CT/US94/05348
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/064,691
PILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,919
PRICEREPRATE 32,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/707-8899
TELEPRAX: 312/707-9155
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INFORMATION FOR SEQ ID NO: 2:
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amino acid
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STATE: Illinois
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TELEFAX: 31
TELEX: 650
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AYRETTDIGIEPLRIGIKKIDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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US-08-819-765-2
US-08-819-765-2
Sequence 2, Application US/08839765
Setent No. 6146631
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: 109
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STEPHEN ADDRESSE:
MANANA STREET AND STREET STATE
CORRESPONDENCE ADDRESS:
STATE OF INVENTION: TOTAL STREET STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE S
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8.6e-125;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BOTON: Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6448
TELEFAX: 312/474-6448
TELEFAX: 312/474-6468
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: THE COMPANIENT TELEFAX: 251 amino acids
TYPE: THE TELEFAX: 251 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
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STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1287;
100.0%; Pred. No. 8.6
ative 0; Mismatches
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Matches 251; Conservative
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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US-09-136-1389-2

Sequence 2, Application US/09136389

Patent No. 6146850

GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studmika, Gary M.
TITLE OF INVENTION: Immunocoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSEE: MACANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1287; DB 3; Length 251;
100.0%; Pred. No. 8.6e-125;
ive 0; Mismatches 0; Indels 0
FILING DATE: 157-FER 1397

CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/425,336

FILING DATE: 18-APR-1995

PRIOR APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

PRIOR APPLICATION NUMBER: US 07/988,430

FILING DATE: 09-DEC-1992

PRIOR DATE: 19-MAY-1993

PRIOR DATE: 19-MAY-1993

PRIOR DATE: 19-MAY-1993

PRIOR DATE: 19-MAY-1992

PRIOR DATE: 19-MAY-1992

PRIOR DATE: 19-MAY-1992

PRIOR DATE: 19-MAY-1991

APPLICATION NUMBER: US 07/901,707

FILING DATE: 04-NOV-1991

APPLICATION NUMBER: 32,918

REGISTRATION NUMBER: 32,918

REGISTRATION NUMBER: 32,918

REGISTRATION NUMBER: 32,918

REGISTRATION NUMBER: 32,918

RELEPHONE: 312/707-8889

TELEFRAX: 610,205-1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISICS:
LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 251 amino acids
amino acid
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Matches 251; Conservative
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1287; DB 3; Length 251; Best Local Similarity 100.0%; Pred. No. 8.6e-125; Matches 251; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                              COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27129/33199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: 22-MAR-1996
ATTORNEY AGENT INFORMATION:
NAME: BOTUM, MICHAEL F.
REGISTRATION NUMBER: 25,447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 2712;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELERAX: 312/474-0448
TELEX: 25-305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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                                                                                                                                                                                                           STREET: 6300 Sea
CITY: Chicago
STATE: Illinois
                             GENERAL INFORMATION:
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                                                                                                                                                                   SCENAIRSE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1994
FILING DATE: 12-MAY-1994
PRIOR APPLICATION NUMBER: WS 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/98,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MANGE: MANGER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDHTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-217-352-247
; Sequence 247, Application US/09217352
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                  Sequence 2. Application US/09711485
Sequence 2. Application US/09711485
Patent No. 6649742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinika, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1287; DB 4; Length 251; 100.0%; Pred. No. 8.6e-125; ive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/711,485
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-NAY-1993
RHIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION UNBER: US 07/901,707
FILING DATE: 19-UN-1992
RILING DATE: 04-NOV-1991
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 1102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 251 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 251; Conservative
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                             241 ALLKFVDKDPK 251
                                                                        241 ALLKFVDKOPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOPOLOGY:
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TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                SOPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
BRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 13-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-AMY-1994
FILING DATE: 13-AMY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: US-MAY-1996
APPLICATION NUMBER: US 08/064,691
FILING DATE: US-MAY-1993
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: US-MAY-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,707
FILING DATE: US -DC-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/91,707
FILING DATE: US -JUN-1992
RRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: US-JUN-1992
RRIOR APPLICATION NUMBER: 20.918
REFERENCE/DOCKET NUMBER: 20.918
REFERENCE/DOCKET NUMBER: 23.918
REFERENCE/DOCKET NUMBER: 23.918
REFERENCE/DOCKET NUMBER: 32.918
TELERPAX: 312/707-9155
TELERPAX: 312/707-9155
TELERPAX: 312/707-9155
TELERPAX: SON 388-1248
INPORMATION FOR SEQ ID NO: 2:
                                                                                           ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
CITY: Chicago
COUNTRY: USA
                                                                                                                                                                                                                             ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-610-838-2
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61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKONTIKTRLHFGGTYPSLEGEK 120
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Pred. No. 1.8e-124;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31,302
TELECOMMUNICATION INFORMATION:
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Marehall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray & STREST: Two First National Plaza, 20 South Clark STREST: Street
CITY: Chicago
CITY: Chicago
STATE: 111inois
COUNTRY: USA
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Patent No. 5416202
GENERAL INFORMATION:
APPLICANT: Berter, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
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AMINO ACID
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Best Local Similarity 99.61
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
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       NUMBER OF
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APPLICANT: LEE-HUANG, Sylvia

TITLE OF INVENTION: Anti-HIV and Anti-tumor Peptides and Truncated Polypeptides of
TITLE OF INVENTION: map30 and gap31

FILE REFERENCE: LEE-HUANG 4A

CURRENT APPLICATION NUMBER: US/09/645,603B

CURRENT FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/150,885

PRIOR FILING DATE: 1999-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07901707

Patent No. 5376546

GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                     181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDOVKPKI 240
                                                                      121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09645603B Patent No. 6652861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                    241 ALLKFVDKDPK 251
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APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lel, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESSE: 101
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                  ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STRATE: Illinois
COUNTRY: USA
ZIP: 60603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAPLICATION NUMBER: PCT/US92/09487
PILING DATE: 19921104
CLASSIPICATION:
PRICE APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
PILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NOLand, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 944-9740
TELERX: 25-3856
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Noland, Greta E. REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6
Matches 250; Conservative
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TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins UNMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
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Pred. No. 1.8e-124;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING.DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NUV-1991
ATION DATE: NOV-1991
ATION DATE: NOV-1991
ATION DATE: NOS 07/787,567
FILING DATE: 10-JUN-1992
REGISTRATION NUMBER: 353022
                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                  STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.84;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 250; Conservative
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                                                                                                                                                                                                                                             ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                                                                                                                                           CITY: Chicago
STATE: Illinois
COUNTRY: USA
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Best Local Similarity
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PCT-US92-09487-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.8%; Score 1284; DB 5; Length 251; 99.6%; Pred. No. 1.8e-124; tive 1; Mismatches 0; Indels 0
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
```

RESULT 15

Sequence 2, Application PC/TUS9209487 GENERAL INFORMATION: APPLICANT: Bernhard, Susan L.

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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                    GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studmika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                    E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT IN ALTONIA CONTROLL OF THING AND ALLIANDS SEATS TOWER, 233 SOUTH WACKET Drive CITY: Chicago SEATS TOWER, 233 SOUTH WACKET DRIVE COUNTRY: USA ZIPE: 60606-6402 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE PACHILIN RCICASOF MS-DOS SOFTWARE: PACHILIN RCICASOF MS-DOS SOFTWARE: PACHILIN RCICASOF MS-DOS SOFTWARE: PACHILIN RATION NUMBER: US/08/425,336 FILING DATE: 18-APR-1995 CLASSIFICATION NUMBER: US/08/64,691 FILING DATE: 19-MAY-1993 APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-WN-1992 PRIOR APPLICATION NUMBER: US 07/787,567 FILING DATE: 19-WN-1992 PRIOR APPLICATION NUMBER: US 07/787,567 FILING DATE: 19-WN-1991 ATTORNEY AGENT INFORMATION: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAME: NAM
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Pred. No. 2.8e-124;
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                                    Sequence 108, Application US/08425336 Patent No. 5621083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 31394
FELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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Best Local Similarity 99.6
Matches 250; Conservative
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US-08-425-336-108
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Search completed: June 20, 2005, 09:49:12 Job time : 31 secs This Police of the Mischery

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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June 20, 2005, 09:34:33 ; Search time 25 Seconds (without alignments) 966.016 Million cell updates/sec Run on:

US-10-717-243-2 Title: Perfect score:

1 GLDIVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

130334 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 251

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Resu] NC

	Descript	ran ranka n-dlycosidase	abrin (clone 7.2)		n-B	luffin-b - smooth	rRNA N-glycosidase	rRNA N-glycosidase	abrin (clone 3.7)	unknown protein, 6	tRNA pseudouridine	HAD superfamily hy	idylate	carbonyl reductase	ica	_	hypothetical prote	acet	conserved hypothet	transcription regu	hypothetical prote	_	hypothetical prote	_	~		>4	hypothetical prote	flavodoxin homolog	GTP pyrophosphokin
		JC4840	C39761	JU0393	JC5032	JN0108	S17574	793	B39761	D96702	B95186	E96957	B98053	A28053	F72769	T47996	T33345	D87031	B70247	AB3024	D86753	G86681	S26074	AE1143	B82472	D72527	A64490	AG2275	AE1714	A84006
	DB	2	~	~	0	0	N	~	~	0	~	~	N	н	N	N	7	~	~	~	~	~	~	N	~	~	N	7	N	7
	ength	۱ ۵	251	247	247	250	40	236	106	220	249	234	249	244	246	249	194	180	245	204	139	139	202	221	220	149	211	112	145	211
•	Query Match	27.1	25.6	24.5	24.1	21.0	15.2	11.6	9.4	6.2	6.2	6.1	6.1	o. 0	5.7	5.7	5.6	-	5.6	•	•	•	•	•	5.5	5.4	5.4	5.4	5.4	5.4
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	o t	¦	7	٣	4	S	9	7	œ	σ	10	11	12	13	14	15	16	11	18	13	20	21	22	23	24	52.	56	27	28	29

d	polyhedrin - Antic	hypothetical prote	hypothetical prote	probable two-compo	nonstructural prot	dTDP-4-dehydrorham	hypothetical prote	hypothetical prote	partial transposas	major fimbrial sub	conserved hypothet	hypothetical prote	hypothetical prote	hypothetical prote	orotidine 5'-monop
S47846	JQ1607	F82403	E97355	T36499	MNIV23	D97187	F96731	T16560	C90330	A43841	AI1682	C75011	AE1826	A90523	AB2613
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232	245	169	180	218	122	185	197	202	211	170	181	191	222	223	235
4.	5.4	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.3	5.2	5.2	5.2	5.2	5.2	5.2
69	69	68.5	68.5	68.5	68	68	68	68	68	67.5	67.5	67.5	67.5	67.5	67.5

## ALIGNMENTS

		trichoar
		(EC 3.2.2.22)
		<u>임</u>
G 1	40	N-glycosidase
ESULT	C4840	ZNA NA

RESULT 1
JC4840

FRNA N-glycosidase (EC 3.2.2.2) trichoanguina - snake gourd

FRNA N-glycosidase (EC 3.2.2.2) trichoanguina - snake gourd

C;Species: Trichosanthes anguina (snake gourd)

C;Species: 15-Aug-1996 #sequence revision 24-Oct-1997 #text_change 05-Dec-1997

C;Accession: JC4840; JT0701; JT0677

R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Wang, S.H.; Ueno, Y.; Tsugita, A.

Biomed Sci. 3, 178-186, 1996

A;Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from 7
A;Reference number: JC4840

A;Accession: JC4840
A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Experimental source: seed
A;Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table
R;Chow, L.P.; Kamo, M.; Lin, J.Y.; Ueno, Y.; Tsugita, A.
A;Description: Anino acid sequence of trichoanguina, a ribosomal-inactvating protein from
A;Reference number: JT0677

A; Accession: J70701
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: TRNA N-glycosidase; prosphoprotein; seed
C; Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F; H-242/Domain: TRNA N-glycosidase homology < RNG>
F; H-242/Domain: TRNA N-glycosidase homology < RNG>
F; H-241/Dinding site: carbohydrate (Asn) (covalent) #status experimental
F; T0, 158, 161/Active site: Tyr, Glu, Arg #status predicted
F; T0, 158, 161/Active site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

7; 21; Gaps 27.1%; Score 348.5; DB 2; Length 245; 35.9%; Pred. No. 1,4e-21; 96; Indels 44; Mismatches Query Match Best Local Similarity 35.9% Matches 90; Conservative

64 9 5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA g ò

61 TVAVDVTNVYIVAYRADAVSYFFEDTPAEAFKLIFAGTKTVKLPYSGNYDKLQSVVGKQ- 119 65 EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE---GEKA 121 ò g

120 -RDMIELGIPAL-----SAITWMVYYDYQSTAAALLVIJGSTAEAARYKYIEQQVS 170 122 YRETTDLGIEPLRIGIKKLDENAIDN---YKPTEIASSLLVVIQMVSEAARFTFIENQIR 178 ò

179 NNFQQRIRPANNTISLENKWGKLSFQIRTSG--ANGMFSEAVELERANGKKYYV--TAVD 234 <del>අ</del> . ઠે g

235 QVKPKIALLKF 245 ò

231 VVKGNIKLLLY 241

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C, Keywords: abortifacient
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                                                                                                        Similarity
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C;Species: Trichosanthes Kirilowii (Mongolian snake-gourd)

C;Species: Trichosanthes Kirilowii (Mongolian snake-gourd)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C;Accession: Jul039; PSG163

R;Tryokawa. S; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.

A;Tryokawa. S; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.

A;Trle: The complete anino acid sequence of an abortifacient protein, karasurin.

A;Reference number: Jul0393 MUID:92005921; PMID:1914000

A;Accession: Jul0393

A;Accession: Jul0393

A;Accession: Jul0393

A;Accession: Jul0393

A;Accession: Jul0393

A;Cross-references: UNIPROT:P24478

A;Cross-references: UNIPROT:P24478

A;Cross-references: UNIPROT:P24478

A;Note: a sequence which lacks Ala-247 is also shown in this publication

C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
                                                                                                                               N; Contains: rRNA N-glycosidase (EC 3.2.2.22)
(c; Species: Abrus precatorius (Indian licorice)
(c; Species: Abrus precatorius (Indian licorice)
(c; Accession: C39761; S14471

R; Evensen, G.; Mathiesen, A.; Sundan, A.
Biol. Chem. 266, 6848-6852, 1991
A; Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A; Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 'M',1-251 «EV2>
A; Residues: 'M',1-251 «EV2>
A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C; Superfamily: ricin; rRNA N-glycosidase homology
C; Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F; 1-251/Product: abrin (clone 7.2) chain A #status predicted «ACH>
F; 7-246/Domain: rRNA N-glycosidase homology «RNG»
F; 7-246/Domain: rRNA N-glycosidase homology «RNG»
F; 7-113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F; 164,167/Active site: Glu, Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV-DQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 VSIRTGTAFQPDPAMLSLENNWDNLSRGVQES-VQDTPPNAVTLRRVNNQPVIVDSLTHQ 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKKCDDPGKC----FVLVALSND
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R;Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
A;Reference number: S14471
A;Accession: S14471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
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                                                                                                        abrin (clone 7.2) precursor - Indian licorice (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 VKPKIALLKFVDKDP 250
                                                                                                                                                                                                                                                                                                                                                   A; Accession: C39761
A; Molecule type: DNA
A; Residues: 1-251 <EVE>
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Carasurin-B - Trichosanthes kirilowii var. japonica
CjSpecies: Trichosanthes kirilowii var. japonica
CjSpecies: Trichosanthes kirilowii var. japonica
CjSpecies: Trichosanthes kirilowii var. japonica
CjSpecies: Trichosanthes kirilowii var. japonica
CjSpecies: Trichosanthes kirilowii var. japonica
CjAccession: JCS032
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and kan
A;Reference number: JCS032,
A;Reference number: JCS032,
A;Reference number: JCS032,
A;Reference: JCS032
A;Reference: JCS032
A;Reference: JCS032
A;Residues: 1-247 < KON>
A;Cross-references: UNIPROT: Q1216; UNIPROT: Q94KE4; UNIPROT: Q81PV7
A;Cross-references: UNIPROT: Q1216; UNIPROT: Q94KE4; UNIPROT: Q81PV7
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic
C;Superfamily: FRNA N-G1ycosidase; rRNA N-G1ycosidase homology < RNG>
F;4-243/Domain: rRNA N-G1ycosidase homology < RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ISVAIDVTNVYVMGYRAGDISYFFNEASATEAAKTVFKDAKRKVTLPYSGNYERLQIAAG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 KIRENIPLGLPALDSAİ----TILFYYNANSAASALMVI. QSTSEAARYKFIEQQIGKR 174
                                                                                                                                                                                                                                                                                                                                                                                                        64 AEIAIDVTSVYVGYQVRNRSYFFKDA-PDAAYEGLFKNT-IKTRLHFGGSYPSLE-GEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 FQQRIRPANNTISLENKWGKLSFQIR-TSGANGMFSEAVELERANGKKYYVŢAVDQ--VK 237
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                                                                                                                                                                                                                                                                                       2 VSFRLSGATSSSYGVFISNLRKALFYERKLYDIPLLRSTL--PGSQRYALIHLTNYADET
                                                                                                                                                                                                                                              5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPG-KCFVLVALSNDNGQL
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                                                                               ; Score 315; DB 2; Length 24; Pred. No. 8.6e-19; 33; Mismatches 105; Indels
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                               24.5%;
                                                                                                                                                              94; Conservative
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11;

Matches

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94

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C;Species: Saponaria officinalis (common soapwort)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S17932; S15458
R;Pordham-Skelton, A.P.; Taylor, P.N.; Hartley, M.R.; Croy, R.R.D.
Mol. Gen. Genet. 229, 460-466, 1991
A;Title: Characterisation of saporin genes: in vitro expression and ribosome inactivation A;Reference number: S17932; MuID:92049247; PMID:1719367
A;Accession: S17932
A;Molecule type: DNA
A;Residues: 1-236 <FOR>
A;Cross-references: UNIPROT:P27560; EMBL:X59256; NID:g21322; PIDN:CAA41949.1; PID:g21323
A;Note: the authors tranalated the codon CTC for residue 75 as Phe and GCA for residue 16;Superfamily: TRNA N-91ycosidase; monomer; toxin
C;Superfamily: TRNA N-91ycosidase; monomer; toxin
F;1-221/Domain: TRNA N-91ycosidase homology (fragment) <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           distinct abrin A-chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 ANOKALEYTEDÝQSIEKNAKIT------EGDKT-ŘKELGLGINLLSTLMDAVNKK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 ARVVKNE-----ARFILIAIQMTAEAARFRYIQNLVTKNFPNKFNSEDKVIQFQVNWSKI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 BIASSLLVVIQMVSEAARFTFIENQIRNNFQ--QRIRPANNTISLENKWGKLSFQIRTSG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 FIRINFQSSRGTVS-LGLKRENLYVVAYLAMDNANVNRAYYFGTEITSAELTTLLPEATV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abrin (clone 3.7) precursor - Indian licorice (fragment)
N;Contains: RRNA Neglycosidase (EC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
C;Species: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 05-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 A--IDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQRIRPANNTISLENKWGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVLVALSNDNGQLAEIAIDVTSVYVVGYQVR----NRSYFFKD-----APDAA-
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R;Evensen, G.; Mathlesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
J. Biol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A;Réference number: A39761; MUID:91201329; PMID:2016300
A;Accession: B39761
A;Molecule type: DNA
A;Residues: 1-106 <EVUS-
A;Cross-references: GB:X54873
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycosidase; hydrolase; lectin; toxin F;1-101/Domain: rANA N-glycosidase homology (fragment) <F:1101/Domain: rRNG-F:1101/Domain: RNG-F:1101/Domain: RNG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.6%; Score 149; DB 2; Length 236; Best Local Similarity 25.2%; Pred. No. 5e-05; Matches 58; Conservative 39; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession: B39761
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                                                                                       C;Species: Luffa cylindrica (smooth loofah)
C;Species: Luffa cylindrica (smooth loofah)
C;Aacession: JN0108
C;Accession: JN0108
R;Islam, M.R.; Hirayama, H.; Funatsu, G.
R;Islam, M.R.; Hirayama, H.; Funatsu, G.
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from A;Reference number: JN0108; MUID:91248488; PMID:1168666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRNA N-glycosidase (BC 3.2.2.22) GAP31 - Gelonium multiflorum (fragment)
C;Species: Gelonium multiflorum
C;Date: 19-Mar-1997 #sequence_revision 24-Oct-1997 #text_change 09-Jul-2004
C;Accession: S17574
R;Lee-Huang, S.; Kung, H.; Huang, P.L.; Huang, P.L.; Li, B.Q.; Huang, P.; Huang, H.I.;
R;Lee-Huang, S.; Kung, H.; Huang, P.L.; Huang, P.L.; Li, B.Q.; Huang, P.; Huang, H.I.;
A;Title: A*new class of anti-HIV agents: GAP31, DAP8 30 and 32.
A;Reference number: S17574; MUID:92037998; PMID:1936243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RETTDLGIEPLRIGIKKLDE--NAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 IR-----EKIPLGFRALDSALTSIFHYDSTAAAAFLVILQTTAEASRFKYIEGQIIER 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FQQRIRPANNTISLENK-WGKLSFQIRTSGA-NGMFSEAVELERANGKKYYVT----A 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 21.0%; Score 270; DB 2; Length 250; 1 Similarity 31.3%; Pred. No. 4.8e-15; 79; Conservative 47; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 195; DB 2; Length 40;
Pred. No. 7.3e-10;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Status: preliminary
A;Nesidues: 1-250 <1SL>
A;Cross-references: UNIPROT: P22851
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;5-246/Domain: rRNA N-glycosidase homology
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C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLL
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95.0%;
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IKDVNSKLLLNK 246
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Best Local Similarity 95.0
Matches 38; Conservative
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A;Molecule type: protein
A;Residues: 1-40 <LEE>
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Best Local Similarity
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C;Species: Clostridium acetoburylicum C;Species: Clostridium acetoburylicum ccispecies: Clostridium acetoburylicum C;Species: Clostridium acetoburylicum C;Species: Clostridium acetoburylicum C;Species: Casesion: E96557
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: E96557
A;Accession: E96557
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pseudouridylate synthase (EC 4.2.1.70) [imported] - Streptococcus pneumoniae (strain R6) C; Species: Streptococcus pneumoniae (journal 22-Oct-2001 #text_change 09-Jul-2004 C; Accession: B98053 C; Accession: B98053 C; Accession: B98053 C; Accession: B98053 C; Accession: B98053 C; Accession: B98053 C; Accession: B98053 C; Accession: B98053 C; Accession: Bown, B.N.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Et e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc y, P.; Sun, P.M.; Winkler, M.B.
J. Bacteriol. 183, 5709-5717, 2001
J. Bacteriol. 183, 5709-5717, 2001
J. AjAuthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
                                                                                                                                                                                                                                                                                                                                                                                           88 IDVISIELVADDFHCRYAKHSKTYEF-----TVDRGRPKNPM--RRHYATHFP------ 133
                                                                                                                                                                                                                                                                                                                                                       172 FIEN-----QIRNNFQQRIRPANN-----TISLENKWGKLSFQIRTSGANGMFSEAVE 219
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                                                                                                  68 IDVTSVYVVG-----YQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKA
                                                                                                                                                                                                                              122 YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAA-----RFT
                                                                                                                                                                                                                                                                                      134 ----YPLDVERMQIAİKKİ-EGTHDPTGFTASGTSVEDKVRTITEASLIVDETGQFLTFT
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                                       49;

    Clostridium acetobutylicum

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                                    60; Indels
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23.6%; Pred. No. 35;
ive 34; Mismatches
   ; Pred. No. 32; 28; Mismatches
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      24.7%;
                                    45; Conservative
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Best Local Similarity
Matches 45; Conserv
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Matches
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                                                                                                                     Ritheologis, M.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., L.; J.H.; Lin, X.; Liu, X.; Liu, Z.A.; Luxos, J.S.; Maiti, E.; Kim, C.C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luxos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Streptococcus pneumoniae
C;Date: 0.3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95186
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
N; T.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
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C;Genetics:
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A;Accession: B95186
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <KUR>
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                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 -NGFSVKKAEDVVNIMVGRGYALGKDAMEKAKAFDDR-----HNLISNASAT-----I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 ITYVNF------LNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSN
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   unknown protein, 64612-65506 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93; Indels
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Best Local Similarity 20.8%
Matches 52; Conservative
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T-LDPSSPKV 211
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A;Residues: 1-220 <STO>
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                                                                                           C, Accession: D96702
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A, Status: prelimina
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A, Map position: 1
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Genetics:

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Query Match

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R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi. T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T47996
R;Choisne, N.; Robert; C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sal submitted to the Protein Sequence Database, February 2000
A;Reference number: 224481
A;Accession: T47996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-246 «KAW»
A;Cross-references: UNIPROT:Q9YFV5; DDBJ:AP000058; NID:g5103388; PIDN:BAA79056.1; PID:dl(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Aeropyrum pernix
Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004;
Accession: F72769
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
                                                                                                                           66 IAIDVTSVY-VVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKAYRE
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                                                     Gaps
                                                41;
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  Length 244;
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C;Superfamily: Aeropyrum pernix hypothetical protein APE0145
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  DB 1;
                                                                                                 94 AYEGLFKNTIKTRLHFGGSYPSLEGEKAYRETTDI
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                         99
                                                   Mismatches
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21.0%; Pred. No. 98;
  Score 75.5;
Pred. No. 66
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                                              32,
  5.9%;
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                                                   Conservative
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  Query Match
Best Local Similarity
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                                                   46;
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                                                                     A,Molecule type: DNA
A,Residues: 1-249 <KUR>
A,Cross-references: UNIPROT:Q8CWQ1; GB:AE007317; PIDN:AAL00255.1; PID:g15459107; GSPDB:G
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Cispecies: Mus musculus (house mouse)
Crispecies: Nus musculus (house mouse)
Crispecies: Nus 203382; 869141; 869142; A28053
R.Navre, M.; Ringold, G.M.
A.Title: A growth factor-repressible gene associated with protein kinase C-mediated inhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Cross-references: UNIPROT:P08074; EMBL:X07411; NID:g50003; PIDN:CAA30309.1; PID:g50004; Experimental source: strain C3H; Signostian C3H; Ni Deyashiki, Y.; Ohshima, K.; Hara, A. ur. J. Biochem. 228, 381-387, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----YPLDVERMOIAİKKI-EGTHDFTGFTASGTSVEDKVRTITEASLIVDETGQFLTFT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 FIEN-----QIRNNFQORIRPANN-----TISLENKWGKLSFQIRTSGANGMFSEAVE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: EMBL:D26123; NID:g440371; PIDN:BAA05120.1; PID:g699608
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                                                                                                                                                                                                                                                                                                                         49;
                                                                                                                                                                                                                                                                        DB 2; Length 249;
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Residues: 1-29,40-80,84-96,110-198,209-223,227-244 <NAW>
Experimental source: lung; strain CD-1
Reference number: A97872; MUID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title: Cloning, expression and tissue distribution of Reference number: S69141; MUID:95220366; PMID:7705352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - mouse
                                                                                                                                                                                                                                                                   6.1%; Score 78.5; D 24.7%; Pred. No. 38; Live 28; Mismatches
                                                                                                                                                                 A Gene: truA
C;Superfamily: tRNA-pseudouridine synthase I
C;Keywords: carbon-oxygen lyase; hydro-lyase
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Matches 45; Conservative
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                                                   A;Status: preliminary
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                                                                                                                                                                                                                  Query Match 5.7%; Score 73; DB 2; Length 249;
Best Local Similarity 20.4%; Pred. No. 1.1e+02;
Matches 46; Conservative 35; Mismatches 91; Indels 54; Gaps
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <CHO>
A;Residues: 1-249 <CHO>
A;Cross-references: UNIPROT:Q9M262; EMBL:AL138642
A;Experimental source: cultivar Columbia; BAC clone F21F14
C;Genetics:
A;Map position: 3
A;Introns: 14/1; 36/1; 68/3; 110/3; 176/3
A;Introns: 14/1; 36/1; 68/3; 110/3; 176/3
C;Superfamily: conserved hypothetical protein YBR037w
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Q9k3e8 staphylococ Q99x19 streptococc Q7p521 fusobacteri Q8re43 fusobacteri Q8re43 plasmodium P58791 pyrococcus Q8ewt mycoplasma Q9c9w1 arabidopsis Q6mry4 mycoplasma Q8rmy4 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q8rmy6 mycoplasma Q9rnostemma Q9yp10 streptococcc	ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο	NGQLAETAIDVTSVYVVGYQVRNRSYFFKDAPDAAYBGLFKNTIKTRLHFGGSYPGLB-G 118
098X38 099XL9 099XL9 R64 FUSNN 078ES9 WCPE 0909W1 066WY4 068WD6 07YU4 069HQ7 081FY4 TRUA_STRPN	PRELIMINARY; PRT; 251 AA.  04 (TERMELrel. 27, Created) 04 (TERMELrel. 27, Last sequence update) 04 (TERMELrel. 27, Last annotation update) 04 (TERMELrel. 27, Last annotation update) 04 (TERMELrel. 27, Last annotation update) 04 (TERMELrel. 27, Last annotation update) 04 (TERMELrel. 27, Last annotation update) 1; Viridiplantae; Streptophyta; Embryophta; Nyta; Magnoliophyta; eudicotyledons; core ev D=3816;  FROM N.A. ed; 413976; PubMed=8307038; 413976; PubMed=8307038; 413976; PubMed=8307038; 413976; PubMed=8307038; 413076; PubMed=8307038; 413076; Ablantagenesis in Escherichia ediochem. 219:83-87(1994) 200692; Pidefense on the 28S FRNA. ARITY: Belongs to the ribosome-inactivating richem. 219:83-87(1994) 201 cadenosine on the 28S FRNA. 16707; Fihydrolase activity; IEA. 1670; Fihydrolase activity; IEA. 1670; Fihydrolase activity; IEA. 1670; Fihydrolase activity; IEA. 1670; Fihydrolase activity; IEA. 1670; Fihydrolase activity; IEA. 1748; Pipathogenesis; IEA. 1748; Pipathogenesis; IEA. 1750, 1AB. 1748; Pipathogenesis; IEA. 1751, AB. 1748; Pipathogenesis; IEA. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751, AB. 1751,	SYQVRNRSYFFKDAPDAAYEC
7.0 6.6 6.6 6.4 6.4 6.3 6.3 6.3 6.2 6.2 6.2 6.2 6.2 6.2 6.2 6.2 6.2 6.2	MLIGNMENT  M12  Q7DM12  O7DM12  O5-JUL-2004 (TERMELrel. 27, Last sequence O5-JUL-2004 (TERMELrel. 27, Last sequence O5-JUL-2004 (TERMELrel. 27, Last annotate Abria A-chain (Fragment). Abria Precatorius (Indian licorice) (Cra Bukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; eudicotyle eurosids 1; Fabales; Fabaceae; Papiliono NCBI_TAXID=3816; SEQUENCE FROM N.A. TISSUE-Seed; MEDLINE=94139756; PubMed=8307038; Chih-Hung H., Lee M.C., Chen J.K., Lin J. "Cloning and expression of three abrin A derived by site-specific mutagenesis in Bur. J. Biochem. 219:83-87(1994) CATALYTIC ACTIVITY: Endohydrolysis of specific adenosine on the 28S FRNA SIMILARITY: Belongs to the ribosome- EMBL; X76720; CAA54138.1; CATALYTIC ACTIVITY: Endohydrolysis of G0; G0:0017148; P: Hydrolase activity; IE G0; G0:001748; P: Hydrolase activity; IE G0; G0:001748; P: Hydrolase activity; IE G0; G0:001748; P: Hydrolase activity; IE C0; G0:001748; P: Hydrolase activity; IE C0; G0:001748; P: Hydrolase activity; IE C0; G0:001748; P: Hydrolase activity; IE C0; G0:001748; P: Hydrolase; Protein synthe NON_TER C0: G0:001748; P: Pred. No. 1 Applorase; PRO0155; SHIGARICIN; PROSTE; PRO0156; P: Pred. No. 1 Atches 91; Conservative 39; Mismatch SUBSICALYITYVNFLMELRVKLKPEGNSE; SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A4; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSBC2 SUBENCE 251 A5; 28098 MM; B17BSC2 SUBENCE 251 A5; 28098 MM; B17BSC2 SUBENCE 251 A5; 28098 MM; B17BSC2 SUBENCE 251 A5; 28098 MM; B17BSC2 SUBENCE 251 A5; 28098 MM; B17BSC2 SUBEN	60 NGQLAEIAIDVISVYVV :
332 334 335 335 335 335 335 335 335 335 335	7DM12 7DM12 5-JUL-20 5-JUL-20 5-JUL-20 5-JUL-20 5-JUL-20 5-JUL-20 5-JUL-20 5-JUL-20 5-JUL-20 6-INDE-9 PERINGE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE-9 PEDLINE	60 NG 60_DT
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64 AEIAIDVTSVYVVGYQVRNRSYFFKDA-PDAAYEGLFKNT-IKTRLHFGGSYPSLE-GEK 120
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Van Chi P., Quoc Truong H., Thuy Ha N., Chung W.I., Binh L.T.;
"Characterization of trichobakin, a type I ribosome-inactivating
protein frichosanthes Bac Kan 8-98.";
Biotechnol. Appl. Blochem. 34:85-92(2001).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTL--PGSQRYALIHLTNYADET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 FQQRIRPANNTISLENKWGKLSFQIR-TSGANGMFSEAVELERANGKKYYVTAVDQ--VK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPG-KCFVLVALSNDNGQL
                                                                                                                                              Trichosanthes sp. Bac Kan 8-98.
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids 1; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                              specific adenosine on the 28S rRNA.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
BENBL; AR039324; BAA92530.1;
--HSSP; P09989; 1J4G.
GO; GO:001787; F:hydrolase activity; IEA.
GO; GO:001598; F:RNA W-9lycosylase activity; IEA.
GO; GO:0010598; F:RNA W-9lycosylase activity; IEA.
GO; GO:001748; F:RNA W-9lycosylase; IEA.
GO; GO:001748; P:Defense response; IEA.
GO; GO:0019405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
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PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.5%; Score 315; DB 2; Length 24' 38.2%; Pred. No. 3.2e-18; ive 33; Mismatches 105; Indels
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
barin A chain (B164A) (Fragment).
Name=pcDNAAC-1-B164A;
Abrus precatorius (Indian licorice) (Crab's eye).
                                                              Last sequence update)
Last annotation update)
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                                            Created)
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                                     (TrEMBLrel. 15, C (TrEMBLrel. 15, I (TremBLrel. 25, I
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les 94; Conservative
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  PRELIMINARY;
                                                                                                        Trichobakin (Fragment).
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                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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120 AHQSRQQIPLGLQALTHGISFFRSGGNDN---EEKARTLIVIIQMVAEAARFRYISNRVR 176
                                     179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ- 235
                                                                       177 VSIQICTARODAAMISLENNWDNLSRGVOES-VODIRPNOVILTNIRNEPVIVDSLSHP 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mi S.-L., Wang Y., Li Y.-Y., Chen Z.-L., An C.-C.;
"Trichosanthes kirilowii trichosanthin (TCS) mature peptide gene.";
submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.
-!-CATALYITC ACTIVIT: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!-SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AN66981; AAT91090.1; -.
GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 VSFRLSGATSSSYGVFISNLRKALPNERRLYDIPLLRSTLQGSQR-YALIHLTNYADETI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                            Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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247 AA; 27172 MW; BCBA762884F89CCE CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Trichosanthin (Fragment).
                                                                                                                                                                                                                                                                                  247 AA
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                                                                                                                          236 VKPKIALLKFVDKDP 250
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                                                                                                                                                                TISSUE-Seed,
MEDLINE=94139756; PubMed=8307038;
MEDLINE=94139756; PubMed=8307038;
MEDLINE=94139756; PubMed=8307038;
MEDLINE=94139756; PubMed=8307038;
Cloning and expression of three abrin A-chains and their mutants derived by site-specific mutagenesis in Escherichia coli.";
Eur. J. Blochem. 219:83-87(1994).
-!- CATALYITC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.
-!- SIMILARITY: Belongs to the zibosome-inactivating protein family.
--- SIMILARITY: CAA54139.1; -.
HSSP: P11140; JABR.
GQ: GO:0016787; F:hydrolase activity; IEA.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
01-OCT-2003 (TrEMBLrel. 25, Last amnotation update)
PCDNAAC-1-E164A/R167L protein (Fragment).
Name=pcDNAAC-1-E164A/R167L;
Abrus precatorius (Indian licorice) (Crab's eye).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales; Fabaceae, Papilionoideae, Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0006552; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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28040 MW; D57FCB182E0EECC9 CRC64;
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MEDLINE=94139756; PubMed=8307038;
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179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ- 235
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Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.;
"Cloning and expression of three abrin A-chains and their mutants derived by site-specific mutagenesis in Bscherichia coli.";
Eur. J. Biochem. 219:83-87 [1934].
-I- CATALYTIC ACTIVITY; Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
-I. SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL: SIMILARITY: Belongs to the ribosome-inactivating protein family.
HSSP; P11140; 1ABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : | | | : | | : | : | : | : | : | IKFSTEGATSQSYKQPIEALRERLR-GGLIHDIPVL----PDPTTLQERNRYITVELSNS
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MEDINE_2156772; PubMed=11710524;
Bark C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.;
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Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                 GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:003598; F:rRNA N-Glycosylase activity; IEA.
GO; GO:003598; P:rRNA N-Glycosylase activity; IEA.
GO; GO:0017148; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:009405; P:pathogenesis; IEA.
InterPro; IPRO1574; RIP.
Pfam; PP00161; RIP; 1.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Santalaceae; Viscum.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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1 Similarity 35.3%; Pred. No. 4.8e-18;
90; Conservative 39; Mismatches 108; Indels
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1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Lectin chain A isoform 2 (Fragment).
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PRINTS, PR00396; SHIGARICIN
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Baramasiavm M., Srinivasan A., Singh T.P.;

Submitted (FRE-2002) to the EMBL/GenBank/DDBJ databases.

-!-CATALYIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

C. -!-SIMILARITY: Belongs to the ribosome-inactivating protein family. RBL; AV891148; AAL87005.1; -.

R HSSP; P81446; AL87005.1; -.

R GO; GO:0015787; F:hydrolase activity; IEA.

R GO; GO:0015787; F:hydrolase activity; IEA.

R GO; GO:0015059; F:rRNA N-glycosylase activity; IEA.

R GO; GO:0015059; F:rRNA N-glycosylase activity; IEA.

R GO; GO:0015059; P:refense response; IEA.

R GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

R InterPro; IPRNO1574; RIP.

R Pfam; PF00161; RIP; 1.
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKK----CDDPGKCFVLVALSNDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 VTHQTTGDQYF---KFITLLRDHVSSGSLSNQIPLLRQSTVPVSDTQR-FVLVELSNQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                      specific adenosine on the 285 rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
BENBL, AF508915; AAM46933.1; -.
BISP, P81446; 10QL.
GO; GO:0010789; F:hydrolase activity; IEA.
GO; GO:0010598; F:rRNA 'Glycosylase activity; IEA.
GO; GO:000552; P:defense response; IEA.
GO; GO:0004952; P:gefense response; IEA.
GO; GO:000405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Santalales, Santalaceae, Viscum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Mismatches 106; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.2%; Score 311.5; DB 2; Length 249; 35.4%; Pred. No. 6.3e-18;
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249 AA; 27821 MW; 3C5870F8338BDAB5 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lectin chain A isoform 2 (Fragment).
Viscum album (European mistletoe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 AA
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236 VIASLAIMLFVCED 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKPKIALLKFVDKD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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-i- SIMILARITY: Belongs to the ribosome-inactivating protein family. EMBL; AF508916; AAM46934.1; -
                                                                                                                                                                                                                                                                                                                                                                                              5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKC--DDPGKCFVLVALSNDNGQ
                                                                                                                                                                                                                               65 SITAAIDVTNIYVVAYQAGDQSYFLRDAPDGAERHLFTGTTRSSLPFTGSYTDLERYAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21566752; PubMed=11710524; Park C.-H., Yoon T.-J., Kim J.-B., Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B., Do M.-S., Song S.K.; "Change and Sequence analysis of the lectin genes of the Korean mistletoe (Viscum album coloratum)."; "Mol. Cells 12:215-220(2001)."
                                                                                                                                                                    11; Gaps
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Park C.-H., Lee D.-W., Kang T.-B., Lee K.-H., Yoon T.-J., Kim J.-B.,
Do M.-S., Song S.K.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016788; F:RNA N-glycosylase activity; IEA.
GO; GO:0016952; P:défense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:009405; P:pzthogenesis; IEA.
InterPro; IPR01574; RIP.
PFGm; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QBLKQ4;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Lectin chain A isoform 3 (Fragment).
Viscum album subsp. coloratum.
Viscum album subsp. coloratum.
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Santalaceae; Viscum.
                                                                                                                        24.1%; Score 310.5; DB 2; Length 249; 34.1%; Pred. No. 7.6e-18; rive 42; Mismatches 109; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00396; SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
NON_TER
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
NON TER 1 1
                                            <1 >249 lectin chain A isoform 2.
249 249 AM; 27944 MW; 89FAFB78309A83B3 CRC64;
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                                                                                                                                                                    84; Conservative
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                                                                                                                                               Similarity
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Matches

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119 EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
                                                                                                                                                                                                                                 179 NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQ- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 YNNAKITIGIDVFDVYVVGFLIGTNSYIFKEAPDLAYNQSLLFPGSVRENLSYTGGYDDL 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VSIQTGTAFQPDAAMİSLENNWDNLSRGVQES-VQDTFPNQVTLTNIRNEPVIVDSLSHP 235
                                                                                    NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
Lin Y., Wu Z.J., Lin Q.Y., Xie L.H.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AY075115; AAL82822.2; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Type I ribosome-inactivating protein (Fragment).

Gynostemma pentaphyllum (diaogulan).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Gynostemma.
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GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:00017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
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PROSITE; PS00275; SHIGA RICIN; UNKNOWN 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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38.3%; Pred. No. 8e-17;
tive 22; Mismatches E
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                                                                                                                                                                                                                                                                                                                                                                                                                                     236 VKPKIALLKFVDKDP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 TVAVLALMLFVCNPP 250
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80; Conserva
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                                                                                    8
                                                                                                                                                                                                                                                                                                                      64 AE---IAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                            65 EDSITAAIDVTNLYVVAYQAGDQSYFLRDAPDGAERHLFTGTTRSSLPFNGSYADLERYA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQQRIR--PANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INSGVSYLPDVYMLELEASWGQOSTQVQQS-TDGVFNNPIRLGISTGNFVWLSNVRDVIA 240
                                                                                                                                                                                                      63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one
                                                                                                                                                                                                                                                          VTHQTTGDEYF --- RFIKLLRDSVSSGSFSNDIPLLPPSIPVSSAQRFVLVELTNQLGKW
                                                                                                                                                                                                      5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCD-DPGKCFVLVALSNDNGQL
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abruce presenterius (Indian licorice) (Crab's eye).

Bukaryota: Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0011148; P:negative regulation of protein biosynthesis; IEA. GO:0009405; P:pathogenesis; IEA.
                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                    23.9%; Score 307.5; DB 2; Length 251; 34.7%; Pred. No. 1.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.9%; Score 307; DB 2; Length 251; 34.9%; Pred. No. 1.5e-17; ive 39; Mismatches 109; Indels
                                                                                                                                             40; Mismatches 111; Indels
251
28090 MW; All777489012E989 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251
27997 MW; 3B60351839AEFB7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Abrin chain E164A/R167L (Fragment).
Name=pcDNAC-1-E164A/R167L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0016787; F:hydrolase activity; IEA.
GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO:0006952; P:defense response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 34.9
Matches 89; Conservative
                                                                                                                                             87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIALLKFVDKD 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLGIMVEVCRD 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
251 AA;
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                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
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SEQUENCE
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096235

RESULT 9

99

18;

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NCBI_TaxID=182084;
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                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=107615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEG--LFKNTIKTRLHFGGSYPSLEGEKAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 RETTDLGIEPLRIGIKKLDENAIDNY---KPTEIASSLLVVIQMVSEAARFTFIENQIRN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 NF--QQRIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYV--TAVD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 INFSLAGAGGOTYKTFIAKLROE------LISIGTOKVA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin Y., Lin Q.Y., Xie L.H.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA
                                                                                                                                                                                                                                                                                                                                                                           Gynostemmin-like protein (Fragment).
Gynostemma pentaphyllum (Jiaogulan).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales, Cucurbitaceae; Gynostemma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SÎMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AY279104; AAP40648.1; -.
HSSP; P24817; ICF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0016787; F.hydrolase activity; IEA.
GO; GO:001598; F.rRNA N-glycosylase activity; IEA.
GO; GO:001598; F.rRNA N-glycosylase activity; IEA.
GO; GO:0017148; F.reneserier response; IEA.
GO; GO:0017148; P.negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P.pathogenesis; IEA.
InterPro; IER001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0MAR-2004 (TrEMBLrel. 26, Last annotation update)
Gynostemmin-like protein (Fragment).
Gynostemma pentaphyllum (Jiaogulan).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PROSITE; PS00275; SHIGA RICIN; UNKNOWN 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 290; DB 2; Length 248; Pred. No. 4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 AA; 27515 MW; 2ACBCE270B018203 CRC64;
                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
172 IAKNLYGTFKPDRAILSLENNWGALSKQI 200
                                                                                                                                                                                                                                                                                   Created
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206 LVQNGIALLKYMSE 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=182084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               -OCT-2003
                                                                                                                                                                                                                                                                                                                                               01-MAR-2004
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D Q7Y1U5
AC Q7Y1U5
AC 07Y1U5
DT 01-OCT--
DT 01-MAR--
DT 01-MAR--
DT 01-MAR--
OS Gynoster
OS Gynoster
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                                                                                                                                             RESULT 11
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Lin Y., Lin Q.Y., Xie L.H.;
Submitted (APR-2003) to the EMEL/GenBank/DDBJ databases.

1. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rkNa.

1. SIMILARITY: Belongs to the ribosome-inactivating protein family.

EMBL; AY279106; AAP40650.1; -.

REBL; AY279106; AAP40650.1; -.

ROG GO:0010598; F:RNA N-glycosylase activity; IEA.

GO; GO:0010598; F:RNA N-glycosylase activity; IEA.

GO; GO:001748; P:negative response; IEA.

ROG GO:001748; P:negative regulation of protein biosynthesis; IEA.

ROG GO:001748; P:negative regulation of protein biosynthesis; IEA.

ROG GO:001748; P:PRO01574; RIP.

ROG GO:001759; SHGA RICIN; UNKNOWN 1.

ROSTIE; PS001275; SHGA RICIN; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 RETTDLGIEPLRIGIKKLDENAIDNY---KPTEIASSLLVVIQMVSEAARFTFIENQIRN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 NLYGENTFKPDQAIISLENNWGALSKQIQKAQDRGGVFPNLVTLTTSSGKPLIIRNDSDP 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEG--LFKNTIKTRLHFGGSYPSLEGEKAY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 NF--QORIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYV--TAVD 234
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Submitted (APR-2004) to the EMBLA (GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AY603353; AAT12448.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92; Indels
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Antivral protein PAPal (Fragment).
                                eurosids I; Cucurbitales; Cucurbitaceae; Gynostemma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%; Score 286; DB 2; 33.5%; Pred. No. 8.6e-16; iive 31; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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206 LVQNGIALLKYMSE 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 33.5
nes 85; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNTIIYNVGSTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTNTNPK--YVLVELQGSN
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Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at o
specific adenosine on the 285 RNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AY603352; AAT12447.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016582; F:rRNA N-glycosylase activity; IEA.
GO; GO:0005929; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0017148; P:pathogenesis; IEA.
FRAM: PRO0157; RIP.
FRAM: PRO0157; RIP.
FRAM: PROS1F: SHIGARICIN.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
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GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO:0006552; P:defense response; IEA.
GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO:0009405; P:pathogenesis; IEA.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Phytolaccaceae; Phytolacca.
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PRINTS; PR00396; SHIGARICIN.
PR053TE; PS00275; SHIGARICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
NON_TER
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Phytolacca americana (Common pokeberry) (Virginian pokeweed)
                                                                                                                                                                                                                                                                                                                                                        96; Indels
                                                                                                                                                                                                                                                          237 AA; 26710 MW; A274F9BA402031DA CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                    ; Score 280; DB 2;
; Pred. No. 2.6e-15;
44; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 AA
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                                                                                                                                                                                                                                                                                                         21.8%;
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                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.64
Matches 76; Conservative
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VDASGAKW 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERANGKKY 228
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::| ||:|| : : : : | ||:|| 113 SRYPTLESKAGVKSRSQVQLGIQILDSNIGKI--SGVMSFTEKTEAEFLLVA 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen D., Wang X., Zhou G., Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL; AF338910; AAK21951.1; -.
                                                                                                                                                                                                                                                                                                  GQLAEIAIDVTSVYVVGYQ-----VRNRSYFFKD-------APDAAYEGLFKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 IQMVSEAARFTFIENQIRNNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVEL
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                                                                                                                                                         2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                      Gaps
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GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:001598; F:rRNA N-glycosylase activity; IEA.

GO; GO:0006952; F:defense response; IEA.

GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.

InterPro; IPR001574; RI.
                                                                                                      32;
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PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phytolacca americana (Common pokeberry) (Virginian pokeweed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Caryophyllales; Phytolaccaceae; Phytolacca.
NCBI_TaxID=3527;
                                                   Length 237;
                                                21.4%; Score 276; DB 2; Length 23 30.2%; Pred. No. 5.6e-15; ive 45; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96; Indels
FE576A3C96A1F6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26534 MW; FE4ADCEE03464783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.4%; Score 276; DB 2; 30.2%; Pred. No. 5.6e-15;
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26622 MW;
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                      Query Match
Best Local Similarity 30.4v
Best Local Similarity 75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 ERANGKKY 228
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237 AA;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM protein - protein search, using sw model Run on:

June 20, 2005, 09:21:47; Search time 113.5 Seconds (without alignments) 855.303 Million cell updates/sec US-10-717-243-2 1287 Title:

1 GLDTVSFSTKGATYITYVNF.....AVDQVKPKIALLKFVDKDPK 251 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2105692 seqs, 386760381 residues Searched:

1545266

Minimum DB seq length: 0 Maximum DB seq length: 251

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:* Database

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* 4 6 6 7 8

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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SUMMAKIES	ID	AAR63903	ADG63044	AAR63923	AAR63921	AAR63918	AAR63920	AAR63919	AAR63924	AAR63922	AAR63917	AAR63912	AAR74177	AAR37291	AAR63914	AAR63915	AAR63916	AAR63913	AAY69048	AAR07518	AAR25573	AAR67359	AAR21605	AAW14228	AAW14232	AAW14231
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*	Query Match	100.0	100.0	99.6	99.4	99.4	99.4	99.4	99.4	99.3	99.3	99.3	99.1	98.6	98.6	98.0	97.3	91.4	24.9	24.9	24.9	24.9	24.5	24.5	24.4	24.4
	Score	1287	1287	1282	1279	1279	1279	1279	1279	1278	1278	1278	1275	1269	1269	1261	1252	1176	321	321	321	320	315	315	314	314
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26 27 28 30		33 3 3 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6	1 4 4 4 4 1 4 6 4 7

## ALIGNMENTS

AAR63903 standard; protein; 251 AA. **AAR**63903

(revised)
(first entry) 25-MAR-2003 27-JUL-1995 AAR63903; 

Type I ribosome-inactivating protein gelonin.

Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.

Gelonium multiflorum.

WO9426910-A1.

24-NOV-1994.

94WO-US005348. 12-MAY-1994; 93US-00064691 12-MAY-1993;

(XOMA ) XOMA CORP.

Studnicka GM; Better MD, Carroll SF,

WPI; 1995-006804/01. N-PSDB; AAQ75532 - which Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents.

Example 1; Fig 1; 221pp; English

AAQ75532 encodes AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytchoxic therapeutic agents (CTA9), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 251 AA;

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Mismatches

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251; Conservative

Matches

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tumour and antiviral activity. Also described is a composition comprising the isolated peptide or polypeptide, and a carrier, excipient or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides or polypeptides. The peptide or polypeptide is useful for treating HIV infection, and tumour. This is the amino acid sequence of Gelonium anti-
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                                                                                                                                                                                                                                                                      GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and antiviral activity, useful for treating human immunodeficiency virus infection or tumor.
                                                         .
Length 251;
                                                         Indels
   '; DB 2;
1.6e-125;
                                                               ö
                                                         0; Mismatches
100.0%; Score 1287; 100.0%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADG63044 standard; protein; 251 AA
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                           Best Local Similarity 100. Matches 251; Conservative
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Score 1287; DB 8; Length 251; Pred. No. 1.6e-125;

100.0%;

Best Local Similarity

Query Match

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AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
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              1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                       121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
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1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                            GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.6%; Score 1282; DB 2; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 187-188; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type I RIP gelonin analog Gel (C103).
                                                                                                                                                                                                                                                                                                                                                                  AAR63923 standard; protein; 251 AA
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                                                                                                                                                                                                                                                                       241 ALLKFVDKDPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-006804/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    correct PN field.)
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27-JUL-1995
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Query Match
Best Local Similarity 99.6
Matches 250; Conservative
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27-JUL-1995
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                                                                                                                                                                                                                                                                                                                                   61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                            61 GQLAEIAIDVTSVYVVGYQVRNRSYFFXDAPDAAYEGLFKNTCKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                    121 AYRETTÜLGIEPLRIGIKKLÜENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                 FQORIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                               1 GLDIVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                   1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                               Gaps
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  Pred. No. 5.3e-125;
0; Mismatches 1; Indels
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  99.68;
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graft-versus-host disease
Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 ALLKFVDKDPK 251
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27-JUL-1995
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Sequence 251 AA;

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                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                240
                                                                                                                                               61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                      GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                       121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                          1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                 1 GLDTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                 181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
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                                         Gaps
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                                        Indels
Score 1279; DB 2;
Pred. No. 1.1e-124;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 183-184; 221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Type I RIP gelonin analog Gel(C248).
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   99.4%;
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(first entry)
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Gaps

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Indels

99.4%; Score 1279; DB 2; 99.6%; Pred. No. 1.1e-124; ive 0; Mismatches 1;

Conservative

250;

Similarity

Local

Length 251;

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180 180

AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 121 AYRETIDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFIFIENQIRNN FOOR I RPANNT I SLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI

121

GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120 61 GOLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120

61

1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN

1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN

240 240

181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI

241 ALLKFVDKDPK 251

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Sequence 251 AA;
                                                     Query Match
                                                                                                           Matches
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                                                                                                                                     GLDTVSFSTKGATY1TYVNFLNELRVKLKPEGNSHG1PLLRKKCDDPGKCFVLVALSNDN
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                         Length 251;
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                                                                            Indels
                         99.4%; Score 1279; DB 2;
99.6%; Pred. No. 1.1e-124;
iive 0; Mismatches 1;
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                                                     Local Similaricy ....
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AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                                                                                                                   Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Better MD, Carroll SF, Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 184; 221pp; English.
                                                                                                                                                                                                  Type I RIP gelonin analog Gel (C239)
                                                                                  AAR63919 standard; protein; 251 AA
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                                                                                                                                                                                                                                                                  graft-versus-host disease.
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(first entry)
241 ALLCFVÖKÖPK 251
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27-JUL-1995
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Gelonium multiflorum.
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  correct PN field.)
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                                               Sequence 251 AA;
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27-JUL-1995
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                                                                                                                                                                                                                                                           61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELBRANGKKYYVTAVDQVKPCI 240
                                                                                                                                                                                                                                     61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                            Score 1279; DB 2;
Pred. No. 1.1e-124;
0; Mismatches 1;
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                                                            Query Match
Best Local Similarity 99.6%;
Matches 250; Conservative
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                      Sequence 251 AA;
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   Length 251;
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                                                       Indels
Score 1279; DB 2;
Pred. No. 1.1e-124;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 187; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR63922 standard; protein; 251 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type I RIP gelonin analog Gel(C60)
99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-00064691.
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(first entry)
                                                          Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Better MD, Carroll SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ALLKFVOKOPK 251
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WO9426910-A1
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27-JUL-1995
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                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR63912;
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                                                                        Query Match
Best Local
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AAR63912
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                                                                                                                                                                                                                                                                                     181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKFKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) galonin, one of the nine RIPs described in AAR63903-R63311. RIPs are key components of cytoxoxic therapeutic agents (CTAS), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the
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  cancer and graft-versus-host disease. (Updated on 25-MAR-2003
                                                                                                                            GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDC
                                                                                                                                                             GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                             GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                             121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFIFIENQIRNN
                                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                              FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents.
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                                                            Length 251;
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                                                                                     Indels
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                                                            Score 1278; DB 2;
Pred. No. 1.4e-124;
                                                                        Pred. No. 1.4e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page 182-183; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type I RIP gelonin analog Gel(C247).
                                                                                                                                                                                                                                                                                                                                                                                                     AAR63917 standard; protein; 251 AA.
                                                            99.3%;
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                                                                        Local Similarity 99.6
                                                                                                                                                                                                                                                                                                              ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                               Carroll SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gelonium multiflorum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-006804/01
disease, cancer an correct PN field.)
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                                     Sequence 251 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1994;
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                                                               Query Match
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Matches
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elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                       61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                            121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                  1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                    GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                                                                                                                           121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                                                                                                                              FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                            1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                            Gaps
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0
                                                                                                           Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
                                                                                                                                           1; Indels
                                                                                                       Score 1278; DB 2;
Pred. No. 1.4e-124;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 179-180; 221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type I RIP gelonin analog Gel (A50/C44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Studnicka GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR63912 standard, protein, 251 AA.
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                                                                                                         99.3%;
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                                                                                                                                            250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ALLKFVDKDPK 251
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                                                                                                                            Similarity
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                                                                          Sequence 251 AA;
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Misc-difference 169
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the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
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                                                                                                                                                                  121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                             FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                              9
                                                                                                        1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKAFVLVALSNDN
                                                                                                                                          61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                             1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                  inactivating protein; RIP; Type I; cytotoxin; immunotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "in ricin A-chain and the Type I RIPs'
                                                          Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Non-Cys residue in claimed analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= non-Cys residue in claimed analogue
                                                                            1; Indels
                                                          Score 1278; DB 2;
Pred. No. 1.4e-124;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Cys in claimed analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Ala in claimed analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= Cys in claimed analogue
                                                                                                                                                                                                                                                                                                                                                               Type I ribosome-inactivating protein gelonin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= invariant residue
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                   AAR74177 standard; protein; 251 AA.
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/label= see above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abel= see above
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                                                          99.3%;
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                           Matches 250; Conservative
                                                                                                                                                                                                                                       ALLKFVDKDPK 251
                                                                                                                                                                                                                                                        ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                      (revised)
                                                                                                                                                                                                                                                                                                                                                                                                   Gelonium multiflorum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 113
                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Misc-difference 10
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                         correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 44
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                                          Sequence 251 AA;
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04-JAN-1980
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Analogues of Type I RIP are defined as non-naturally occurring polypeptides that share the ribosome-inactivating activity of the natural protein but differ in As sequence. Preferred analogues have a Cys available for disulfide bonding located at a posn. it its Ah sequence from the posn. corresp. to posn. 251 in ricin A-chain RTA to the carboxy cerminus of the analogue. (AAR74176 is the sequence of ricin A-chain RTA, which is a Type II RIP). The primary Ah sequence of ricin A-chain RTA, which is a Type II RIP). The primary Ah sequence of the Type I RIPS glonin, BRIP, mormordin II, luffin [see Islam et al. Agricultural biological Chem., 545, 1343-45.1991], alphatrichosanthin ([see Chow et al., J. Biol. Chem., 265, 8670-74.1990], momordin I [see Ho et al., J. BA, 108], Mirabilis antiviral protein [see Habuka et al., J. BA, 108], Mirabilis antiviral protein [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, 108], momordin I [see Habuka et al., J. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. BA, I. B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotide(s) encoding gelonin analogues - having a cysteine residue for intermolecular bonding for the prodn. of immuno-toxin(s).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                              239. .251
/label= location of Cys in claimed analogue
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Pred. No. 2.8e-124;
1; Mismatches 1;
                                                                                                                                                                                                                                                   label= Cys in claimed analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bernhard SL,
                                                                                 label= see above
                                                                                                                                                                                                                                                                                                                                                                                  247. .248
/label= see above
label= see above
                                                                                                                                                                                                                                                                                                                                         'label= see above
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92US-00901707,
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Best Local Similarity 99.2%;
Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-193480/25
                                             Misc-difference 198
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AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLDIVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDN
                 FQQR1RPANNT1SLENKWGKLSFQ1RTSGANGMFSEAVELERANGKKYYVTAVDQVKPK1
                               1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents.
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                                                                                                                                                                                                                                                                                                                      Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 181-182; 221pp; English
                                                                                                                                                                                                                                                                                           Type I RIP gelonin analog Gel(A44/A50)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Studnicka GM;
                                                                                                                                                                                  AAR63914 standard, protein, 251 AA.
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                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                     graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 249; Conservative
                                                                                              Better MD, Carroll SF,
                                                                          241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                              (revised)
                                                                                                                                                                                                                                                                                                                                                                                  Gelonium multiflorum.
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Best Local Similarity
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27-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention covers analogues of Type I RIPS. Gelonin is a Type I RIP and the analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment. (Updated on 25-MAR-2003 to correct PN field.)
                 181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDOVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQLAEIAIDVTSVYVVGYQVRNRSYFFKHAPDAAYEGLFKNTIKTRLHFGETYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                       Type I ribosome-inactivating protein; ricin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin; Buphorbiaceae family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Analogues of type I ribosome inactivating protein - useful as cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYYTTAVDQVKPKI
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                                                                                                                                                                  AAR37291 standard; protein; 251 AA.
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92US-00901707
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Matches 248; Conservative
                                                                                                                                                                                                                                                                         Plant type I RIP Gelonin.
                                                            ALLKFVDKDPK 251
                                                                           (revised)
                                                                                                                                                                                                                                                                                                                                                    Gelonium multiflorum.
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19-JUN-1992;
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13-SEP-1993
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 181
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AAR37291
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protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63901. RPBs are key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
                             FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                              181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polynucleotide(s) encoding type I ribosome-inactivating proteins - which are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                              Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.
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Pred. No. 8.2e-123;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                   Type I RIP gelonin analog Gel(C10/A44/A50).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Studnicka GM;
                                                                                                                                                                                           AAR63915 standard; protein; 251 AA.
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Best Local Similarity 98.8%;
Matches 248; Conservative
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                                                                                                      241 ALLKFVDKDPK 251
                                                                                     241 ALLKFVDKDPK 251
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                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                           Gelonium multiflorum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, cancer ar correct PN field.)
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27-JUL-1995
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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                             181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
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                                                                                                            241 ALLKFVDKDPK 251
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Sequence 1 Sequence 5 Sequence

Sequence 99, Appl Sequence 100, App Sequence 100, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 111, App Sequence 111, App Sequence 39, Appl Sequence 39, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 5, Appl Sequence 11, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

Sequence:

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Run on:

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Result

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TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
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Patent No. US2002000665381
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 265
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Sequence 103,
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 251
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Sequence 2, Application US/10717243

Publication No. US20050054835A1

GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANGTews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-889
TELEPHONE: 312/707-889
TELER: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                              ;
**TOPOLOGY: linear
;
**MOLECULE TYPE: protein
;
**SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-127-890-2
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COMPUTER READABLE FORM:
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COUNTRY: USA
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Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                            1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                          Score 1287; DB 9;
Pred. No. 5.8e-117;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
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APPLICATION NUMBER: US/10/127,890
FILING DATE: 23.Apr-2002
CLASSIFICATION: <Unknown>
                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 247:
                                                                                                                                                                                          100.0%; Scc.
100.0%; Pre
                            SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
    INFORMATION FOR SEQ ID NO: 247:
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STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                         Matches 251; Conservative
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Best Local Similarity
                                                                                                                                                             US-09-765-527-247
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US-10-127-890-2
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61 ĠQLABIAIDVTSVYVVĠYQVRNRSYFFKDAPDAAYEGLFKNTCKTRLHFGGSYPSLEGEK 120
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Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1282; DB 14;
Pred. No. 1.8e-116;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                 FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNV-1992
FILING DATE: 04-NOV-1991
                                                                                                                                                                                APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
PPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MCMIACholas, Janet M.
REGISTRATION NUMBER: 32, 918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                     APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 108, Application US/10717243 Publication No. US20050054835A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relephone: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312/707-9155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.64;
                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ALLKFVDKDPK 251
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Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                             NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1287; DB 17;
100.0%; Pred. No. 5.8e-117;
ive 0; Mismatches 0;
                                  FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-M2-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT THORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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Publication No. US20030166196A1
GENERAL INFORMATION:
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15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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COMPUTER READABLE FORM:
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Best Local Similarity
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US-10-127-890-108
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Sequence 103, Application US/10127890
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                                                                                                                                                                         NUMBER OF SEQUENCES: 173
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Best Local Similarity 99.6
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                              CURENT AFAILLE FORPY disk
CONGUTER: IBM PC Compatible
CONGUTER: IBM PC Compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 18-Nov-2003
CLASSIFICATION BATE: 15-APR-1997
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-APR-1995
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-APR-1993
APPLICATION NUMBER: US 07/984,107
FILING DATE: 19-DEC-1992
APPLICATION NUMBER: US 07/981,777
FILING DATE: 19-DU-1992
APPLICATION NUMBER: US 07/981,567
FILING DATE: 19-UN-1991
FILING DATE: 19-UN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
                 ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

NOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 108:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 251 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 108:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                          ZIP: 60661
COMPUTER READABLE FORM:
                                   STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLKFVDKDPK 251
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RESULT 6 US-10-127-890-103

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
Publication No. US20030166196A1
GENERAL INFORMATION:
CATTOIL, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                CITY: Chicago
COUNTX: USA
COUNTX: USA
ZIP: GOGG1
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <underweenseleccture
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ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 1279; DB 14; 99.6%; Pred. No. 3.5e-116; iive 0; Mismatches 1;
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APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCMICACIOLAS, Janet M.
REFERENCE/DOCKET NUMBER: 20.918
REFERENCE/DOCKET NUMBER: 20.918
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9889
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-127-890-103
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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMPSEAVELERANGKKYYTAVDQVKPCI 240
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                                                                                                                121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTBIASSLLVVIQMVSBAARFTFIENOIRNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BELLER, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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FLIANG DATE: 33-Apr-2002
FLASTELATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FLILNG DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70,P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-127-890-105
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Illinois
COUNTRY: USA
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  181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                 Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunocoxins Comprising Ribosome-Inactivating
Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ); DB 14;
3.5e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: McNicholas, Janet M.
REGIGTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
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Pred. No. 3.
                                                                                                                                                                                                      Sequence 104, Application US/10127890 Publication No. USZ0030166196A1 GENERAL INFORMATION: APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 104
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60661
COMPUTER READABLE FORM:
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Best Local Similarity 99.6
Matches 250; Conservative
                                               241 ALLKFVDKDPK 251
                                                                                        241 ALLKFVDCDPK 251
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61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKONTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                          61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                     1 GLDTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPLLLLLLLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 109, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
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                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                            Length 251;
                                                                                                                                                                                                                                                                             Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                          Query Match 99.4%; Score 1279; DB 14; Best Local Similarity 99.6%; Pred. No. 3.5e-116; Matches 250; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION CONTINUALLY
APPLICATION NUMBER: US/08/646,360
RILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/97,567
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APPLICATION NUMBER: US/10/127,890
FILING DATE: 23Apr-2002
CLASSIFICATION: «Unknown»
                         | LENGTH: 251 amino acids | TYPE: amino acids | TYPE: amino acid | TYPE: amino acid | TYPE: TYPE: protein | SEQUENCE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 106: US-10-127-890-106
     INFORMATION FOR SEQ ID NO: 106:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 173
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US-10-127-890-109
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                                                                                                                                                                                                                                                                                                                                                  180
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                                                                                                    1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carroll, Stephen F. Studnika, Gary M. TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                     Gaps
                                                     ;
     Score 1279; DB 14; Length 251;
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COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

CORFWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360

FILING DATE: 12-APY-1996

APPLICATION NUMBER: PCT/US94/05348

FILING DATE: 12-MAY-1996

APPLICATION NUMBER: US 08/064,691

FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/988,430

FILING DATE: 10-MAY-1997

APPLICATION NUMBER: US 07/981,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/991,707

FILING DATE: 19-JUN-1992

APPLICATION NUMBER: US 07/991,707

FILING DATE: 19-JUN-1992

ATTORNEY/AGENT INFORMATION:
                                                     IndelB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                         Pred. No. 3.5e-116;
0; Mismatches 1;
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REGIGTRATION NUMBER: 32,918
REFERNCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-889
TELEFAX: 312/707-9155
TELEFAX: 550 388-1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 106, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Better, Marc D.
Query Match 99.4%;
Best Local Similarity 99.6%;
Matches 250; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60661
COMPUTER READABLE FORM:
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STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLKFVDKDPK 251
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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AYRETTDLGIEPLKIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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Sequence 104, Deplication US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxing Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
0
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                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFRENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMULCATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.4%; Score 1279; DB 17; 99.6%; Pred. No. 3.5e-116; ive 0; Mismatches 1;
                                                                  FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 05-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 15-UNV-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                        FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
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MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-717-243-103
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 251 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins
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INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ALLKFVDCDPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 103, Application US/10717243
Publication No. US20050054835A1
GENERAL INPORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE: MCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111,1nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                           99.4%; Score 1279; DB 14; 99.6%; Pred. No. 3.5e-116; ive 0; Mismatches 1;
                                  REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/707-9155
TELESTAX: 312/707-9155
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                         LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 60661
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-127-890-109
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셤 ò 쉽 ò g ò 유 ઠે 240

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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GLDTVSFSTKGATYITTVNPLNPLRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION: 330
PRIOR APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APPL1997
FILING DATE: 18-APPL1997
FILING DATE: 18-APPL1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DOWN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCHACHOLAS, Janet M.
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 31,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MABER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
IE: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.4%; Score 1279; DB 17;
99.6%; Pred. No. 3.5e-116;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-10-717-243-106
; Sequence 106, Application US/10717243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 251 amino acids TYPE: amino acid
  ADDRESSEE: McAndrews,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 105:
                                                                                                                  ZIP: 60661
COMPUTER READABLE FORM:
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Best Local Similarity 99.6
Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: MANIcholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/707-9889
TELEFAX: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.5e-116;
                                                                                                                                                    APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.4%; Score 1279; D 99.6%; Pred. No. 3.5e
                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-717-243-104
  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105, Application US/10717243 Publication No. US20050054835A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 251 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ALLKFVDKDPK 251
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                                                                                                                                                                                                                    Sequence 109, Application US/10717243
Publication No. US20050054835A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxing Comprising Ribosome-Inactivating Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
TELEFAK: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: MCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APP.1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/87,567
FILING DATE: 04-NOV-1991
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FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                      241 ALLKFVDKDPK 251
                                       241 ALLKFVDKDPK 251
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US-10-717-243-109
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                                                                                     Carroll, Stephen F. Studnika, Gary M. IIILE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYYTAVDQVKPKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-NOV-2003
CLASSIFICATION: 530
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/908,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 106;
                                                                                                                                                                       Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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                                                           APPLICANT: Better, Marc D.
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                                                                                                                                                                                                NUMBER OF SEQUENCES: 169
Publication No. US20050054835A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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Search completed: June 20, 2005, 10:05:45 Job time : 105.5 secs

241 ALLKFVDKDPK 251 ||||||||||| 241 ALLKFVDKDPK 251

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NAME: Meyers, Thomas C.
REGIGSTRATION NUMBER: P-36,98:
REPERENCE/DOCKET NUMBER: 313:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-425-336-2
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25, App
259, App
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251, App
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Sequence 2, Appli
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-621-803-247

US-08-631-803-247

US-09-136-389-2

US-09-136-389-2

US-09-217-355-247

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US-09-217-355-247

US-09-610-838-2

US-09-610-838-2

US-09-645-603B-2

US-09-645-603B-2

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US-09-621-803-259

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09-610-838-108
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
TITLE OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
Sequence
Sequence
Sequence
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STATE: 111inois
COMPUTE: 105A
ZIP: 6606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PREN: US/08/425,336
FLING DATE: 18-ARR-1995
RELOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
RELOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-JUN-1991
ATPONEY/AGENT INFORMATION:
WANDER: MAINTENAMENTION:
WANDER: MAINTENAMENTION:
WANDER: MAINTENAMENTION:
WANDER: MAINTENAMENTION:
WANDER: MAINTENAMENTION:
                 US-08-425-336-103
US-08-425-336-104
US-08-425-336-105
US-08-425-336-105
US-08-488-1138-104
US-08-488-1138-105
US-08-488-1138-105
US-08-488-1138-105
US-08-488-1138-106
US-08-477-4848-109
US-08-477-4848-105
US-08-477-4848-105
US-08-477-4848-105
US-08-477-4848-105
US-08-477-4848-105
US-08-477-4848-105
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US-08-646-360-104
                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-425-336-2
; Sequence 2, Application US/08425336
; Patent No. 5621083
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FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
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                                        TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 251 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein
312/707-8889
                                                                                                                                                                                                                                                                                   Matches 251; Conservative
                      312/707-9155
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241 ALLKFVDKDPK 251
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  TELEPHONE: 3
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                                                                                                          1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
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                      100.0%; Score 1287; DB 1; Length 251; 100.0%; Pred. No. 8.6e-125; tive 0; Mismatches 0; Indels 0;
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FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
FILING DATE: 19-JUN-1992
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 130,7087,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
FORDRESSEE: MCANTERWS! Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08488113B Patent No. 5744580
                                                                Matches 251; Conservative
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241 ALLKFVDKDPK 251
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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STATE: Illinois
COUNTRY: USA
                                            Similarity
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US-08-488-113B-2
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APPLICANT: Better, Marc D.

APPLICANT: Carroll, Stephen F.

APPLICANT: Carroll, Stephen F.

APPLICANT: Carroll, Stephen F.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins

NUMBER OF SEQUENCES: 169

CORRESPONDENCE ADDRESS:

ADDRESSEE: MCANdrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor

CITY: Chicago

STATE: Illinois

COUNTY: USA
                                                                                                                                                          1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                              Gaps
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100.0%; Score 1287; DB 1; Length 251; 100.0%; Pred. No. 8.6e-125;
                                                           0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
COMPUTER: The PC compatible
COMPUTER: The PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION NUMBER: US 08/64,691
FILING DATE: 12-APR-1995
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-APR-1993
PRIOR APPLICATION NUMBER: US 08/064,691
                   100.0%; Prec. ...
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Sequence 247, Application US/08621803
Fatent No. 5851802
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Fatent No. 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: MCMICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPAX: 312/707-9155
TELEPX: 650 389-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                     PAPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
FILING DATE: 04-NOV-1991
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 251 amino acids TYPE: amino acid
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US-08-621-803-247
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Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1287; DB 1; Length 251; Best Local Similarity 100.0%; Pred. No. 8.6e-125; Matches 251; Conservative 0; Mismatches 0; Indels 0
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OFFER.: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                       11022US07/200-70.P3.C2A
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STREET: 500 West Madison Street, 34th floor
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, JANEE M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/2
TELECHANKI 312/707-8889
TELECHANK: 312/707-8889
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TELEFAX: 650 388-1248
FILEX: 650 388-1248
FINFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
TYPE: amino acids
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61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKOTIKTRLHFGGSYPSLEGEK 120
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US-09-136-389-2
; Sequence 2, Application US/09136389
; Fatent No. 614680
; Patent No. 614680
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 PQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
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                CLASSIPTCATION 15.76 LIANGE APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILING DATE: 18-ARR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
NAME: MCANICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFRAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 251 amino acids
amino acid
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Best Local Similarity 100.
Matches 251; Conservative
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    FILING DATE:
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TELEX: 69
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Patent No. 6146631
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Batter, Marc D.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 251;
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                                                           CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,803

FILING DATE: 22-MAR-1996

ATTORNEY/AGBNT INFORMATION:

NAME: BOTUN, Michael F.

REFERENCE/DOCKET NUMBER: 27129/33199

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: 312/474-6408

TELEFRAX: 312/474-6408

TELEFRAX: 25-3856

INFORMATION FOR SEQ ID NO: 247:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 60661

ZIP: 60661

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 100.0%; Score 1287; DB 2; Local Similarity 100.0%; Pred. No. 8.6e-125;
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APPLICATION NUMBER: US/08/839,765
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 251; Conservative
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CITY: Chicago
STATE: Illinois
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US-08-839-765-2
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61 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                              APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
TITLE OF INVENTION: Methods for Recombinant Wicrobial Production of
TITLE OF INVENTION: Pusion Proteins and BPI-Derived Peptides
NUMBER OF SEQUENCES: 265
CORRESPONDENESS:
CORRESPONDENESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                             CITY: Chicago State Lower, 233 South Market Lilve STATE: Illinois COUNTRY: United States of America ZIP: G6060-6402 COMPUTER READABLE FORM: WEDLUM TYPE: Ploppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/09/217,352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,80
FILING DATE: 22-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BOTUN, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/POCKET NUMBER: 25,447
REFERENCE/POCKET NUMBER: 2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INPOMATION FOR SEQ ID NO: 247:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
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TELEFAX: 312/474-0448
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amino acid
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Matches 251; Conservative
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                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA: 94
PRIOR APPLICATION DATA: 98/064,691
PRIOR APPLICATION DATA: 98/064,691
PRIOR APPLICATION DATA: US 07/988,430
PRIOR APPLICATION DATA: US 07/988,430
PRIOR APPLICATION DATA: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-0NN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
PERGESTRATION NUMBER: 32,918
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US-09-217-352-247
; Sequence 247, Application US/09217352
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 251 amino acids
TYPE: amino acid
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Best Local Similarity 100.
Matches 251; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Illinois
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Patent No. 6643742
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDERSS:
ADDRESSEE: MCANDERSS:
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/711,485
FILING DATE:
CLASSPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/839,765
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500 West Madison Street, 34th floor
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APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAX-1993
PRICR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/97,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Jane MARE: MCNicholas, Jane MCSICATION NUMBER: 33,918
REFERENCE/DOCKET NUMBER: 33,918
REFERENCE/DOCKET NUMBER: 31,918
REFERENCE/DOCKET NUMBER: 31,918
TELEPHONE: 312/707-8889
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INFORMATION FOR SEQ ID NO: 2:
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amino acid
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Matches 251; Conservative
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                                                               241 ALLKFVDKDPK 251
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Illinois
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US-09-711-485-2
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TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDERSWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS PROPED TO SERVED TO SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED SERVED 
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APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG.
PILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-UN-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTOCNEY/AGGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 200-70.P4
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                               STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC compatible

COMPUTER IBM PC compatible

COMPUTER IBM PC compatible

COMPUTER IBM PC compatible

COMPUTER IBM PC compatible

COMPUTER IBM PC compatible

COMPUTER IBM PC compatible

COMPUTER IBM PC compatible

APPLICATION NUMBER: US/07/901,707

FILING DATE: 19920619

FILING DATE: 04-NOV-1991

ATTORNEY/AGENT INFORMATION:

NAME: NO. 5376546and, Greta E.

REGISTRATION NUMBER: 35.302

REFERENCE/DOCKET NUMBER: 27129/30910

TELECOMMUNICATION INFORMATION:

THE TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY TOWNEY T
       NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                        STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
CITY: 1111nois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/07988430 Patent No. 5416202 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (312) 346-5750
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TELEFX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (312) 984-5750
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-988-430-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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APPLICANT: LEE-HUANG, Sylvia

APPLICANT: LEE-HUANG, Sylvia

TITLE OF INVENTION: map30 and Anti-tumor Peptides and Truncated Polypeptides of

TITLE OF INVENTION: map30 and gap31

FILE REFERENCE: LEE-HUANG 4A

CURRENT APPLICATION NUMBER: US/09/645, 603B

CURRENT FILING DATE: 2000-08-25

PRIOR APPLICATION NUMBER: US 60/150,885

PRIOR PLING DATE: 1999-08-26

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.2
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Patent No. 5376546
GENERAL INFORMATION:
APPLICANT: Berthard, Susan L.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
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FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09645603B Patent No. 6652861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Gelonium multiflorum US-09-645-603B-2
                                                                                                                                                                                                                                                                                                                                                                                           241 ALLKFVDKDPK 251
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241 ALLKFVDKDPK 251
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US-09-645-603B-2
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LENGTH: 251
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APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STREET: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER
SOFTWARE: PATCHION DATA:
APPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO.land, Greta E
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 31133
TELEFRAX: (312) 346-5750
TELEFRAX: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: AMINO ACID
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Best Local Similarity 99.6
Matches 250; Conservative
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PCT-US92-09487-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60603
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TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION:
Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES:
ORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLIASSIFICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
RICHARD APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5416202and, Greta E.
REGISTRATION NUMBER: 35323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: AMINO ACID
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PCT-US92-09487-2
; Sequence 2, Application PC/TUS9209487
Sequence 1, Application PC/TUS9209487
; APPLICANT: Bernhard, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.6
Matches 250; Conservative
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MOLECULE TYPE: protein
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143 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 202
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                                                                                                                                                                                                                                                                                                                                                                                                                     99.8%; Score 1284; DB 2; Length 293; 99.6%; Pred. No. 2.2e-124; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.6'
Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-621-803-259
US-08-621-803-259
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Sequence Sequence Sequence

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Sequence 100, App Sequence 102, App Sequence 102, App Sequence 100, App Sequence 100, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 110, App Sequence 110, App Sequence 110, App

4, Appli 1, Appli 1, Appli 1, Appli 1, Appli 1, Appli

Sequence 1 Sequence 1 Sequence 1

Sequence 111, P Sequence 4, App Sequence 4, App

Appli Appli

Sequence 1, Sequence 2, Sequence 39,

Sequence 39, Appl

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Result Š.

us-10-717-243-2.open.rapb

OM protein -

Run on:

Sequence:

Title: Perfect

Searched:

Database

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Sequence 247, Application US/09765527
Patent No. US2002000663BA1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Born STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: 11linois COUNTRY: United States of America ZIP: 6060-6400 CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER : IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
US-10-127-890-104
US-10-127-890-105
US-10-127-890-105
US-10-127-890-106
US-10-127-890-109
US-10-717-243-103
US-10-717-243-104
US-10-717-243-106
US-10-717-243-106
US-10-717-243-106
US-10-127-890-100
US-10-127-890-100
US-10-127-890-101
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REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27129/33199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/765,52:
FILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
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    US-09-765-527-247
    RESULT 1
    Sequence 247, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 11, Appl
Sequence 259, App
Sequence 259, App
Sequence 259, App
Sequence 259, App
                                                                                                                             (without alignments)
913.544 Million cell updates/sec
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Sequence 108,
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                                                                                                              June 20, 2005, 09:20:52 ; Search time 105.5 Seconds
                   version 5.1.6
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US-10-127-890-108

US-10-127-890-103
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100%
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Maximum DB seq length: 200000000
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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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MEDIUM TERE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSUT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIPICATION: 530
PRIOR APPLICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSER: MCANDTews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                         ATTORNEY/AGENT INFORMATION:
NAME: MCNIcholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
                                                                                                                                                       TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 100.
Matches 251; Conservative
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COUNTRY: USA
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Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
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COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <underween
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STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                    Query Match
100.0%; Score 1287; DB 9;
Best Local Similarity 100.0%; Pred. No. 5.8e-117;
Matches 251; Conservative 0; Mismatches 0;
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FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UUN-1992
                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 247:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                LENGTH: 251 amino acids
                    INFORMATION FOR SEQ ID NO: 247: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCES: 173
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CORRESPONDENCE ADDRESS
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STATE: Illinois
COUNTRY: USA
                                                                                         TYPE: amino acid
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  TELEX: 25-3856
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100.0%; Pred. No. 1.5e-116;
trive 0; Mismatches 0;
                                              DB 14;
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0; Mismatches 0
                                            100.0%;
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Best Local Similarity 100.0
Matches 251; Conservative
                                                            al Similarity 100.
251; Conservative
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Matches 251
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Sequence 1, Application US/10074596
Publication No. US20030176331A1
GENERAL INFORMATION:
APPLICANT: CHEUNG, LAWRENCE
APPLICANT: CHEUNG, LAWRENCE
TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF TITLE OF INVENTION: MAKING THEOFF FILE OF INVENTION: WINDER: US/10/074,596
CURRENT APPLICATION NUMBER: US/10/074,596
PRIOR APPLICATION NUMBER: 60/268,402
PRIOR APPLICATION NUMBER: 60/268,402
PRIOR FILING DATE: 2001-02-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match : 100.0%; Score 1287; DB 17; Length 251; Best Local Similarity 100.0%; Pred. No. 5.8e-117; Matches 251; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 3.2, 918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/797,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-717-243-2
                                                                                                                                                                                                                                                                                               TELEÇOMMUNICATION INFORMATION
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                              INCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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TYPE: PRT
ORGANISM: Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                        TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 2:
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US-10-074-596-1
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| Publication No. US2030176331A1
| GENERAL INFORMATION:
| APPLICANT: ROSENBLUM, MICHAEL G. |
| APPLICANT: ROSENBLUM, MICHAEL G. |
| TITLE OF INVENTION: MODIFIED PROTEINS, DESIGNER TOXINS, AND METHODS OF |
| TITLE OF INVENTION: MAKING THEOF |
| TITLE OF INVENTION: MAKING THEOF |
| TITLE OF INVENTION: MUMBER: US/10/074,596 |
| CURRENT APPLICATION NUMBER: 60/268,402 |
| PRIOR FILING DATE: 2002-02-12 |
| PRIOR FILING DATE: 2001-02-12 |
| NUMBER OF SEQ ID NOS: 11 |
| SEQ ID NO 11 |
| LENGTH: 507 |
| TYPE: PRI |
| TYPE: PRI |
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Length 316;
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US-09-765-527-253
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                                                                                                                                                   APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of FITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                           CUNTRY: United States of America

CUNTRY: United States of America

ZIP: 6060-6402

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/765,527

FILING DATE: 18-Jan-2001

PRIOR APPLICATION NUMBER: 08/621,803

FILING DATE: CUNKNOWN:
APPLICATION NUMBER: 25,447

REGISTRATION MICHAEL F.
REGISTRATION MICHAEL F.
REGISTRATION MICHAEL F.
REGISTRATION MICHAEL F.
TELECOMMUNICATION INFORMATION:
TELEFAX: 312/474-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 259: US-09-765-527-259
                                                                                           Sequence 259, Application US/09765527
Patent No. US20020006638A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 293 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 259:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 265
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497 ALLKFVDKDPK 507
                                                                             US-09-765-527-259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
Sequence 253, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 GLDTVSFSTKGATYITYVNFLNBLRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                              CITY: Chicago
COMPUTER: 111inois
COMPUTER: 111inois
COMPUTER READABLE FORM:
MEDIUM TYPES: POGG-6402
COMPUTER: 110 PC COMPALIDIS
COMPUTER: 110 PC COMPALIDIS
COMPUTER: 110 PC COMPALIDIS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,527
PRICH APPLICATION NUMBER: 08/621,803
PTILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BOTUM, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 25,447
TELEPRAIS 312/474-6300
TELEFORMUNICATION INFORMATION:
TELEFAR: 312/474-6300
TELEFAR: 312/474-6300
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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99.8%; Score 1284; DB 9;
Best Local Similarity 99.6%; Pred. No. 1.5e-116;
Matches 250; Conservative 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
US-09-765-527-251
; Sequence 251, Application US/09765527
; Patent No. US20020006638A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 309 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 253:
                                                                                                                                                                              NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 ALLKFVDKOPK 273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 GQLAEIAIDVTSVYVVGYQVRNRSYFFXDAPDAAXEGLFKNTIKTRLHFGGTYPSLEGEK 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLIRKKCDDPGKCFVLVALSNDN 82
APPLICANT: Better, Marc D.
TITLE OF INVENTION: Methods for Recombinant Microbial Production of
Fusion Proteins and BPI-Derived Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carroll, Stephen F. Studnika, Gary M. Studnika, Gary M. TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLDTVSFSTKGATY1TYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                            CITY: Clicago
CITY: Clicago
CITY: Clicago
COMPUTE: Illinois
COMPUTE: Illinois
COMPUTE: Ellinois
COMPUTE: Ellinois
COMPUTE: READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 18-Jan-2001
PRIOR APPLICATION NUMBER: US/09/765,527
PRILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BOTUM, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/OCKET NUMBER: 25,447
TELEPHONE: 312/474-0448
TELEPHONE: 312/474-0448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.8%; Score 1284; DB 9;
Best Local Similarity 99.6%; Pred. No. 1.7e-116;
Matches 250; Conservative 1; Mismatches 0;
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 251:
US-09-765-527-251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 332 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 251:
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                                                                     NUMBER OF
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US-10-127-890-108
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121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
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                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <UNknown>
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.6%; Score 1282; DB 14;
99.6%; Pred. No. 1.8e-116;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION SOURCES AND PRIOR APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993 APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992 APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992 APPLICATION NUMBER: US 07/901,707 FILING DATE: 09-UN-1992 APPLICATION NUMBER: US 07/901,707 FILING DATE: 09-UN-1992 APPLICATION NUMBER: US 07/901,707 FILING DATE: 09-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MCM.cholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
US-10-127-890-108
                                                                                                                                                                 ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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INFORMATION FOR SEQ ID NO: 108:
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Matches 250; Conservative
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181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI 240
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                       181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                            GLDTVSFSTKGATY I TYVNFLNELRVKLKPEGNSHGI PLLRRKKCDDPGKCFVLVALSNDN
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.4%; Score 1279; DB 14; 99.6%; Pred. No. 3.5e-116; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1991
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-UN-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-UN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEC ID NO: 103:
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60661
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6
Matches 250; Conservative
                                                                                                                 241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                    RESULT 11
US-10-127-890-103
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                                                                                                     APPLICANT: Better, Marc D.
Carroll, Srephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMULCATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAX-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/717,243
FILING DATE: 18-Nov-2003
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19-UNN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 108:
                                     Sequence 108, Application US/10717243 Publication No. US20050054835A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312/707-9155
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                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60661
COMPUTER READABLE FORM:
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Matches 250; Conservative
                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-717-243-108
                     -10-717-243-108
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61 GQLAEIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                                                        GOLAEIAIDVTSVYVVGYOVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                         1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 60
                                                                                                                                                                                                                                                                                                                                                                                                         FOOR I RPANN'TI SLENKWGKL, SFOI RTSGANGMFSEAVELERANGKKYYVTAVDOVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 105, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
                                                                                         Gaps
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                                               Length 251;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS: ADDRESSE: MCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                            DB 14;
                                          Score 1279; DB 14;
Pred. No. 3.5e-116;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/064,691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 12-MAY-1994
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                                            99.4%;
                                          Query Match
Best Local Similarity 99.6%
Matches 250; Conservative
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US-10-127-890-104
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                       GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                            61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                            AYRETTDIGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                           121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                             181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYYTAVDQVKPKI 240
                                                                                                                                                                                                   FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: MCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 200-70.P4 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 104, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                     ALLKFVDCDPK 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carroll, Stephen F. Studnika, Gary M. TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
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COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1279; DB 14;
Pred. No. 3.5e-116;
O; Mismatches 1;
                   APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 106:
US-10-127-890-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 109, Application US/10127890
; Publication No. US2003166196A1
; GENERAL INFORMATION:
APPLICANT: Better, Marc D.
                                                                                                                                                     TELECOMMUNICATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELERAX: 650 388-1248
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                    LENGTH: 251 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins
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COMPUTER READABLE FORM:
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Best Local Similarity 99.6
Matches 250; Conservative
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Carroll, Srephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY. Chicago
STATE: 111inois
COUNTRY: USA
                                                                                                                                                                                                                                                   Query Match 99.4%; Score 1279; DB 14;
Best Local Similarity 99.6%; Pred. No. 3.5e-116;
Matches 250; Conservative 0; Mismatches 1;
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APPLICATION NUMBER: US/08/646,360
FILING DATE: 13 MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1993
APPLICATION NUMBER: US 07/980,707
                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-10-127-890-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 106, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
                                                                                      LENGTH: 251 amino acids
TYPE: amino acid
                     TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
TELEFAX: 312/707-9155
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COMPUTER READABLE FORM:
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US-10-127-890-106
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             PILING DATE: 13-MAY-1996

APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994

APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993

APPLICATION NUMBER: US 07/984,430
FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-DEC-1992

APPLICATION NUMBER: US 07/97,567
FILING DATE: 09-DEC-1991

ATTORNEY/AGNT INFORMATION:

REGISTRATION NUMBER: 200-70.P4

FELECOMMUNICATION NUMBER: 200-70.P4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-9889

TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 109:

SEQUENCE CHARACTERISTICS:

LENGTH: 251 amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: AMINO ACID

SEQUENCE DESCRIPTION: SEQ ID NO: 109:

SEQUENCE DESCRIPTION: SEQ ID NO: 109:

SEQUENCE DESCRIPTION: SEQ ID NO: 109:
APPLICATION NUMBER: US/08/646,360
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Best Local Similarity 99.61
Matches 250; Conservative
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Search completed: June 20, 2005, 09:39:26 Job time : 106.5 secs

ALLKFVDKOPK 251

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

June 20, 2005, 09:09:06; Search time 25.5 Seconds (without alignments) 947.075 Million cell updates/sec

US-10-717-243-2 1287 1 GLDTVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Ø	Description	RNA	rRNA N-glycosidase	rRNA N-glycosidase	. ricin D precursor	rRNA N-glycosidase	agglutinin precurs	abrin-b precursor	rRNA N-glycosidase	abrin (clone 7.2)	rRNA N-glycosidase	rRNA N-glycosidase	abrin-a precursor	karasurin - Mongol	karasurin C - Tric	antiviral protein	karasurin-B - Tric	rRNA N-glycosidase	mistletoe lectin I	abrin-d precursor	abrin-c precursor	rRNA N-glycosidase	agglutinin I precu	beta-luffin - smoo	luffin-b - smooth	rRNA N-glycosidase	betavulgin - beet	ribosome-inactivat		rRNA N-glycosidase
SUMMARIES		! ! !																												
SUM	ID	T075	JC4840	\$25560	RLCSD	JC4235	RLCSAG	S32430	\$28421	C39761	S17757	RLTZT	TZLSA	JU0393	JC5606	<b>JE0401</b>	JC5032	\$22494	PD0018	S32431	S16022	RLPUGG	862627	823519	3N0108	A39817	JC4811	S46239	S17574	528542
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•	ouery Match	100.0	27.1	26.9	26.7	26.5	26.0	25.9	25.7	25.6	25.3	4.	24.9	24.5	24.5		24.1		23.3	23.2	23.2	22.6	22.3	22.0	21.0	16.7	16.3	15.7	15.2	14.1
	Score	1287	348.5	346	343	341	334.5	333.5	330.5	329	325	321	320	315	315	311.5	310	306.5	300.5	298	298	291	287.5	283.5	270	215.5	210	202	2	181.5
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rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	abrin (clone 3.7)	N conserved hypoth	tritin - wheat	rRNA N-glycosidase	30K ribosome inact	protein synthesis	hypothetical prote
RLQHG2	T12573	S17519	805205	S28541	528539	S29931	A58923	S17932	B39761	B69511	S33631	RLBH	B38664	JC5848	T05612
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# ALIGNMENTS

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6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	47-316/PF 53-294/Do Duery Mat Best Loca Matches 1 1 1 2 2	F;47-316/Product: ribosomal RNA N-glycosidase #status predicted <mat> F;53-294/Domain: rRNA N-glycosidase homology <rng>  Query Match  100.0%; Score 1287; DB 2; Length 316; Best Local Similarity 100.0%; Pred. No. 2.1e-99; Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 GLDTVSFSTKGATYITYVNFLNELRYKLKPEGNSHGIPLIRKKCDDPGKCFVLVALSNDN 60                                       </rng></mat>

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A, Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1.576 cHAL>
A;Cross-references: UNIPROT: P02879; GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083
A;Cross-references: UNIPROT: D.M.
Biol. 18, 515-525, 1992
A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene A;Reference number: S20513; MUID:92163016; PMID:1371405
A;Accession: S20513
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C;Species: Ricinus communis (castor bean)
C;Species: 13-Dec-1993 #sequence_revision 31-Dec-1993 #text change 09-Jul-2004
C;Date: 13-Dec-1993 #sequence_revision 31-Dec-1993 #text change 09-Jul-2004
C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R;Halling, K.C.; Halling, A.C.; Murray, B.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic, Acids Res. 13, 8019-8013, 1985
A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A;Reference number: A24041; MUID:86067214; PMID:2999712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 SVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNNFQQ 183
                                                                                                                                                                                                                                                                                                                                                                                     25 VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISD-SRRFILLDLTSYAYETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 RIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI
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A; Molecule type: DNA
A; Residues: 1-576 < RTES.
A; Cross-references: EMBL:X52908; NID:921084; PIDN:CAA37095.1; PID:921085
A; Cross-references: EMBL:X52908; NID:921084; PIDN:CAA37095.1; PID:921085
B; Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Bischem. 148, 265-270, 1985
A; Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A; Reference number: A24614; MUID:85179479; PMID:3838723
                                                                                                                                                                                                                10;
                                                                                                                            26.9%; Score 346; DB 2; Length 28 37.4%; Pred. No. 2.8e-21; ive 34; Mismatches 108; Indels
C; Keywords: glycosidase; hydrolase
F;27-264/Domain: rRNA N-glycosidase homology <RNG>
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A;Molecule type: DNA
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A.Reference number: 470677
A.Accession: 470701
A.Accession: 470701
A.Molecule type: protein
A.Molecule type: protein
A.Residues: 1-50, 12, 52-245 <CHO2>
C.Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C.Keywords: glycoprotein; glycosidase; hydrolase; phosphoprotein; seed
F.4-242/Domain: rRNA N-glycosidase homology <RNG>
F.51,201/Binding site: carbohydrate (Asn) (covalent) #status experimental
F.70,158,161/Active site: Tyr, Glu, Arg #status predicted
F.70,558,Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Momordica balsamina (balsam apple)
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S25560
R;Ortigao, M.; Better, M.
Nucleic Acids Res. 20, 4662, 1992
A;Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homol A;Reference number: $25560; MUID:93027170; PMID:1408771
A;Accession: $25560
A;Status: preliminary
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A;Modlecule type: mRNA
A;Modlecule type: mRNA
A;Cross-references: UNIPROT:P29339; EMBL:Z12175; NID:g19525; PIDN:CAA78166.1; PID:g19526
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: Amino acid of sequence of trichoanguina, a ribosomal-inactivating protein from A,Reference number: JC4840
A,Accession: JC4840
A,Accession: JC4840
A,Bolecule type: protein
A,Residues: 1-132,'S', J34-245 <CHO1>
A,Experimental source: seed
A,Note: the sequence in Fig. 2 is inconsistent with the sequence data presented in Table submitted to JIPID, August 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE---GEKA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHISSNEYPNQAVISLENKWGALSKQIQIANRIGHGQPENPVELYNPDGTRFSVTHTSAG 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                               rRNA N-glycosidase (EC 3.2.2.2) trichoanguina - snake gourd
C;Species: Trichosanthes anguina (snake gourd)
C;Date: 15-Aug-1996 #sequence revision 24-Oct-1997 #text_change 05-Dec-1997
C;Accession: JC4840; JT0011; JT0677
C;Accession: JC4840; JLD1, JY.; Wang, S.H.; Uèno, Y.; Tsugita, A.
Biomed. Sci. 3, 178-186, 1996
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ALLKFVDKDPK 297
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A; Molecule type: protein
A; Residues: 315-335, NY, 337-342, NH, 345-362,364-383, PS, 386-399, T', 401, 'D', 403, 'E', 40
A; Residues: 315-335, NY, 566, 'H, 567-570, 'LI', 573-574, 'F' <FUN>
A; NC E: (E, 520-544, WW, 566, 'H, 567-570, 'LI', 573-574, F' <FUN>
A; NC E: this paper, one of a series, summarizes the experimental details for the determinence in Proteins 10, 270-278, 1991
A; Title: 31c-directed mutagenesis of ricin A-chain and implications for the mechanism c
A; Reference number: A48237; MUID: 91352006; PMID: 1881883
A; Contents: annotation, active site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Concents: annotation; X-ray crystallography, 2:5 angstroms
R; Katzin, B.J.; Collins, E.J.; Robertus, J.D.
R; Katzin, B.J.; Collins, E.J.; Robertus, J.D.
R; Katzin, B.J.; Collins, E.J.; Robertus, J.D.
R; Title: Structure of ricin A-chain at 2.5 angstroms.
A; Reference number: A48239; MUD:91352004; PMID:1881881
A; Reference number: A48239; MUD:91352004; PMID:1881881
A; Reference number: A48239; MUD:91352004; PMID:1881881
A; Reference number: A48239; MUD:91352004; PMID:1881881
C; Comment: The A chain inhibits protein synthesis; it inactivates the 60s ribosomal subuto the cell of the A chain; B chains are also responsible for cell agglutination (lectic C; Comment: This protein is cytotoxic and very poisonous to animals.
C; Superfamily: ricin; rRNA N-glycosidase homology C; Keywords: duplication; glycosidase homology content is a sinal sequence #status predicted (SIG)
F; 1-35/Domain: signal sequence #status experimental catter catter of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the coll of the c
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F;315-576/Product: ricin or chain B #status experimental <BCH>
F;331-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats
F;455,409,449/Bainding site: carbohydrate (Asn) (covalent) #status experimental
F;115,159,243,244/Bainding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;212/Active site: Arg #status experimental
F;215/Active site: Arg #status predicted
F;249,364-318,334-353,377-394,465-478;504-521/Disulfide bonds: #status experimental
F;349,360/Bainding site: N-acetylgalactosamine (Asp, Asn) #status experimental
F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 GEMRTRIRYNRRSADDPSVITLENSWGRLSTAIQESN-QGAFASPIQLQRRNGSKFSVYD 279
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; Pred. No. 1.2e-20;
45; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Rutenber, E.; Robertus, J.D.
Proteins 10, 260-269, 1991
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A;Reference number: A48238; MUID:91352005; PMID:1881882
R; Functous: 315-383,'PS',386-576 <ARA>
R; Functou, G.; Kimura, M.; Functou, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A; Title: Primary structure of Ala chain of ricin D.
A; Rccession: A03374
A; Molecule type: profred-
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precursor - balsam pear

rRNA N-glycosidase (EC 3.2.2.22) map30 p N,Alternate names: anti-HIV 30K protein

RESULT 5

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C;Species: Momordica charantia (balsam pear, bitter gourd)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Date: Subset of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the constant of the const
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A, Note: The authors translated the codon TAC for residue 37 as Thr and ACT for residue 18
R, Lee-Huang, S.; Huang, P.L.; Nara, P.L.; Chen, H.C.; Kung, H.; Huang, P.; Huang, H.I.; F
FBBS Lett. 272, 12-18, 1990
A, Title: MAP 30: a new inhibitor of HIV-1 infection and replication.
A, Reference number: $12869; MUID: 91032105; PMID: 1699801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein A;Residues: 24-36,'T',38-66,'P' <LEW>
A;Residues: 24-36,'T',38-66,'P' <LEW>
C;Comment: This plant protein has anti-HIV activity. It possesses antiviral action, antiactivation activities. It is capable of acting against multiple stages of the viral life C;Comment: This protein has conserved unique residues Trp-213 and Met-277.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reaidues: 1-564 <ROB>
A;Cross-references: UNIPROT:P06750; GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701
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C, Superfamily: rRNA N-glycosldase; IRNN N-317001.
C, Reywords: antiviral; glycoprotein; glycosldase; hydrolase
F.1-23/Domain: signal sequence #status predicted <SIO.
F, 24-286/Product: rRNA N-glycosidase (EC 3.2.2.22) map30 #status predicted <MAT>
F, 27-264/Domain: rRNA N-glycosidase homology <RNG>
F, 27-264/Domain: rRNA N-glycosidase homology <RNG>
F, 27-264/Domain: gle: carbohydrate (Asn) (covalent) #status predicted
F, 33, 181, 184/Active site: Tyr, Glu, Arg #status predicted
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C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A24261; A24210
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
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A, Title: The primary sequence of Ricinus communis agglutinin.
A, Reference number: A24261; MUD:86059449; PMID:2999130
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37.0%; Pred. No. 7.2e-21;
tive 34; Mismatches 109
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233 HQSVAVLALMLFVCNPP 249
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A;Molecule type: DNA
A;Residues: 1-294 <KAT>
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                                                                                                                                    A; Molecule type: protein
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 553-
C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C; Superfamily: ricin; rRNA N'glycosidase homology
C; Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F; 12-24/Domain: signal sequence #status predicted <SIG>
F; 25-290/Product: agglutinin chain A #status predicted <ACH>
F; 35-281/Domain: RRNA N'glycosidase homology <RNG</br>
F; 303-564/Product: agglutinin chain B #status experimental <BCH>
F; 303-564/Product: agglutinin chain B #status experimental seque repeats
F; 313-261/Ac2-402,405-4043,405-485,450-485,489-528,531-564/Region: 40-residue repeats
F; 314,259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F; 202-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F; 334,337,348/Binding site: Carbohydrate (Asn) (covalent) #status experimental
F; 356,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F; 356,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti
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A;Residues: 260-281, D', 283-290, N', 292-349, 'PQ', 352-377,'N', 379-425,'M', 427,'D', 429-430
A;Residues: 260-281, D', 286-4
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQLGGLRENIELGTGPLEDAISALYYYSTCGTQIPTLARSFWVCIQMISEAARFQYIEGE 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
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C;Species: Abrus precatorius (Indian licorice)
C;Species: Abrus precatorius (Indian licorice)
C;Accession: S32430; UG1399
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA stancerence number: S32429; MUID:93132798; PMID:8421313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VSFSTKGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKCDDP-GKCFVLVALSNDNGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.0%; Score 334.5; DB 1; Length 564; 36.3%; Pred. No. 6.1e-20; tive 42; Mismatches 105; Indels 13
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                                                                                          A; Reference number: A24210
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A; Residues: 1-527 <HUN>
                                                                                                                        A; Accession: A24210
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A;Cross-references: UNIPROT:Q03464; EMBL:D10600; NID:g218010; PIDN:BAA01451.1; PID:g21801
C;Superfamily: RRNA N-g1ycosidaes; RRNA N-g1ycosidase homology
C;Keywords: g1ycosidase; hydrolase
F;30-278/Domain: rRNA N-g1ycosidase homology <RNG>
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S28421
R;Kataoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koiwai, A.
R;Kataoka, J.; Habuka, N.; Masuta, C.; Miyano, M.; Koiwai, A.
R;Tatha Mol. Biol. 20, 879-886, 1992
A;Title: Isolation and analysis of a genomic clone encoding a pokeweed antiviral protein.
A;Reference number: S28421; MUID:93099240; PMID:1281438
F;7-25/Domain: rRNA N-glycosidase homology <RNG-
F;7-25/Domain: rRNA N-glycosidase homology <RNG-
F;260-527/Product: abrin-b chain B #status experimental <BCH-
F;282-324,325-365,368-406,413-448,452-491,494-5527/Region: 40-residue repeats
F;10/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;10,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163,166/Active site: Glu, Arg #status predicted
F;246-268,285-304,328-345,416-429,455-412/Disulfide bonds: #status predicted
F;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 NGQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEG- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.9%; Score 333.5; DB 2; Length Best Local Similarity 37.7%; Pred. No. 6.7e-20; Matches 97; Conservative 34; Mismatches 103; Indels
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A; Accession: $17757
A; Molecule type: DNA
A; Readidues: 1-313 <LIN-
A; Molecule type: DNA
A; Readidues: 1-313 <LIN-
A; Cross-references: UNIPROT: P10297; EMBL: X55383; NID: 920421; PIDN: CAA39054.1; PID: 920422
R; Rearbieri, L; Bologomesi, A; Cenini, P.; Falasca, A.I.; Minghetti, A.; Garofano, L.; G.
B; Cross-references: UNIPROT: 1989
A; Title: Ribosome-inactivating proteins from plant cells in culture.
A; Riccession: S02792; MUD: 89193489; PMID: 2930487
A; Accession: S02792
A; Molecule type: protein
A; Robidues: 23-55, X', 57-65 < RAR>
A; Molecule type: protein
A; Redidues: 23-55, X', 57-65 < RAR>
A; Molecule type: protein
B; Molecule type: protein
A; Reference number: S13469; MUD: 91064383; PMID: 248976
A; Reference number: S13469; MUD: 91064383; PMID: 248976
A; Residues: 23-54 < Rob.
A; Residues: 23-54 < Rob.
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A; Reference number: Jrosof, MUID:91153657; PMID:1999291
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A;Residues: 1-289 sSHA-
A;Cross-references: UNIPROT:P09989; GB:M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537
A;Experimental source: tuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GQLAEIAIDVTSVYVVGYQ-----VRNRSYFFKD-------APDAAYEGLFKNT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 KKTITLMLRRNNLYVMGYSDPFETNKCRYHIFNDISGTERQDVETTLCPNA-----NSR 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 IKTRLHFGGSYPSLEGEKAY--RETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 IOMVSEAARFTFIENOIRNNFOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVEL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 IQMVSEAARFKYIENQVKTNFNRAFNPNPKVLNLQETWGKISTAIH-DAKNGVLPKPLEL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.3%; Score 325; DB 2; Length 31 Best Local Similarity 31.6%; Pred. No. 1.7e-19; Matches 84; Conservative 49; Mismatches 101; Indels
   Reference number: S17757; MUID:92003676; PMID:1912488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 ERANGKKYYVTAVDQVKPKIALLKFV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JT0566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠે
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N;Alternate names: pokeweed antiviral protein; protein synthesis inhibitor; ribosome-ina
C;Species: Phytolacca americana (Virginian pokeweed)
C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S1757; S02792; S13469; S32611
R;Lin, Q.; Chen, Z.C.; Antoniw, J.F.; White, R.F.
Plant Mol. Biol. 17, 609-614, 1991
A;Title: Isolation and characterization of a cDNA clone encoding the anti-viral protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Molecule type: DNA

A; Residues: 'M',1-251 (EV2>

A; Residues: 'M',1-251 (EV2>

A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089

C; Superfamily: ricin; rRNA N-glycosidase homology

C; Keywords: duplication; glycosidase; hydrolase; lectin; toxin

F; 1-251 (Product: abrin (clone 7.2) chain A #setatus predicted «ACH>

F; 7-246/Domain: rRNA N-glycosidase homology «RNG>

F; 7-46/Domain: rRNA N-glycosidase homology (RNG>

F; 74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             distinct abrin A-chains
NGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERESIEVGIDVTNAYVVAYRAGSQSYFLRDAPASASTYLFTGTQRYSLRFDGSYGDLERW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 AHQTREQISLGLQALTHAISFLRSGASND---BEKARTLIVIIQMASEAARYRYISNRVG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV-DQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 VSIRTGTAFQPDPAMLSLENNWDNLSRGVQES-VQDTFPNAVTLRRVNNQPVIVDSLTHQ 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKC----FVLVALSND 59
                                                                                                                                                                                                                                                                                                                                                                                                                Contains: rRNA N-glycosidase (EC 3.2.2.2)
Species: Abrus precatorius (Indian licorice)
Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-251 sENE>
A; Cross-references: UNIPROT: Q38760
A; Cross-references: UNIPROT: Q38760
B; Bvensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A; Description: Direct molecular cloning of two distinct abrin A-chains.
A; Accession: S14471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 329; DB 2; Length 251; Pred. No. 6e-20; 40; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                 abrin (clone 7.2) precursor - Indian licorice (fragment) N;Contains: rRNA N-glycosidase (EC 3.2.2.2) C;Species: Abrus precatcorius (Indian licorice) C;Deceies: Abrus precatcorius (Indian licorice) C;Accession: C39761; S14471 S;Evensen, G.; Mathiesen, A.; Sundan, A. J:Biol. Chem. 266, 6848-6852, 1991 A;Title: Direct molecular cloning and expression of two A;Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                           NGKKYYVTAVDQVKPKIALLKFVD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 36.5%;
Matches 93; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVAVLALMLFVCNPP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DN
                                                                                                                224
                                                                                                                                                                                          256
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us-10-717-243-2.open.rpr

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A; Molecule type: mENA
A; Residues: 'E', 2-28 «4UN>
A; Residues: 'E', 2-28 «4UN>
A; Residues: 'E', 2-28 «4UN>
A; Cross references: UNIPROT: 11140; GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295
A; Cross references: UNIPROT: 1140; GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295
A; Mote: the conding region for the sequence shown is preceded by an ATG codon
A; Note: residues: 'E', 2-28 «4UN>
A; Reference number: 'J0202
A; Reference number: 'J0202
A; Accession: 'J0202
A; Accession: 'J0202
A; Molecule type: protein
A; Reference number: 'A: Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan, A.; Sundan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S32429; JT0202; Ā39761; JC1398; S14472; S24133; S74110; S74111
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Reference number: S32429; MulD:93132798; PMID:8421313
A;Reference number: S32429
A;Reference number: acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: GB:X54872
A,Note: residues 1-8 were derived from the synthesized primer
R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Bisci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A,Reference number: JC1398; MUID:93169023; PMID:7763422
A;Contents: seeds
     121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                              143 KIRENIPLGLPALDSAI-----TTLFYYNANSAASALMVLIQSTSEAARYKFIEQQIGKR 197
                                                                                                                                                                                                        181 FOORIRPANNTISLENKWGKLSFOIR-TSGANGMFSEAVELERANGKKYYVTAVDQ--VK 237
                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 'ME',2-251 <EV2>
A;Cross-references: EMEL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
R;Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
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A,Residues: 261-347, T',349-351,'A',353-357,'L',359-528 <KIM>
A,Residues: 261-347, T',349-351,'A',353-357,'L',359-528 <KIM>
A,Experimental source: seed
R,Evensen, G., Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A,Description: Direct molecular cloning of two distinct abrin A-chains.
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A;Reference number: S24133; MUID:92371656; PMID:1505674
A;Accession: S24133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            abrin-a precursor - Indian licorice (fragment)
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A,Status: nucleic acid sequence not shown
A,Molecule type: DNA
A,Residues: 'E',2-251 <EVE>
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A; Accession: $14472
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                                                                                                                                                                                                                                                                                                                                                                                                           238 PKIALL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 SNIALL 263
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A; Molecule type: DNA
A; Residues: 1-72, VV, 74-90, SV, 92-233, TV, 235-267, VD', 269-289 < ZHE>
A; Cross-references: GB:S70176; NID:9547148; PIDN:AB31048.1; PID:9547149
B; Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
Chan. CSF, 8665-8669, 1990
A; Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abx
A; Reference number: A36273; MUID:90256789; PMID:2341399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24 R;Xiong, J.P.; Xia, Z.X.; Wang, Y. Submitted to the Brookhaven Protein Data Bank, December 1994 A;Reference number: A66711; PDB:11CS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
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Nat. Struct. Biol. 1, 695-700, 1994
A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
A;Fitle: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re
A;Feference number: A58622; MUD:95360714; PMID:7634073
A;Contents: annotation; X-ray crystallography, 1.7 angstroms
C;Comment: Alpha-trichosanthin has been used to induce abortions.
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                                          J. Biol. Chem. 265, 8670-8674, 1990
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rik
A;Reference number: A36274; MUID:90256790; PMID:2341400
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A,Residues: 24-270 <COL>
R;Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A;Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A,Reference number: JT0003
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A, Molecule type: protein
A, Residues: 24-56,'L',561-71,'I',73-81,85-86,'L',88-92,'DAGLPRNAVL',93-142,'GL'
A, Experimental source: tuber
A, Experimental source: tuber
R; Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
B, Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
A, Reference number: A67091; PDB:1MRN
A, Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-87, Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
Bubmitted to the Brookhaven Protein Data Bank, July 1994
A, Reference number: A67092; PDB:1MRK
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                                                                                                                                                                                                                                                                                       A;Reaidues: 1-233, TT, 235-246, MY, 248-289 <CHO>
A;Cross-references: GB:J05434; NID:g170534; PIDN:AAA34206.1; PID:g170535
R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
A;Zta Genet. Sin. 21, 42-51, 1994
A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A;Reference number: JC1093; MUID:94271613; PMID:8003348
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R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 37.89
Matches 93; Conservative
                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                        A; Accession: A36274
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Nicontains: karasurin A
C;Species: Trichosanthes kirilowii var. japonica
C;Species: Trichosanthes kirilowii var. japonica
C;Accession: JC5506; JC5033
R;Mizukami, H; Iida, K:; Kondo, T:; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A;Telle: Cloning and bacterial expression of a gene encoding ribosome-inactivating protesi
A;Reference number: JC5606; MUID:97356562; PMID:9212998
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A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and kas A;Reference number: JC5032; MUID:97108848; PMID:8951169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 KIRENIPLGLPALDSAI-----TTLPYYNANSAASALMVLIQSTSEAARYKFIEQQIGKR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 FQQRIRPANNTISLENKWGKLSFQIR-TSGANGMFSEAVELERANGKKYYVTAVDQ--VK 237
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                                        Length 247;
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                                    24.5%; Score 315; DB 2; Length 24 38.2%; Pred: No. 8.6e-19; ive 33; Mismatches 105; Indels
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                                                                                                                 Conservative
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A,Residues: 22-270 <KON>
C,Comment: This protein i
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A; Residues: 1-289 <MIZ>
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A, Status: preliminary
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Best Local S:
Matches 94
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A. Residues: 262-76./%./%./278-280;329-348;369-388;399-418 LIW>
A. Residues: 262-76./%./%./278-280;329-348;369-388;399-418 
C. Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh
C. Comment: Abrin-a is more toxic than A and B chains are linked by a single disulfi
C. Superfamily: ricin; rRNA N-glycosidase homology
C. Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
F. 7-246/Domain: rRNA N-glycosidase homology RNC F: 7-251/Product: abrin-a chain A #status experimental <a href="https://domain:rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-246/Domain: rRNA N-glycosidase homology <a href="https://domain:rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-246/Domain: rRNA N-glycosidase homology <a href="https://domain:rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-256-528/Product: abrin-a chain B #status experimental <a href="https://domain.rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-256-528/Product: abrin-a chain B #status experimental <a href="https://domain.rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-256-728/Product: abrin-a chain B #status experimental <a href="https://domain.rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-256/Product: abrin-a chain B #status experimental <a href="https://domain.rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-266/Product: abrin-a chain B #status experimental <a href="https://domain.rrnAN N-glycosidase">domain:rrnAN N-glycosidase</a>, hydrolase; lectin; pyroglutamic acid
F. 7-413,195,196/Binding site: substrate (Tyr, Tyr, Tyr, Glu, Asn) #status predicted
F. 164,167/Active site: substrate (Tyr, Tyr, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JU0393; PS0163
R;Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A;Reference number: JU0393; MUID:92005921; PMID:1914000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fi261-528/Product: abrin-a chain B #status experimental <BCH>
Fi261-528/Product: abrin-a chain B #status experimental <BCH>
Fi283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
Fi283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
Fi24/Aprilided site: pyronidone carboxylic acid (Gln) #status experimental
Fi364,167/Active site: Glu, Arg #status predicted
Fi364,267-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
Fi288,312/Binding site: Carbohydrate (Asp, Asn) #status experimental
Fi361,401/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-G 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 VSIQTGTAFQPDAAMISLENNWDNLSRGVQES-VQDTFPNQVTLTNIRNEPVIVDSLSHP 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 262-297, 'Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 < CHE>
R; Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.

Bur. J. Biochem. 240, 564-569, 1996
A; Title: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: S74110
A; Accession: S74110
A; Molecule type: protein
A; Residues: 89-108; 154-172 < LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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35.7%; Pred. No. 8.9e-19;
+ive 39; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: JU0393
A,Molecule type: protein
A,Residues: 1-247 <TOY>
A,Cross-references: UNIPROT: P24478
A,Note: a sequence which lacks Ala-247 is also shown in this pi
C,Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: abortifacient
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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karasurin - Mongolian snake-gourd
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198 VDKTFLPSLAIISLENSWSALSKQIQIASTNNGQFETPVVLINAQNQRVTITNVDAGVVT 257

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A Accession: JE0401
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-261 < KUN>
A; Cross-references: UNIPROT: P23339
A; Cross-references: UNIPROT: P23339
A; Experimental source: seed
C; Comment: This protein prevents the replication of a number of plant viruses, and inhib C; Superfamily: rRNA N-glycosidase, rRNA N-glycosidase homology
C; Keywords: disulfide bond; glycoprotein
F; 6-254/Domain: rRNA N-glycosidase homology < RNG>
F; 6-254/Domain: rRNA N-glycosidase homology < RNG>
F; 6-10,44,255/Blinding site: carbohydrate (Asn) (covalent) #status experimental
F; 34-258,84-105/Disulfide bonds: #status experimental
                                                                                                                                                                                                                              antiviral protein - Virginian pokeweed
Cispecies: Phytolacca americana (Virginian pokeweed)
Cispecies: Phytolacca americana (Virginian pokeweed)
Cibate: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
CiAccession: JEO401
Rikung, S.S.; Kimura, M.; Funatsu, G.
Rikung, S.S.; Kimura, M.; Punatsu, G.
A; Fila Siol.: Chem. 54, 3301-3118, 1990
A; Title: The complete amino acid sequence of antiviral protein from the seeds of pokewee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GQLAEIAIDVTSVYVVG----YQVRNRSYFFKDAPDAAYEGLFKNT-----IKTRLH 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LKTITLMLRRNNLYVMGYSDPYDNKCRYHIFNDIKGTEYSDV-ENTLCPSSNPRVAKPIN 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 FGGSYPSLEGEKA---YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVS 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LDTVSFSTKGATYITYVNFLNELRVKLK-PEGNSHGIPLLRRKKCDDPGKCFVLVALSNDN 60
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      238 PKIALL 243
                                                                    258 SNIALL 263
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Matches 85; Conserv
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166

8 8 8

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Search completed: June 20, 2005, 09:21:37 Job time : 27.5 secs

us-10-717-243-2.open.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

June 20, 2005, 09:00:50; Search time 114.5 Seconds (without alignments) 1122.549 Million cell updates/sec

Title: Perfect score:

Sequence:

US-10-717-243-2 1287 1 GLDTVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	P33186 gelonium mu	Q989e4 gelonium mu		Q94bw3 cinnamomum	Q9fv22 cinnamomum	Q8gzn9 euphorbia s				P33183 sambucus ni	Q945s2 sambucus ni	004367 sambucus ni	Q684j5 momordica c	P29339 momordica b	P24817 momordica c		P02879 ricinus com	P34967 phytolacca	P56626 trichosanth	Q9avr2 sambucus eb		-			Q38760 abrus preca	Q8vyu0 jatropha cu	Q8hlwl phytolacca	Q841j1 gynostemma			Q84jr1 gynostemma
QI QI	RIPG GELMU	Q9S9 <u>E</u> 4	Q94BW5	Q94BW3	Q9FV22	OBGZN9	Q94BW4	Q8GT32	Q8GZP0	NIGB SAMNI	Q945 <u>S</u> 2	004367	Q684J5	RIP2 MOMBA	RIP3 MOMCH		RICI_RICCO	RIP2 PHYDI	RIP1_TRIAN	Q9AVR2	AGGL RICCO		RIP2_BRYDI	RIPA PHYAM	Q387 <u>6</u> 0	QBVYU0	Q8H1W1	Q84LJ1	RIP1_PHYAM	Q6PWU4	Q84JR1
DB	-	7	7	~	~	~	~	7	~	-	7	N	0	-	Н	~	-		-	~	ч	-	-	-	~	~	N	N	-	~	N
% Query Match Length DB	316	258	581	580	549	299	580	563	297	263	563	563	264	286	286	541	576	265	294	564	564	527	282	294	252	293	294	275	313	313	277
% Query Match	100.0	96.5	30.7	30.6	30.5	30.1	30.0	28.1	27.8	27.4	27.4	27.1	26.9	26.9	26.9	26.7	26.7	26.5	26.3	26.3	26.0	25.9	25.9	25.7	25.6	25.4	25.4	25.3	25.3	25.3	25.2
Score	1287	1242.5	394.5	393.5	392.5	388	386.5	361.5	357.5	352	352	348.5	346	346	346	344	343	341.5	338.5	337.5	334.5	333.5	333	330.5	329	327.5	327.5	325.5	325	325	324.5
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Q88452 jatropha cu Q41216 trichosanth Q8909 gynostemma Q8h1y4 gynostemma Q8h1y4 gynostemma P09989 trichosanth Q64Ket trichosanth Q657 viecum albu Q8gy11 gynostemma Q4071 sambucus ni Q7dm12 abrus preca Q38761 abrus preca Q848v8 trichosanth P11140 abrus preca Q6bgq trichosanth
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                                                                                                                                                                                                                                Matches 248; Conservative
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Rosemblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
Rosemblum M.G., Kohr W.A., Beattie K.L., Beattie W.G., Marks W.,
Toman P.D., Cheung L.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
12-OCT-2003 (TrEMBLrel. 22) (TRNA N-glycosidase)
Gelonium multiflorum (Euphorbiaceae himalaya).
Bukaryota, Viridiplantae, Streptophyta; Empryophyta; Tracheophyta;
Bernaryophyta; Magnoliophyta; eudicoryladons; core eudicots; rosids;
eurosids I; Malpighiales, Euphorbiaceae; Crotonoideae; Gelonieae;
HSSP; P09989; ILLO, ILRODIST4; RIP.
INCEPTRO; IRRODIST4; RIP.
PRINTS; PR001396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN.
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Removed in mature form.
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-> D (in Ref. 2).
1252F3E710901B85 CRC64;
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-- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-- SIMILARITY: Belongs to the ribosome-inactivating protein family.
EMBL, AY03801, AAK82458.1; -.
EMBL, AY03801, AAK82458.1; -.
EMSL, AY03801, AAK82458.1; -.
ENGL, AY03801, AAK82458.1; -.
GO, GO:0016787; F:hydrolase activity, IEA.
GO, GO:0016787; F:hydrolase activity, IEA.
GO, GO:0016787; F:hydrolase response; IEA.
GO, GO:0016787; F:hydrolase sequilation of protein biosynthesis; IEA.
GO, GO:00107405; P:pathogenesis; IEA.
InterPro; IPR008997; RicinB like.
InterPro; IPR008997; RicinB like.
-- InterPro; IPR008997; RicinB like.
-- InterPro; IPR00897; RicinB like.
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Pfam; PF00161; RIP; 1.
PRINTS, PF00396; SHIGARICIN.
SMART; SM0458; RICIN, 2.
PROSITE; P550231; RICIN B_LECTIN, 2.
PROSITE; P550231; RICIN B_LECTIN, 2.
PROTOCOLABE; Protein synthesis inhibitor; Signal; Toxin. 31 SIGNAL 32 Potential.
CHAIN 33 581 type 2 ribosome-inactivating protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I precursor.
Cinnamomum camphora (Camphor tree).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                 96.5%; Score 1242.5; DB 2; Length 258; 95.8%; Pred. No. 6.9e-96; 1; Mismatches 1; Indels 9;
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR001574; RIP.
Pfan; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PHYGROLASE; Plant defense; Protein synthesis inhibitor; Toxin.
SEQUENCE 258 AA; 28826 MW; 13D68E673F4D6B06 CRC64;
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Best Local Similarity
Matches 101; Conserv
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              101;
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                                                                                                                                            153 VAGERREEILLGMDPLENAISALWISNINQQR--ALARSLIVVIQWVAEAVRFRFIEYRV 210
                                                                                                                                                                                                                                          EKA-YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENOI 177
                                                                                                                                                                                                                           RNNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV-D 234
                                                                                   29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3; Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.; Yang Q. of three genes encoding Cinnamomin (a type II RIP) isolated from the seeds of camphor tree and their expression patterns."; Gene 284:215-223(2002).

-I - CAPALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-I - SIMILARITY: Belongs to the ribosome-inactivating protein family.
                                                                                              TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDP-GKCFVLVALSN---D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGURES, PRO0396, SHIGARICIN.
SMART; SM00458; RICIN, 2.
PROSITE; PS5021; RICIN B LECTIN; 2.
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016787; Fibydrolase activity; IEA.
GO; GO:0030598; F:rRNA N-glycosylase activity; IEA.
GO; GO:0006952; P:defense response; IEA.
GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, magnoliids, Laurales, Lauraceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                           Indels 13;
                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin III precursor.
Cinnamomum camphora (Camphor tree).
                                       DB 2; Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type 2 ribosome-inactivating cinnamomin III.
    cinnamomin I.
6E8F5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      940D10F01E7FB558 CRC64;
                                                           94;
                                   ; Score 394.5; DB 2
; Pred. No. 2.1e-24;
45; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                            580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 393.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro, IPR008997; RičinB like.
InterPro, IPR000772; Ricin B lectin.
InterPro, IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00652; Ricin B_lectin; 6.
Pfam; PF00161; RIP; 1.
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              64215 MW;
                                     30.7%;
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                                                                                                                                                                                                                                                                         QVKPKIALLKFV 246
                                                  Best Local Similarity 39.73
Matches 100; Conservative
                                                                                                                                                                                                                                                                                               RVISGLAIMLFI 282
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     580 AA;
               581 AA;
                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                    094BW3;
01-DEC-2001
01-DEC-2001
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                                                                                                                                                                                                                                                   211
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               SEQUENCE
                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 --GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIEN 175
                                                                                                                                                                                                                                                                                           94
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
                                                                                                                                                                                                                                                 35 TVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVWRERSTVPDSKRFILVELSNWAAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S SP--VILAVDVINAXVVAXRIGSQSFFIREDNPDPAIENLLPDTKRYTFPFSGSYTDLER
                                                                                                                                                                                                                                                                                                                                                                                                              60 NGQLAEIAIDVTSVYVVGYQVRNRSYFFK-DAPDAAYEGLFKNTIKTRLHFGGSYPSLE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDP-GKCFVLVALSN---D
                                                                                                                                                                              4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDP-GKCFVLVALSN---D
                                                                  17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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GO; GO:0016787; E:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:001698; F:rRNA N-glycosylase activity; IEA.

GO; GO:001748; P:negative regulation of protein biosynthesis; IEA.

GO; GO:000405; P:pathogenesis; IEA.

InterPro; IPR008997; RicinE like.

InterPro; IPR001574; RicinE like.

InterPro; IPR001574; RIP.
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Cinnamomum camphora (Camphor tree).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Cinnamomum.
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Hydrolase, Plant defense; Protein synthesis inhibitor; Toxin.
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                                                                  90; Indels
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39.8%; Pred. No. 2.5e-24; ive 46; Mismatches 90
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Pfam; PF00161; RIP; 1.
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SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:| :|:: |:
269 SDRVISGLAIMLFI 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 -DQVKPKIALLKFV 246
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                                                                  Conservative
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C. I. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

C. I. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

C. I. STMILARITY: Belongs to the ribosome-inactivating protein family. BRBL; AV03802; AAR8459.1; -..

DR GO; GO:0016787; Fibydrolase activity; IEA.

GO; GO:0016787; Fibydrolase activity; IEA.

GO; GO:001748; P:RNA N-glycosylase activity; IEA.

GO; GO:001748; P:RNA N-glycosylase activity; IEA.

GO; GO:0009405; P:Regative regulation of protein biosynthesis; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

RITERPRO; IPR0001574; RIP.

RITERPRO; IPR0001574; RIP.

RITERPO; IPR001574; RIP.

REPRO; PR001561; RIP. I.

PERM; PR001561; RIP. I.

PR PRINTS; PR00396; SHIGARICIN.

REPROSORUEL: RIP. I.

PR PRINTS; PR00396; RICIN. 2.
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179 NNFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKP 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SE--VALAVDVINAXVVAYRIGSQSFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21888636; PubMed=11891062; DOI=10.1016/S0378-1119(01)00890-3;
Yang Q., Liu R.S., Gong Z.Z., Liu W.Y.;
"Studies of three genes encoding Cinnamomin (a type II RIP) isolated
from the seeds of camphor tree and their expression patterns.";
Gene 284:215-223(2002).
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Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin II precursor.
Cinnamomum camphora (Camphor tree)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae;
Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Potential.
type 2 ribosome-inactivating protein
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                                                                                                                                                                                                                                                                                              580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Mismatches
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                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                     |::| :
263 DISILLY 269
                                                                                                      239 KIALLKF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=13429;
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                                                                           234
                                                                                                                                                                                          147 DRSKVGLGIGPLSRSIDTLNKFNGVSVNNV----FKESLLVVIQWVAEAARFKFIQLKIE 202
SP--VTLAVDVTNAYVVAYRTGSQSFFLREDNPDPAIENLLPDTKRYTFPFSGSYTDLEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LA-EIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEKA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 YRETTDLGIEPLRIGI --- KKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENQIR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Girbes T., Arias F.J., Benvenuto E.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 285 rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVKFTTHLASVGSYQSFMSSLRKELDSGSESHDIPLLRKPTEITNNNKYLLVNLINYDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKA-YRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENQI
                                                                                                                                                        RNNFQ--QRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAV-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCD-DPGKCFVLVALSNDNGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential. ribosome inactivating protein Euserratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I, Malpighiales, Euphorbiaceae, Euphorbioldeae, Buphorbieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA. GO; GO:0030598; F:rRNA N-glycosylase activity; IEA. GO; GO:0005975; P:carbohydrate metabolism; IEA. GO; GO:0006952; P:carbohydrate metabolism; IEA. GO; GO:0006952; P:edfense response; IEA. GO; GO:0011148; P:negative regulation of protein biosynthesis; IEA. GO; GO:0009405; P:pathogenesis; IEA. InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the ribosome-inactivating protein family. BMBL; AF457875; AA015531.1; -. HSSP; Q9AVR2; 1HWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00275; SHIGA RICIN; 1.
Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.1%; Score 388; DB 2; Length 299; 41.3%; Pred. No. 3.1e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosome inactivating protein Buserratin 2 precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 AA; 33115 MW; DE791872B9CE2A7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00396; SHIGARICIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jest Local Similarity 41.37
Matches 102; Conservative
                                                                                                                                                                                                                                                                  QVKPKIALLKFV 246
                                                                                                                                                                                                                                                                                                                    RVISGLAIMLFI 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=196589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euphorbia serrata.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 AYRETTDLGIEPLRIGIKKLDENAIDNYK-PTEIASSLLVVIQMVSEAARFTFIENQIRN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 NFQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 GLLTQYLPKPDTISYQNNWSALSKSIQLADANGRLSESVTLKYEDGKDRVVFWVEQVQRD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 --RSKVGLGIPALKNAINIL--NQFDGVSTDQDFKHSLLIVIOMVSBAARFKFIQLKIEG 201
                                                                                                                                                                                                                                                                                                                                                                               4 TVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCD--DPGKCFVLVALSN-DN
                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Malpighiales, Euphorbiaceae, Euphorbioideae, Euphorbieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ribosome inactivating protein Euserratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIGB SAMNI STANDARD; PRT; 563 AA.
P3163; P33184; P93542;
P3167-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Nigrin b precursor (Agglutinin V) (SNAV) (Contains: Nigrin b A chain (RC 3.2.22) (rRN N-9]ycooidase); Nigrin b B chain].
Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GG; GG: 0016798; F: Hydrolase activity, acting on glycosyl bonds; IEA. GG; GG: 0035598; F: FRNA N-glycosylase activity; IEA. GG; GG: 0035595; P: Carbohydrate metabolism; IEA. GG; GG: 0005975; P: Carbohydrate metabolism; IEA. GG; GG: 0017148; P: Defense response; IEA. GG; GG: 0017148; P: Pachogenesis; IEA. InterPro; IPR001574; RIP. PERN; PF00161; RIP; 1. PRINTS; PR00156; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00275; SHIGA RICIN; 1.
Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.8%; Score 357.5; DB 2; Length 297; 39.8%; Pred. No. 1.1e-21; iive 39; Mismatches 98; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A5269E1DDB91287A CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosome inactivating protein Euserratin 1 precursor
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nes 98; Conservative
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262 ISLLLY 267
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                                                                                                                                                      Euphorbia serrata.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF24280; AAN86130.1; -- SIMILARITY: Belongs to the ribosome-inactivating protein family. R BEBL; AF24280; AAN86130.1; -- SIMILARITY: Belongs to the ribosome-inactivating protein family. R BSP; Q34782; HWM.

R GO; GO:0016798; F:HWM. N-glycosylase activity, IEA.

R GO; GO:0016979; F:RNA N-glycosylase activity; IEA.

R GO; GO:0005975; P:Carbohydrate metabolism; IEA.

R GO; GO:001748; P:negative response; IEA.

R GO; GO:001748; P:negative response; IEA.

R GO; GO:001748; P:negative response; IEA.

R GO; GO:0009405; P:pathogenesis; IEA.

R InterPro; IPR001574; RIP.

R Pfam; PF001657; Ricin B lectin.

R Pfam; PF001651; RICIN B lectin.

R PRINTS; PR001396; RICIN; C.
                                                                                                                                                                                                                  o.1-mar-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Type 2 ribosome-inactivating protein Nigrin I (EC 3.2.2.22).
Sambucus nigra (European elder).
Bukaryorat, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Girbes T., Arias F.J., Antolin P.,;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one.
specific adenosine on the 28S TRNA.
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PROSITE; PS00275; SHIGA_RĪCIN; 1.
Glycosidase; Hydrolase; Plant defense; Protein synthesis inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Indels 17;
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                                                                                                                         TISSUE=Bark;
MEDLINE=96215449; PubMed=8647092;
Wan Damme E.J. Barre A., Rouge P., Van Leuven F., Peumans W.J.;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
"Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GalNAG-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
Eur. J. Blochem. 237:505-513(1996).
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
campanulids; Dipsacales; Adoxaceae; Sambucus.
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Plant Mol. Biol. 22;1181-1186(1993).
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REPEAT
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Van Damme E.J.M.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

1. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 288 rRNA.

1. SIMILARITY: Belongs to the ribosome-inactivating protein family.

REMBL; AF409135; AAL04123.1; -.

ROS (GO:0016787; F:HYMA N-glycosylase activity; IEA.

GO; GO:0016787; F:HYMA N-glycosylase activity; IEA.

GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

GO; GO:0017148; P:negative regulation of protein biosynthesis; IEA.

GO; GO:0017148; RicinB like.

InterPro; IPR008997; RicinB like.

InterPro; IPR001574; RIP.

REPROS (RicinB like.)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 LE-GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIE 174
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GLD--TVSFSTKGATYITYVNFLNEIRVKLKPEG--NSHGIPLLRKKCDDPGKC-FVLVA
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                                                                                                                                                                                       (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                         (Potential)
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SWART; SW00458; RICIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PS00275; SHIGA RICIN; 1.
SROSITE; PS0275; SHIGA RICIN; 1.
SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79; Indels
                                                                                                                                                                                                                                                                                                                                                                                        -> V (in Ref. 2). F250CBE24621BF14 CRC64;
By similarity.
By similarity.
By similarity.
N-linked (GloNAc. . . ) (N-linked (GloNAc. . . ) (N-linked (GloNAc. . . ) N-linked (GloNAc. . . ) N-linked (GloNAc. . . ) N-linked (GloNAc. . . ) (N-linked (GloNAc. . . ) (N-linked (GloNAc. . . ) (N-linked (GloNAc. . . ) (N-linked (GloNAc. . . ) (N-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-linked (GloNAc. . . ) (M-li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 NQIRNNFQQ--RIRPANNTISLENKWGKLSFQIRTSGAN 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0945S2;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 27.4%; Score 352; DB 1; Similarity 41.1%; Pred. No. 7.3e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosome-inactivating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               62300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90; Conservative
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360
448
489
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                                                 DISULFID
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CARBOHYD
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CARBOHYD
CARBOHYD
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Best Local
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E-GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIEN 175
                                                                                                                                                                                                                                                                                              184 RIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 EIAIDVTSVYVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOWVSEAARFTFIENOIRNNFOO 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENIDLGLPALSSAI----TTLFYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKKCDDPGKCFVLVALSNDNGQLA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 GIDYPSVSFNLAGAKSATYRDFLKNLRIIVATGTYEVNGLPVLRRESEVQVKNRFVLVLL
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                                                                                                                                SNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Momordica charantia (Bitter gourd) (Balsam pear).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
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29775 MW; AD9E1175B70521AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Nguyen Dinh C., Nguyen Thuy D., Le Thi Thu H., Nguyen Huy H.,

Tran Thi Phuong L., Nong Van H.;

"Expression of a gene encoding ribosome inactivating protein from
bitter melon (Momordiac charantla).";

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                     QIRNNFQQR--IRPANNTISLENKWGKLSFQIRTSGAN-GMFSEAVELE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Type I ribosome inactivating protein precursor (Fragment).
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ive 34; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%; Score 346; DB 2; 37.4%; Pred. No. 8.8e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                    LSNDNGQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPS 115
                                                                                                                                                                                                                                                                                    LE-GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIE 174
                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ribosome inactivating protein precursor.
Sambucus nigra (Buropean elder).
Elwaryora, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feundals W.J.;
Feundals W.J.;
"The major elderberry (Sambucus nigra) fruit protein is a lectin
derived from a truncated type 2 ribosome-inactivating protein.";
Plant J. 12:1251-1260(1997).
-I CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.
-I SIMILARITY: Belongs to the ribosome-inactivating protein family.
                                                                                                                                                             1 GLD--TVSFSTKGATYITYVNFLNELRVKLKPEG--NSHGIPLLRKKCDDPGKC-FVLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50231; RICIN B LECTIN, 2.
PROSITE; PS00275; SHIGA RĪCIN; 1.
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
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HSSP; Q9AVR2; 1HWM.
GQ; GQ:000125; C.Clathrin vesicle coat; IEA.
GQ; GQ:000125; C.Clathrin vesicle coat; IEA.
GQ; GQ:000125; F.hydrodase activity; IEA.
GQ; GQ:0001697; F.hqfense response; IEA.
GQ; GQ:0001748; P:negative response; IEA.
GQ; GQ:0009405; P:pathogenesis; IEA.
InterPro; IPR001473; Clathrin propl_N.
InterPro; IPR008997; RicinB 11Ke.
InterPro; IPR00172; RicinB 11Ke.
InterPro; IPR00172; RicinB 11Ke.
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                                                                      16;
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      Length 563;
                                                                79; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 NQIRNNFQQ--RIRPANNTISLENKWGKLSFQIRTSGAN 211
   ; Score 352; DB 2;
; Pred. No. 7.3e-21;
34; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=98112023; PubMed=9450339;
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      27.4%;
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                                                             90; Conservative
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Acta Crystallogr. D 55:1144-1151(1999).
-!- FUNCTION: Possesses anti-HIV and anti-tumor activities. Inhibits
HIV-1 integrase, irreversibly relax supercoiled DNA and catalyzes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 23-286 FROM N.A.
Wei Y.-F., Cai L.-B., Zhuang W.;
"Cloning rip gene and identification of its resistance to Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Momordica charantia (Bitter gourd) (Balsam pear).
Momordica charantia (Bitter gourd) (Balsam pear).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
NCBI_TaxID=3673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huang H.I., Kung H.-F.;
"Anti-HIV and anti-tumor activities of recombinant MAP30 from bitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95394347; PubMed=7665070; DOI=10.1016/0378-1119(95)00186-A; Lee-Huang S., Huang P.L., Chen H.-C., Huang P.L., Bourinbaiar A., Huang H.I., Kung H.-F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10571185; DOI=10.1016/5092-8674(00)81529-9; Wang Y.-X., Neamati N., Jacob J., Palmer I., Stahl S.J., Kaufman C., Huang P.L., Huang P.L., Winslow H.E., Pommier Y., Wingfield P.T., Hee-Huang S., Bax A., Torchia D.A.; Solution structure of anti-HIV-1 and anti-tumor protein MAP30: structural insights into its multiple functions."; Cell 99:433-442(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nguyen Huy H., Nghiem Ngoc M., Dao Huy P., Le Tran B., Nong Van P. "Expression of a RIP gene from Momordica charantia in E. coli."; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 24-272. PubMed=10329776; DOI=10.1107/S0907444999003297; Yuan Y.-R., He Y.-N., Xiong J.-P., Xia Z.-X., "Three-dimensional structure of beta-momorcharin at 2.55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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EIAIDVISVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
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"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologome to other plant proteins.";
Nucleic Acids Res. 20:4662-4662(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: Belongs to the ribosome-inactivating protein family.
-!- Type I RIP subfamily.
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Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Momordica balsamina (Bitter gourd) (Balsam apple).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids I; Cucurbitales, Cucurbitaceae, Momordica.
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05-JUL-2004 (Rel. 44, Last annotation update)
Ribosome-inactivating protein momordin II precursor (BC 3.2.2.22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       By similarity.
3B89FF1AE6B25986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93027170; PubMed=1408771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 181 B
286 AA; 32031 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z12175; CAA78166.1; -. PIR; S25560; S25560.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286
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TISSUE=Seed;
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01-DEC-1992
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 BIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLE-GEKAYR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 ENIDLGLPALSSAİ----TTLFYYNAQSAPSALLVIJQTTABARFKYİBRHVAKYVAT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 RIRPANNTISLENKWGKLSFQI-RTSGANGMFSEAVELERANGKKYYVTAVDQ--VKPKI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 ETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENQIRNNFQQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA 64
            protein.
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S IRNA.
FTM: Bound to a branched hexasaccharide.
MISCELLANDOUS: Manganese or zinc required for enhancing substrate binding rather than catalysis.
MISCELLANEOUS: The oligosaccharide does not influence the fold of the polypeptide chain and probably does not play a role in the enzymatic function.
MISCELLANDOUS: Is not toxic to uninfected normal cells as it cannot enter into them.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00275; SHIGA RICIN; 1.
3D-structure; Antiviral; Direct protein sequencing; Glycoprotein;
Hydrolase; Plant defense; Protein synthesis inhibitor; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 346; DB 1; Length 286;
; Pred. No. 9.7e-21;
34; Mismatches 108; Indels 10; Gaps
                                                                                                                                                                            SIMILARITY: Belongs to the ribosome-inactivating protein family. Type 1 RIP subfamily.
double-stranded breakage. Acts also as a ribosome inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribosome-inactivating protein beta-
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6B2DF55A41D8F921 CRC64;
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By similarity.
By similarity.
By similarity.
N-linked (GlCNP
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L; AYS2412; AAS17014.1; -.
L; AJ294541; CAC08217.1; -.
; B61318; B61318.
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PRINTS; PR00396; SHIGARICIN
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1D8V; NMR; A=-.
Pro; IPR001574; RIP.
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Oy 241 ALL 243
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Search completed: June 20, 2005, 09:20:41 Job time : 117.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model OM protein - Run on:

June 20, 2005, 09:00:05; Search time 117 Seconds (without alignments) 829.717 Million cell updates/sec

US-10-717-243-2

Perfect score:

1287 1 GLDTVSFSTKGATYITYVNF......AVDQVKPKIALLKFVDKDPK 251 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:* Database :

geneseqp1980s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aar63903 Type I ri	Adq63044 Gelonium	Abg71551 G. multif			Aaw29303 BPI pepti	Aaw29294 BPI pepti	Aar63923 Type I RI	1 Type	Type I	Aar63920 Type I RI	н	H	н	Aar63917 Type I RI	н	Aar74177 Type I ri	Plant	Aar63914 Type I RI			Aar22227 Gelonin t	Aar63913 Type I RI	Aar63905 Type I ri	Aar74179 Type I ri
ID	AAR63903	ADG63044	ABG71551	ABG71552	AAW29300	AAW29303	AAW29294	AAR63923	AAR63921	AAR63918	AAR63920	AAR63919	AAR63924	AAR63922	AAR63917	AAR63912	AAR74177	AAR37291	AAR63914	AAR63915	AAR63916	AAR22227	AAR63913	AAR63905	AAR74179
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% Query Match	100.0	100.0	100.0	100.0	8.66	8.66	99.8	99.66	99.4	99.4	99.4	99.4	99.4	99.3	99.3	99.3	99.1	98.6	98.6	98.0	97.3	96.5	91.4	26.9	26.9
Score	1287	1287	1287	1287	1284	1284	1284	1282	1279	1279	1279	1279	1279	1278	1278	1278	1275	1269	1269	1261	1252	1242.5	1176	346	346
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	Aap70326 Sequence Aaw25787 Castorbea
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ALIGNMENTS

AAR63903 standard; protein; 251 AA (revised)
(first entry) 25-MAR-2003 27-JUL-1995 AAR63903; AAR63903

Type I ribosome-inactivating protein gelonin.

Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer; graft-versus-host disease.

Gelonium multiflorum.

WO9426910-A1.

24-NOV-1994.

12-MAY-1994;

94WO-US005348

93US-00064691. 12-MAY-1993;

(XOMA) XOMA CORP.

Better MD, Carroll SF, Studnicka GM;

WPI; 1995-006804/01. N-PSDB; AAQ75532.

- which Polynucleotide(8) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents.

Example 1; Fig 1; 221pp; English.

AAQ75532 encodes AAR65903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R65911. RIPs are key components of cytcoxic therapeutic agents (CTAS), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 251 AA;

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Gaps

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Indels

Mismatches

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tumour and antiviral activity. Also described is a composition
comprising the isolated peptide or polypeptide, and a carrier, excipient
or auxiliary agent. Specifically claimed are MAP30 or GAP31 peptides
or polypeptides. The peptide or polypeptide is useful for treating HIV
infection, and tumour. This is the amino acid sequence of Gelonium anti-
HIV protein 30kDa (MAP30).
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                                                                  GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                  GQLAEIAIDUTSVIVVGYQVRNRSYPFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                       FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                 GLDTVSFSTKGATY I TYVNFLNELRVKLKPEGNSHGI PLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                        AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                          FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-HIV; cytostatic; peptide therapy; anti-tumour; antiviral; MAP30;
GAP31; HIV; tumour; gelonium anti-HIV protein 31kDa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New MAP30 or GAP31 peptides or polypeptides having an anti-tumor and antiviral activity, useful for treating human immunodeficiency virus infection or tumor.
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  Length 251;
                          Indels
287; DB 2;
5. 1.6e-125;
100.0%; Score 1287;
100.0%; Pred. No. 1.6
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                Gelonium anti-HIV protein 31kDa (GAP31).
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                                                                                                                                                                                                                                                                                                                                                     ADG63044 standard; protein; 251 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                        251; Conservative
                                                                                                                                                                                                                                                             ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                            Gelonium multiflorum.
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            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 251 AA;
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Score 1287; DB 8; Length 251; Pred. No. 1.6e-125;

100.0%;

Best Local Similarity

Query Match

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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Generating a modified protein with reduced antigenicity for treating cancer, AIDS, autoimmune diseases, comprises identifying a protein region antigenic in the first subject using antiserum from either the first or a
                                                                                                         120
                                                                                                                                                                               180
                                                                                                                                                                                                                                                       240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a method of generating a modified protein with reduced antigenicity while maintaining its biological activity. The method comprises identifying a region of the protein that is antigenic in a first subject using antiserum from either the first subject or a second subject of the same species as the first subject. In particular the invention discloses modified toxin compounds, for example gelonin toxin derived from Gelonium multiflorum, that are truncated
                                   9
                                                                     9
                                                                                                                            61 GQLAEIAIDVTSVYVVGYQVRNRSYFPKDAPDAAYBGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                                                                          FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                         GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                               121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                     FQQRIRPANNTI SLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                   1 GLDTVSFSTKGATYITYVNFLNBLRVKLKPBGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                     1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified protein; reduced antigenicity; modified toxin; gelonin;
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiflorum recombinant gelonin (rGel) toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 63; Page 169-170; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG71551 standard; protein; 316 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-FEB-2001; 2001US-0268402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant gelonin; rGel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
251; Conservative
                                                                                                                                                                                                                                                                                                                               241 ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                    Rosenblum MG, Cheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RERE-) RES DEV FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-750431/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABS56021
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                                                                                                         61
Matches
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c and/or possess reduced antigenicity. Such designer toxins have
therapeutic, diagnostic, and preventative benefits, particularly as
immunotoxins. The method of the invention is useful for generating
proteinaceous compounds with less antigenicity. The immunotoxin and
gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain.
Stin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic,
bone, bone marrow, head and neck, cervical, oesophagus, eye, gall
bladder, kidney, adrenal glands, heart, colon, or blood cancer. The
compositions of the invention are also useful for treating microbial
pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune
diseases, hyperproliferative disorders including cancer, leukaemias,
carthritis, inflammatory diseases, cardiovascular diseases pathogenic
diseases, and diabetes. The method provides less antigenic proteins,
peptides and polypeptides, which are more effective than prior art. The
present sequence represents G. multiflorum recombinant gelonin (rGel)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified protein; reduced antigenicity; modified toxin; gelonin; designer toxin; immunotoxin; proteinaceous compound; cancer; microbial pathogenesis; acquired immunodeficiency syndrome; AIDS; autoimmune disease; hyperproliferative disorder; leukaemia; arthritis; inflammatory disease; cardiovascular disease; diabetes; pathogenic disease; oryostatic; antiarthitis; antidiabetic; virucide; protozoacide; fungicide; antibacterial; murine; single-chain ZME-018 antibody; recombinant gelonin; rGel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLDIVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOOR I R PANN'T I SLENKWGKLS FOIR TSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMYSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOORIRPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1287; DB 5; Length 316; 100.0%; Pred. No. 2.2e-125; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine scfvMEL/G. multiflorum rGel fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG71552 standard; protein; 507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         scfvMEL/rGel; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-2002; 2002WO-US004195.
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                                                                                                                                                                                                                                                                                                                                                                                                         fatches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALLKFVDKDPK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gelonium multiflorum Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                       Sest Local Similarity
                                                                                                                                                                                                                                                                                                                           Sequence 316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200269886-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG71552;
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The present invention relates to a method of generating a modified protein with reduced antigenicity while maintaining its biological activity. The method comprises identifying a region of the protein that is antigenic in a first subject using antiserum from either the first subject or a second subject of the same species as the first subject. In particular the invention discloses modified toxin compounds, for example gelonin toxin derived from Gelonium multiflorum, that are truncated and/or possess reduced antigenicity. Such designar toxins have therapeutic, diagnostic, and preventative benefits, particularly as immunotoxins. The method of the invention is useful for generating proteinaceous compounds with less antigenicity. The immunotoxin and gelonin toxin are useful for treating cancer, e.g. prostate, lung, brain, skin, liver, breast, lymphoid, stomach, testicular, ovarian, pancreatic, bund, bone marrow, head and neck, cervical, oseophagus, eye, gall bladder, kidhey, adrenal glands, heart, colon, or blood cancer. The compositions of the invention are also useful for treating microbial pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune compositions of the invention are also useful for treating microbial pathogenesis, acquired immunodeficiency syndrome (AIDS), autoimmune arthaltis, inflammatory diseases, cardiovascular diseases, pathogenic diseases, and diabetes. The method provides less antigenic proteins, microbial and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                  Generating a modified protein with reduced antigenicity for treating cancer, AIDS, autoimmune diseases, comprises identifying a protein region antigenic in the first subject using antiserum from either the first or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 AYRETTDLGIEPURIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptides and polypeptides, which are more effective than prior art. The present sequence represents murine single-chain ZME-018 antibody/G. multiflorum recombinant gelonin (rGel) (scfvMEL/rGel) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 GLDTVSFSTKGATYITYVNFLNBLRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1287; DB 5;
100.0%; Pred. No. 4.4e-125;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 174-176; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW29300 standard; protein; 293 AA
                      12-FEB-2001; 2001US-0268402P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 251; Conservative
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                                                                                                                  Rosenblum MG, Cheung
                                                                (RERE-) RES DEV FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 ALLKFVDKDPK
                                                                                                                                                            WPI; 2002-750431/81.
N-PSDB; ABS56029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 507 AA;
                                                                                                                                                                                                                                                                                                          second subject.
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AAW29300
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A new recombinant DNA vector construct has been developed which encodes a fusion protein and is suitable for introduction into a bacterial host. The vector comprises: (a) DNA encoding at least one cationic bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a carrier protein, and (c) DNA encoding an amino acid (a) Encayage site located between (d) and (b). The present sequence represents the protein from the pING3797 vector construct which codes for a BPI fusion protein. The peptides have many uses including the treatment of bacterial and fungal infections. BPI peptides also bind to endocaxins and hegarin, neutralising their effects. The peptides have further been shown to inhibit angiogenesis (partly due to heparin-binding activity). The fusion proteins have been found to be expressed in large amounts without significant proteolysis, and in some cases are actually secreted from the host cells. This allows the indirect production of anti-microbial BPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; anglogenesis; fungicidal; recombinant DNA; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant production of bactericidal/permeability increasing protein - by expression as a fusion protein in microbial host cells, then cleaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIOMVSEAARFTFIENOIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLDTVSFSTKGATYI TYVNFLNELRVKLKPEGNSHGI PLLRKKCDDPGKCFVLVALSNDN
                                                   BPI peptide fusion protein pING3797 vector construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1284; DB 2;
Pred. No. 4.1e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 160-161; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.8%;
                                                                                                                                                                                                                                                                                                                  97WO-US005287
                                                                                                                                                                                                                                                                                                                                                       96US-00621803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptides in microbial hosts
                                                                                                                                                                      Pectobacterium carotovorum.
Homo sapiens.
                20-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT86336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 293 AA;
                                                                                                                                                                                                                                                                                                                                                       22-MAR-1996;
                                                                                                                                                                                                                                                                                                                    18-MAR-1997;
                                                                                                                                                                                                                                             WO9735009-A1
                                                                                                                                                                                                                                                                                 25-SEP-1997,
                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                              Chimeric
셤
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A new recombinant DNA vector construct has been developed which encodes a fusion protein and is suitable for introduction into a bacterial host. The vector comprises: (a) DNA encoding at least one cationic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic actionic acti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN 82
                                                                                                                                                                                                                                                                                                                                                                                    Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant production of bactericidal/permeability increasing protein -
by expression as a fusion protein in microbial host cells, then cleaving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                   BPI peptide fusion protein pING3795 vector construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 4.4e-125;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 152-153; 186pp; English.
                                                                                                                                                                               AAW29303 standard; protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptides in microbial hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pectobacterium carotovorum
                                                                                                                                                                                                                                                                                   (first entry)
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Matches 250; Conservative
241 ALLKFVDKDPK 251
                          263 ALLKFVDKOPK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-480215/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT86341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                   20-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                  AAW29303;
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Length 332;

Score 1284; DB 2; Pred. No. 4.9e-125; L; Mismatches 0; 1; Mismatches

99.8%;

Conservative

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61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYBGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                                                                                                                                                                             121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN 180
                                                                                                                                                                                                                                                               83 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK
                                                                                                                                                                                                                                                                                                                                                                              143 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                   23 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                  1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSBAVELERANGKKYYTAVDQVKPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 ALLKFVDKDPK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALLKEVDKDPK
                              Similarity
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Local S...
250;
Query Match
Best Local Si
Matches 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR63923
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The vector comprises: (a) DNA encoding at least one cationic cartical/permeability increasing peptide (BPI), (b) DNA encoding at least one cationic cartier protein, and (c) DNA encoding an amino acid (aa) cleavage site located between (a) and (b). The present sequence represents the protein from the pING3793 vector construct which codes for a BPI fusion protein. The peptides have many uses including the treatment of bacterial and fungal infections. BPI peptides also bind to endotoxins and heparin, neutralising their effects. The peptides have further been shown to inhibit angiogenesis (partly due to heparin-binding activity). The fusion proteins have been found to be expressed in large amounts without significant proteolysis, and in some cases are actually secreted from the peptides in microbial hosts
                                                                                                                                                                                                                              262
GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGTYPSLEGEK 142
                                                            180
                                                                                                                  202
                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          new recombinant DNA vector construct has been developed which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bactericidal/permeability increasing peptide; BPI; fusion protein; bacterial infection; fungal infection; endotoxin; heparin; angiogenesis; fungicidal; recombinant DNA; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant production of bactericidal/permeability increasing protein - by expression as a fusion protein in microbial host cells, then cleaving
                                                                                                                                                                  AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQWYSEAARFTFIENQIRNN
                                                         AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BPI peptide fusion protein pING3793 vector construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 148-150; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW29294 standard; protein; 332 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by expression as a fusion proteir
the BPI peptide from the carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US005287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                        ALLKFVDKDPK 273
                                                                                                                                                                                                                                                                                    ALLKFVDKDPK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-480215/44.
N-PSDB; AAT86332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (XOMA ) XOMA CORP.
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Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9735009-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                          263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW29294;
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83
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AAW'2

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AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. The are key components of cytocoxic therapeutic agents (CTAS), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                               - which
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) encoding type I ribosome-inactivating proteins - are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                         Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Page 187-188; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Studnicka GM;
                                                                                                            Type I RIP gelonin analog Gel(C103).
AAR63923 standard; protein; 251 AA
                                                                                                                                                                                                                                                                                                     94WO-US005348.
                                                                                                                                                                                                                                                                                                                                    93US-00064691.
                                                              (revised)
(first entry)
                                                                                                                                                                           graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                               Better MD, Carroll SF,
                                                                                                                                                                                                         Gelonium multiflorum
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-006804/01
                                                                                                                                                                                                                                                                                                                                                                (XOMA ) XOMA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 251 AA;
                                                                                                                                                                                                                                                                                                     12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                    12-MAY-1993;
                                                                                                                                                                                                                                        WO9426910-A1
                                                            25-MAR-2003
27-JUL-1995
                                                                                                                                                                                                                                                                       24-NOV-1994.
                               AAR63923;
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Sequence 332 AA

Length 251;

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Similarity
Sequence 251 AA;
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27-JUL-1995
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                                                                                                           GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
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0
           Length 251;
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                                   Indels
         99.6%; Score 1282; DB 2;
99.6%; Pred. No. 5.3e-125;
iive 0; Mismatches 1;
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                                  250; Conservative
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                                                                                                                                                                                                                                        1 GLDTVSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                             181 FQORIKPANNTISLENKWGKLSFOIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                       1 GLDTVSFSTKGATYITYVNFLNBLRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                              61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                     AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
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                                     Gaps
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                                     Indels
99.4%; Score 1279; DB 2; 99.6%; Pred. No. 1.1e-124; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3, Page 183-184; 221pp; English.
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                                     Conservative
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AAR63912-R63924 are analogs of AAR63903 type I ribosome-inactivating protein (RIP) gelonin, one of the nine RIPs described in AAR63903-R63911. RIPs are key components of cytotoxic therapeutic agents (CTAB), which include gene fusion products and immunoconjugates. CTAB may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune
                                                                                                                                                                             61 GQLABIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                                                                                            61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                                                        121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                         1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                      GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                                                                                                                                                                                   FQQRIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                        Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type I ribosome-inactivating proteins; RIPs; gelonin; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                     Indels
                                                         Score 1279; DB 2;
Pred. No. 1.1e-124;
                                                                                     0; Mismatches
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                                                        99.4%;
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                                                                                       Matches 250; Conservative
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correct PN field.)
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                             Sequence 251 AA;
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                                                                                                                                                                                                                                                                                                       PQQRIRPANNTISLENK#GKLSFQIRTSGANGMFSEAVELERANGKKYYTAVDQVKPKI 240
                                                                                                                                                                GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
                                                                                                                                                                                GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK 120
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                                                                                                                      GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                     GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                          Gaps
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                                          Length 251;
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                                          Score 1279; DB 2;
Pred. No. 1.1e-124;
0; Mismatches 1;
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                                           99.4%;
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                                                                      Matches 250; Conservative
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                                          Query Match
Best Local Similarity
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               Sequence 251 AA
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elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                  Sequence 251 AA;
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disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 correct PN field.)
                                                                                                                                                                                                                                                                                                                                            61 GOLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
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                                                                                                                       99.4%; Score 1279; DB 2; Length 251; 99.6%; Pred. No. 1.1e-124; ive 0; Mismatches 1; Indels
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Matches 250; Conservative
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                                                                       Sequence 251 AA;
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                                                                                     1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
                                                                                                                                       GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                       61 GQLAEIAIDVTSVYVVGYQVRNRSYFFKDAPDAAYEGLFKNTIKTRLHFGGSYPSLEGEK
                                                                                                                                                                                                         121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                           121 AYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRNN
                                                                                                                                                                                                                                                                                               181 FQQCIRPANNTISLENKWGKLSFQIRTSGANGMFSEAVELERANGKKYYVTAVDQVKPKI
                                                                   1 GLDTVSFSTKGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDN
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                                   Gaps
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                                 1; Indels
 Length
Score 1279; DB 2;
Pred. No. 1.1e-124;
0; Mismatches 1;
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the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-MAR-2003 to
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                                                                                               Length 251;
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                                                                                                                           1; Indels
                                                                                               Score 1278; DB 2;
Pred. No. 1.4e-124;
0; Mismatches 1;
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(first entry)
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                                         correct PN field.)
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                                                                      Sequence 251 AA;
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targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host disease. (Updated on 25-WAR-2003 correct PN field.)
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Matches 250; Conservative
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